

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:36:10 ; Search time 77.9211 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKWIFQNRKMKKKTALDASALQTE 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubppa/PTC_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*

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7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*

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15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	100.0	28	10	US-09-847-940B-19
2	148	100.0	28	11	US-09-847-946A-19
3	134	90.5	28	11	US-09-847-940B-18
4	134	90.5	28	11	US-09-847-946A-18
5	101	68.2	26	15	US-10-097-175-101
6	100	67.6	36	9	US-09-731-023A-12
7	100	67.6	36	12	US-10-358-365-12
8	98	66.2	17	15	US-10-229-915-11
9	95	64.2	21	8	US-08-610-220A-11
10	95	64.2	21	9	US-09-150-623-11
11	95	64.2	30	15	US-10-188-947-11
12	94.5	63.9	26	12	US-10-116-275-190
13	94	63.5	34	15	US-10-161-499-79
14	94	63.5	36	9	US-09-731-023A-11
15	94	63.5	36	12	US-10-358-365-11

16	94	63.5	64	15	US-10-118-079-44	Sequence 44, Appl
17	94	63.5	217	15	US-10-097-340-129	Sequence 129, App
18	94	63.5	233	12	US-10-420-940-4	Sequence 4, Appl1
19	94	63.5	295	15	US-10-118-079-4	Sequence 4, Appl1
20	93	62.8	22	12	US-10-369-226-50	Sequence 50, Appl
21	93	62.8	28	9	US-09-214-371-9	Sequence 9, Appl1
22	93	62.8	115	9	US-09-925-299-1169	Sequence 1169, Ap
23	93	62.8	115	11	US-09-925-299-1169	Sequence 1169, Ap
24	93	62.8	257	15	US-10-118-079-6	Sequence 6, Appl1
25	92	62.2	16	8	US-08-610-220A-9	Sequence 9, Appl1
26	92	62.2	16	9	US-09-214-371-43	Sequence 43, Appl
27	92	62.2	16	9	US-09-780-070-38	Sequence 38, Appl
28	92	62.2	16	9	US-09-150-623-9	Sequence 9, Appl1
29	92	62.2	16	9	US-09-731-023A-10	Sequence 10, Appl
30	92	62.2	16	9	US-09-854-204-1	Sequence 1, Appl1
31	92	62.2	16	10	US-09-900-147-8	Sequence 8, Appl1
32	92	62.2	16	10	US-09-792-480-29	Sequence 29, Appl
33	92	62.2	16	10	US-09-786-802A-2	Sequence 2, Appl1
34	92	62.2	16	10	US-09-785-802A-5	Sequence 5, Appl1
35	92	62.2	16	10	US-09-902-432-32	Sequence 32, Appl
36	92	62.2	16	10	US-09-953-031A-10	Sequence 10, Appl
37	92	62.2	16	10	US-09-981-286A-3	Sequence 3, Appl1
38	92	62.2	16	11	US-09-963-967A-6	Sequence 6, Appl1
39	92	62.2	16	11	US-09-912-414-6	Sequence 6, Appl1
40	92	62.2	16	11	US-09-775-032-54	Sequence 54, Appl1
41	92	62.2	16	11	US-09-295-189-4	Sequence 4, Appl1
42	92	62.2	16	11	US-09-965-876A-1	Sequence 1, Appl1
43	92	62.2	16	12	US-10-017-672-11	Sequence 11, Appl
44	92	62.2	16	12	US-10-201-389A-14	Sequence 14, Appl
45	92	62.2	16	12	US-10-161-051-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1

US-09-847-940B-19

; Sequence 19, Application US/09847940B

; Patent No. US20020156000A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J.

; APPLICANT: Ghosh, Sanjay

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-117CP

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides

US-09-847-940B-19

Query Match 100.0%; Score 148; DB 10; Length 28;

Best Local Similarity 100.0%; Pred. No. 6.6e-14;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRKMKKKTALDASALQTE 28

DB 1 DRQIKWIFQNRKMKKKTALDASALQTE 28

RESULT 2

US-09-847-946A-19

; Sequence 19, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

```
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19
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Query Match          100.0%; Score 148; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.6e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 DROIKIFQNRBMKKTALDASALQTE 28
Db 1 DROIKIFQNRBMKKTALDASALQTE 28
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RESULT 3
US-09-847-940B-18
Sequence 18, Application US/09847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-18
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Query Match          90.5%; Score 134; DB 10; Length 28;
Best Local Similarity 92.9%; Pred. No. 6e-12;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 DROIKIFQNRBMKKTALDASALQTE 28
Db 1 DROIKIFQNRBMKKTALDASALQTE 28
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RESULT 4
US-09-847-946A-18
Sequence 18, Application US/09847946A
Patent No. US2003005999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
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TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-18
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Query Match          90.5%; Score 134; DB 11; Length 28;
Best Local Similarity 92.9%; Pred. No. 6e-12;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 DROIKIFQNRBMKKTALDASALQTE 28
Db 1 DROIKIFQNRBMKKTALDASALQTE 28
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RESULT 5
US-10-097-175-101
Sequence 101, Application US/10097175
Patent No. US20030045680A1
GENERAL INFORMATION:
APPLICANT: JOYAL, JOHN L.
APPLICANT: MUELLER, JOHN
APPLICANT: OZA, VIBHA B.
APPLICANT: FINDEIS, MARK A.
TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
FILE REFERENCE: PPI-110
CURRENT APPLICATION NUMBER: US/10/097,175
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/275,240
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/352,399
PRIOR FILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 101
LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-101
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Query Match          68.2%; Score 101; DB 15; Length 26;
Best Local Similarity 73.9%; Pred. No. 2.4e-07;
Matches 17; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 ROIKIFQNRBMKKTALDASALQTE 24
Db 1 ROIKIFQNRBMKKTALDASALQTE 23
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RESULT 6
US-09-731-023A-12
Sequence 12, Application US/09731023A
Patent No. US20020077283A1
GENERAL INFORMATION:
APPLICANT: Seese, William
TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
FILE REFERENCE: 44574-5076-US
CURRENT APPLICATION NUMBER: US/09/731,023A
CURRENT FILING DATE: 2000-12-07
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PRIOR APPLICATION NUMBER: US 60/231,327
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-09-731-023A-12

Query Match 67.6%; Score 100; DB 9; Length 36;
Best Local Similarity 69.2%; Pred. No. 4.5e-07;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 RQIKWFOQRMMKKTALDASALQ 27
DB 1 RQIKWFOQRMMKKTALDASALQ 26

RESULT 7
US-10-358-365-12
Sequence 12, Application US/10358365
Publication No. US20030165510A1
GENERAL INFORMATION:
APPLICANT: Sease, William
TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
FILE REFERENCE: 44574-5076-US
CURRENT APPLICATION NUMBER: US/10/358,365
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: US 09/731,023
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/231,327
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-10-358-365-12

Query Match 67.6%; Score 100; DB 12; Length 36;
Best Local Similarity 69.2%; Pred. No. 4.5e-07;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 RQIKWFOQRMMKKTALDASALQ 27
DB 1 RQIKWFOQRMMKKTALDASALQ 26

RESULT 8
US-10-229-915-1
Sequence 1, Application US/10229915
Publication No. US20030083262A1
GENERAL INFORMATION:
APPLICANT: Lazarus, Douglas
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
FILE REFERENCE: PPI-127
CURRENT APPLICATION NUMBER: US/10/229,915
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: US 60/316,328
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1

LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: anti-inflammatory compound
US-10-229-915-1

Query Match 66.2%; Score 98; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFOQRMMKKT 17
DB 1 DRQIKWFOQRMMKKT 17

RESULT 9
US-08-610-220A-11
Sequence 11, Application US/08610220A
Publication No. US2003009638A1
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/610,220A
FILING DATE: MAR-04-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 48332/JPM/JML
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-610-220A-11

Query Match 64.2%; Score 95; DB 8; Length 21;
Best Local Similarity 94.4%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RQIKWFOQRMMKKT 19
DB 1 RQIKWFOQRMMKKT 18

RESULT 10
US-09-150-623-11
Sequence 11, Application US/09150623
Patent No. US20020044931A1
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL

TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/150,623
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/610,220
FILING DATE: MAR-04-1996
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 48332/JPW/JML
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-150-623-11

Query Match 64.2%; Score 95; DB 9; Length 21;
Best Local Similarity 94.4%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RQIKIWFQNRRMKWKKTA 19
DB 1 RQIKIWFQNRRMKWKKTA 18

RESULT 11
US-10-188-947-11
Sequence 11, Application US/10188947
Publication No. US2003002393A1
GENERAL INFORMATION:
APPLICANT: MEDHOTOV, Ruslan
APPLICANT: HORNG, Tiffany
TITLE OF INVENTION: TOLL/INTERLEUKIN-1 RECEPTOR ADAPTER PROTEIN (TIRAP)
FILE REFERENCE: 044574-5101US
CURRENT APPLICATION NUMBER: US/10/188,947
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/289,738
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/289,815
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/289,866
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: TIRAP/Antennapedia fusion protein
NAME/KEY: MISC_FEATURE

OTHER INFORMATION: TIRAP/Antennapedia fusion protein
US-10-188-947-11

Query Match 64.2%; Score 95; DB 15; Length 30;
Best Local Similarity 78.3%; Pred. No. 1.9e-06;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 RQIKIWFQNRRMKWKKTA 24
DB 1 RQIKIWFQNRRMKWKKTA 23

RESULT 12
US-10-116-275-190
Sequence 190, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: Egan Pharmaceutical Technology
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Byrne, Daragh
APPLICANT: Lambkin, Imelda
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
SEQ ID NO 190
LENGTH: 269
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-275-190

Query Match 63.9%; Score 94.5; DB 12; Length 269;
Best Local Similarity 67.9%; Pred. No. 2e-05;
Matches 19; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DRQIKIWFQNRRMKWKK-TALDASALQ 27
DB 235 ERQIKIWFQNRRMKWKKKXKLSMSLAT 262

RESULT 13
US-10-161-499-79
Sequence 79, Application US/10161499
Publication No. US20030044427A1
GENERAL INFORMATION:
APPLICANT: Howley, Peter M.
APPLICANT: Benson, John
APPLICANT: Kasukawa, Hiroaki
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
FILE REFERENCE: HMV-041.01
CURRENT APPLICATION NUMBER: US/10/161,499
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US/09/347,504
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 79
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
US-10-161-499-79

Query Match 63.5%; Score 94; DB 15; Length 34;
Best Local Similarity 94.1%; Pred. No. 3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRRMKWKK 17

Db 1 EROIKWFONRMRMKKDGIMKASFTT 17

Job time : 77.9766 secs

RESULT 14
US-09-731-023A-11
; Sequence 11, Application US/09731023A
; Patent No. US20020077283A1
; GENERAL INFORMATION:
; APPLICANT: Seesee, William
; TITLE OF INVENTION: Caveolin peptides and Their Use as Therapeutics
; FILE REFERENCE: 44574-5076-US
; CURRENT APPLICATION NUMBER: US/09/731,023A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/231,327
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Antennapedia-caveolin-1 scaffolding domain fusion
US-09-731-023A-11

Query Match 63.5%; Score 94; DB 9; Length 36;
Best Local Similarity 65.4%; Pred. No. 3,1e-06;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 ROIKWFONRMRMKKKTALDASALQT 27
DB 1 ROIKWFONRMRMKKDGIMKASFTT 26

RESULT 15
US-10-358-365-11
; Sequence 11, Application US/10358365
; Publication No. US20030165510A1
; GENERAL INFORMATION:
; APPLICANT: Seesee, William
; TITLE OF INVENTION: Caveolin peptides and Their Use as Therapeutics
; FILE REFERENCE: 44574-5076-US
; CURRENT APPLICATION NUMBER: US/10/358,365
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 09/731,023
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/231,327
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Antennapedia-caveolin-1 scaffolding domain fusion
; OTHER INFORMATION: peptide
US-10-358-365-11

Query Match 63.5%; Score 94; DB 12; Length 36;
Best Local Similarity 65.4%; Pred. No. 3,1e-06;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 ROIKWFONRMRMKKKTALDASALQT 27
DB 1 ROIKWFONRMRMKKDGIMKASFTT 26

Search completed: February 18, 2004, 15:42:02

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 106.289 Seconds

(without alignments)
41,814 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148
Sequence: 1 DRQIKWFOHMKKXTRALDASALQTE 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
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- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	100.0	28	23	ABB08741 Mutated IKKbeta NR
2	148	100.0	28	23	AAW48524 NBD peptide SEQ ID
3	148	100.0	28	24	ABU08435 Human mutant NEMO
4	134	90.5	28	23	ABB08740 IKKbeta NEMO bindi
5	134	90.5	28	23	AAW48523 NBD peptide SEQ ID
6	134	90.5	28	24	ABU08434 wild-type human NE
7	101	68.2	26	24	AAE31836 Androgen receptor
8	100	67.6	36	23	AAU79345 Antennapedia-caveo
9	98	66.2	20	21	AAI13423 Synthetic alpha sm

10	98	66.2	26	18	AAW1630
11	98	66.2	41	22	AAB80924
12	98	66.2	41	22	AAB80925
13	95	64.2	21	18	AAW45976
14	95	64.2	24	19	AAW82957
15	95	64.2	30	24	ABP58107
16	95	64.2	36	21	AAV78416
17	95	64.2	36	21	AAV58610
18	94	63.5	27	18	AAW1629
19	94	63.5	27	20	AAV27444
20	94	63.5	27	23	ABP83151
21	94	63.5	34	21	AAV79919
22	94	63.5	36	23	AAU79344
23	94	63.5	42	23	ABP53779
24	94	63.5	60	20	AAV42291
25	94	63.5	60	20	AAV27403
26	94	63.5	60	20	AAV04364
27	94	63.5	60	23	ABP84470
28	94	63.5	61	22	AAE00811
29	94	63.5	64	24	AAE32060
30	94	63.5	128	24	ABP97229
31	94	63.5	217	22	AAE10922
32	94	63.5	217	23	ABG96337
33	94	63.5	295	24	AAE32047
34	94	63.5	378	22	ABP72035
35	94	63.5	417	22	ABP57755
36	94	63.5	589	22	ABP58929
37	93	62.8	22	20	AAW91049
38	93	62.8	22	21	AAE27063
39	93	62.8	106	21	AAE21030
40	93	62.8	115	21	AAE53629
41	93	62.8	220	22	AAW41487
42	93	62.8	236	22	AAW39701
43	93	62.8	243	19	AAW48885
44	93	62.8	257	24	AAE32048
45	92.5	62.5	42	23	ABP53778

ALIGNMENTS

RESULT 1
ID ABB08741 standard; peptide; 28 AA.
XX
AC ABB08741;
XX
DT 14-JUN-2002 (first entry)
XX
DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 19.
XX
XX IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
XX kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
XX autoimmune disease; transplant rejection; osteoporosis; cancer;
XX Alzheimer's disease; viral; infection; asthma; anaphylaxis; peritasis;
XX Rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
XX corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
XX osteopontin; cytostatic; neurotrophic; neuroprotective; anti-HIV; human;
XX antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
XX dermatological; antibacterial; antiparasitic; antineoplastic;
XX antiarthritic; osteopathic; antidiabetic; antitumor; mutant; mutagen.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 22 /note= "Wildtype Trp substituted by Ala"
XX FT Misc-difference 24 /note= "Wildtype Trp substituted by Ala"
XX FT
XX PN
XX WO200103547-A2.

Anti-apoptotic pro
Mixer SIM peptide.
Mixer SIM mutant p
Cysteine protease
Oestrogen receptor
Mouse TRAP-antenn
Drosophila antenna
Protein regulating
Anti-apoptotic pro
Antennapedia inter
Transduction domai
Human papillomavir
Antennapedia-caveo
Antennapedia helix
Drosophila antenna
D. melanogaster PA
S. cerevisiae Antp
D. melanogaster an
Antennapedia C3APL
Amino acid sequenc
Human HOXB7 varian
Human ovarian can
Clostridium botuli
Drosophila melanog
Drosophila melanog
Internalization se
Beta-catenin deriv
Human nucleic acid
Human colon cancer
Human polypeptide
Human polypeptide
Amino acid sequenc
Clostridium botuli
Antennapedia helix

[illegible]

DE
XX NBD peptide SEQ ID NO 19.

XX Actin inflammatory, antiasthmatic, cytoprotective, antiproliferative, neurotrophic;
KW antirheumatic, antiallergic, osteoprotective, antibacterial, virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NK-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECTIS PHARM INC.
PA (UYTA) UNIV YALE.

PI May MJ, Ghosh S, Firdaia MA, Phillips K;
XX WPI, 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -

XX Example 5; Fig 5; 86pp; English.

XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytoprotective, antiproliferative, antirheumatic, antiallergic, osteoprotective,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neurotrophic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursts, autoimmune diseases such as lupus, polyarthritis, scleroderma,
CC Alzheimer's disease, atherosclerosis; transplant rejection; osteoporosis;
CC rheumatoid arthritis; multiple sclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.

XX Sequence 26 AA;

XX Query Match 100.0%; Score 148; DB 23; Length 28;
Best Local Similarity 100.0%; Freq. No. 5, 6e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIMFQNRKMKKTALDASALQTE 28
Db 1 DROIKIMFQNRKMKKTALDASALQTE 28

RESULT 3

ID	ABU08435	standard; peptide; 28 AA.
AC	ABU08435;	
DT	12-JUN-2003	(first entry)
DE	Human mutant NEMO binding site (NBD) peptide.	
XX		
KW	Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;	
KM	Ikkapab kinase-beta; Ikkapab kinase-alpha; IKKalpha; NF-kappaB;	
KM	nuclear factor-kappaB induction; inflammatory disorder;	
KW	autoimmune disease; osteoporosis; cancer; Alzheimer's disease;	
KM	atherosclerosis; viral infection; Ataxia telangiectasia;	
KW	transplantation detection; immunosuppressive; osteopathic;	
KM	cytostatic; nootropic; neuroprotective; antiatherosclerotic; vitruclide;	
KW	vasotropic; antirheumatic; antiarthritic; mutant; mutein.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	US2002156000-A1.	
XX		
PD	24-OCT-2002.	
XX		
PE	02-MAY-2001; 2001US-0847940.	
XX		
PR	02-MAY-2000; 2000US-201261P.	
PR	22-AUG-2000; 2000US-0643260.	
XX		
PA	(MAYM/) MAY M J.	
XX	(GHOS/) GHOSH S.	
XX		
P1	May MJ, Ghosh S;	
DR	WPI, 2003-209142/20.	
XX		
PT	Novel antiinflammatory peptide compounds comprising NEMO binding	
PT	domain, useful for modulating NF-kappaB induction in a cell and for	
PT	treating NF-kappaB-mediated inflammation disorders e.g., asthma,	
PT	psoriasis, vasculitis -	
XX		
PS	Claim 22; Fig 5A; 47p; English.	
XX		
CC	The present invention relates to antiinflammatory compounds comprising	
CC	NEMO binding domain (NBD) peptides. The NEMO binding domains are	
CC	found on Ikkapab kinase-beta (IKKbeta) and Ikkapab kinase-alpha	
CC	(IKKalpha) proteins. The antiinflammatory compounds of the invention	
CC	are useful for modulating nuclear factor-kappaB (NF-kappaB) induction	
CC	in a cell, where the compounds are capable of blocking the interaction	
CC	between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The	
CC	antiinflammatory compound further comprises at least one membrane	
CC	translocation domain. The compounds are useful for treating	
CC	inflammatory disorders, autoimmune diseases, osteoporosis, cancer,	
CC	Alzheimer's disease, atherosclerosis, viral infections, Ataxia	
CC	telangiectasia, and for transplantation detection. The compounds of	
CC	the invention block NF-kappaB induction by IKK but do not inhibit	
CC	the basal activity of NF-kappaB. The present sequence represents	
CC	a human mutant NBD peptide.	
XX		
XX		
SQ	Sequence 28 AA;	
Query Match	100.0%; Score 148; DB 24; Length 28;	
Best Local Similarity	100.0%; Pred. No. 5.6e-15;	
Matches 28; Conservative	0; Mismatches 0; Indels 0; Gaps	0;
QY	1 DROIKIWFQNRMRKKWKTKTALDASALQTE 28	
DB	1 DROIKIWFQNRMRKKWKTKTALDASALQTE 28	

ID	ABB08744	standard; peptide; 28 AA.
XX	ABB08740;	
AC	ABB08740;	
DT	14-JUN-2002	(first entry)
XX	14-JUN-2002	(first entry)
DE	IKKbeta NEMO binding domain peptide SEQ ID NO 18.	
XX	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
KM	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
KM	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KM	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
KM	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KM	corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;	
KM	osteopathic; cytotoxic; nocotropic; neuroprotective; anti-HIV; human;	
KM	antiarteriosclerotic; vinorelbine; antitubercular; antiallergic;	
KM	dermatological; antibacterial; antipsoriatic; antirheumatic;	
KM	antiarthritic; osteopathic; antitumor.	
XX		
OS	Homo sapiens.	
PN	W0200183547-A2.	
XX	08-NOV-2001.	
PD		
XX	02-MAY-2001; 2001WO-US40654.	
PE	02-MAY-2000; 2000US-201261P.	
PR	22-AUG-2000; 2000US-0643260.	
XX	(UYTA) UNITV YALE.	
PA		
XX	May MJ, Ghosh S;	
P1	WPI; 2002-179350/23.	
DR		
XX		
PT	Modulating NF-kappaB induction in a cell, useful for treating e.g.	
PT	inflammatory disorders, osteoporosis and cancer, comprises contacting a	
PT	cell with an anti-inflammatory compound comprising at least one NEMO	
PT	binding domain -	
XX		
PS	Claim 23; Fig 5; 82pp; English.	
XX		
CC	The invention relates to modulating NF-kappaB (NF-kB) induction in a cell	
CC	comprises contacting a cell with an anti-inflammatory compound	
CC	(ABB08725-ABB08742) comprising at least one NEMO binding domain	
CC	(ABB77133). The compound has acts through selective inhibition of	
CC	cytokine-mediated NF-kB activation by blocking the interaction of NEMO	
CC	with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO	
CC	interaction results in inhibition of IKKbeta kinase activation and	
CC	subsequent decreased phosphorylation of Ikbappab. The compound may also	
CC	act (directly or indirectly) by blocking the recruitment of leukocytes	
CC	into sites of acute and chronic inflammation, by down-regulating the	
CC	expression of E-selectin on leukocytes or by blocking osteoclast	
CC	differentiation. The compound is useful in treating NF-kB mediated	
CC	conditions, where the condition is an inflammatory disorder, an	
CC	autoimmune disease, transplant rejection, osteoporosis, cancer,	
CC	Alzheimer's disease, atherosclerosis, a viral infection or ataxia	
CC	relating to osteoarthritis. The inflammatory disorder is asthma, allergies,	
CC	urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,	
CC	rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory	
CC	bowel disease, chronic obstructive pulmonary disease, vasculitis and	
CC	burns. The inflammatory disorder may also be dermatitis, eczema,	
CC	psoriasis, osteoarthritis, psoriatic arthritis, lupus and	
CC	spontaneous urticaria. Also for Crohn's disease, ulcerative colitis,	
CC	polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,	
CC	cryoglobulinemia or multiple sclerosis. For chronic viral infections	
CC	caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral	
CC	diseases include HIV and influenza. The compound may also be useful for	
CC	treating anaphylaxis, drug and food sensitivity, contact dermatitis,	
CC	sunburn or aging. The compound may be used to replace corticosteroids in	
CC	any application in which corticosteroids are used, including	
CC	immunosuppression in transplants and cancer therapy. Also for identifying	

CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of the NEMO
 CC binding domain of IKKbeta.
 CC
 CC Sequence 28 AA;
 CC
 CC Query Match 90.5%; Score 134; DB 23; Length 28;
 CC Best Local Similarity 92.9%; Pred. No. 6.7e-13;
 CC Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC 1 DROIKIWFQNRKMKKKTALDASALQTE 28
 CC |||||
 CC 1 DROIKIWFQNRKMKKKTALDMSWLQTE 28
 CC
 CC RESULT 5
 CC ID AAM48523 standard; Peptide: 28 AA.
 CC
 CC AAM48523;
 CC
 CC 20-MAR-2002 (first entry)
 CC
 CC NBD peptide SEQ ID NO 18.
 CC
 CC Antiinflammatory; antiaesthetic; cytostatic; antipruritic; nootropic;
 CC antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;
 CC immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 CC antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 CC cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 CC rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 CC autoimmune disorder; multiple sclerosis; transplant rejection;
 CC osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 CC ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 CC
 CC Synthetic.
 CC
 CC WO200183554-A2.
 CC
 CC 08-NOV-2001.
 CC
 CC 02-MAY-2001; 2001WO-US14346.
 CC
 CC 02-MAY-2000; 2000US-201261P.
 CC
 CC 22-AUG-2000; 2000US-0643260.
 CC
 CC (PRAE-) PRAECIS PHARM INC.
 CC (UYVA) UNIV YALE.
 CC
 CC May MJ, Ghosh S, Firdels MA, Phillips K;
 CC
 CC WPI, 2002-121889/16.
 CC
 CC Novel antiinflammatory compound comprising membrane translocation
 CC domain fused to NEMO binding sequence, useful for blocking nuclear
 CC factor kappaB activation, and for treating asthma, lung inflammation,
 CC psoriasis
 CC
 CC Example 5; Fig 5; 88pp; English.
 CC
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48625-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antipruritic, antineumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virocidic and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC burns; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis, transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 CC Sequence 28 AA;
 CC
 CC Query Match 90.5%; Score 134; DB 23; Length 28;
 CC Best Local Similarity 92.9%; Pred. No. 6.7e-13;
 CC Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC 1 DROIKIWFQNRKMKKKTALDASALQTE 28
 CC |||||
 CC 1 DROIKIWFQNRKMKKKTALDMSWLQTE 28
 CC
 CC RESULT 6
 CC ID ABU08434 standard; peptide: 28 AA.
 CC
 CC ABU08434;
 CC
 CC 12-JUN-2003 (first entry)
 CC
 CC Wild-type human NEMO binding site (NBD) peptide.
 CC
 CC Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 CC IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 CC nuclear factor-kappaB induction; inflammatory disorder;
 CC autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 CC atherosclerosis; viral infection; Ataxia telangiectasia;
 CC transplantation detection; immunosuppressive; osteopathic;
 CC cytostatic; nootropic; neuroprotective; antiatherosclerotic; virocidic;
 CC vasotropic; antirheumatic; antiarthritic.
 CC
 CC Homo sapiens.
 CC
 CC US2002156000-A1.
 CC
 CC 24-OCT-2002.
 CC
 CC 02-MAY-2001; 2001US-0847940.
 CC
 CC 02-MAY-2000; 2000US-201261P.
 CC
 CC 22-AUG-2000; 2000US-0643260.
 CC
 CC (MAYM/) MAY M J.
 CC (GHOSH/) GHOSH S.
 CC
 CC May MJ, Ghosh S;
 CC
 CC WPI, 2003-209142/20.
 CC
 CC Novel antiinflammatory peptide compounds comprising NEMO binding
 CC domain, useful for modulating NF-kappaB induction in a cell and for
 CC treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 CC psoriasis, vasculitis
 CC
 CC Claim 35; Page 22; 47pp; English.
 CC
 CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The

CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. The present sequence represents
 CC an antiinflammatory compound of the invention.

XX
 SQ Sequence 28 AA;

Query Match 90.5%; Score 134; DB 24; Length 28;
 Best Local Similarity 92.9%; Pred. No. 6.7e-13;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 DRQIKWPNRRMKKKTKALDASALQTE 28
 DB 1 DRQIKWPNRRMKKKTKALDMSWLQTE 28

RESULT 7
 AAE31836
 ID AAE31836 standard; peptide; 26 AA.
 AC AAE31836;
 XX
 DT 07-MAR-2003 (first entry)
 XX
 DE Androgen receptor binding peptide #87.
 XX
 KW Androgen receptor; androgen-associated disorder; prostate cancer; acne;
 KW benign prostatic hypertrophy; hirsutism; androgen insensitivity syndrome;
 KW male pattern baldness; Stein-Leventhal syndrome; infertility; cytostatic;
 KW X-linked spinal bulbar muscular atrophy; antiseborrheic; dermatological;
 KW depilatory; androgen receptor binding peptide.
 XX
 OS Unidentified.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 26 /note= "C-terminal amide"
 FT
 PN WO200272612-A2.
 PD 19-SEP-2002.
 PF 12-MAR-2002; 2002WO-US07487.
 XX
 PR 12-MAR-2001; 2001US-275240P.
 PR 28-JAN-2002; 2002US-352399P.
 XX
 PA (PRAE-) PRAECTS PHARM INC.
 PI Joyal JL, Mueller J, Oza VB, Findeis MA;
 PI WPI; 2003-067363/06.
 DR
 XX
 PT New peptide modulators of androgen receptor, useful for treating
 PT androgen-associated disorder, e.g. prostate cancer, particularly
 PT hormonally refractive prostate cancer, colon cancer, lung cancer, acne,
 PT or hirsutism -
 XX
 PS Example; Page 30; 68pp; English.
 CC The present invention relates to novel peptide modulators of androgen
 CC receptor. The peptides of the invention are useful for treating androgen-
 CC associated disorders such as prostate cancer, particularly hormonally
 CC refractive prostate cancer, colon cancer, lung cancer, benign prostatic
 CC hypertrophy, acne, hirsutism, male pattern baldness, Stein-Leventhal
 CC syndrome, androgen insensitivity syndrome, infertility, endometrial
 CC cancer and X-linked spinal bulbar muscular atrophy. The present sequence

CC is an androgen receptor binding peptide.
 XX
 SQ Sequence 26 AA;

Query Match 68.2%; Score 101; DB 24; Length 26;
 Best Local Similarity 73.9%; Pred. No. 4.9e-08;
 Matches 17; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 RQIKWPNRRMKKKTKALDASA 24
 DB 1 RQIKWPNRRMKKKTKLTISSSS 23

RESULT 8
 AAU79345
 ID AAU79345 standard; Peptide; 36 AA.
 AC AAU79345;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Antennapedia-caveolin-X fusion peptide.
 XX
 KW Caveolin; scaffolding domain; endothelial nitric oxide synthase; eNOS;
 KW vasodilation inhibitor; inflammation inhibitor; tumour cell angiogenesis;
 KW tumour cell proliferation; osteoporosis; arthritis; atherosclerosis;
 KW asthma; Alzheimer's disease; allergy; allergic rhinitis; urticaria;
 KW anaphylaxis; dry sensitivity; food sensitivity; dermatitis; eczema;
 KW psoriasis; sunburn; aging; osteoarthritis; psoriatic arthritis; lupus;
 KW sporadic arthritis; chronic obstruction pulmonary disease; cancer; Cav;
 KW chronic inflammatory bowel disease; tumour growth; malignant neoplasm;
 KW human; fruit fly; antennapedia internalisation signal.
 XX
 OS Drosophila melanogaster.
 OS Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 1..16 /label= "Antennapedia internalisation signal"
 FT Misc-difference 17..32 /note= "Specifically claimed in claim 9"
 FT Misc-difference 17..32 /label= "Cav-X"
 FT FT /note= "Control peptide based on a human caveolin-1
 FT FT scaffoldng domain shown in AAU79340 residues
 FT FT 82-101"
 PN WO200220768-A2.
 PD 14-MAR-2002.
 PF 10-SEP-2001; 2001WO-US42069.
 XX
 PR 08-SEP-2000; 2000US-231327P.
 PR 07-DEC-2000; 2000US-0731023.
 XX
 PA (UYVA) UNIV YALB.
 PI
 PI Seesa WC;
 PI WPI; 2002-329877/36.
 DR
 XX
 PT New peptide having caveolin scaffolding domain, useful for modulating
 PT activity of endothelial nitric oxide synthase and inhibiting
 PT inflammation and tumour cell angiogenesis proliferation -
 XX
 PS Claim 16; Page 72; 73pp; English.
 CC The invention describes an isolated caveolin scaffolding domain peptide
 CC (I). A fusion peptide (II) containing (I) and at least a membrane
 CC translocation sequence is useful for down regulating endothelial nitric
 CC oxide synthase (eNOS) activity in a cell, resulting in blockage of
 CC vasodilation. (II) is therefore useful for inhibiting inflammation and

CC tumour cell angiogenesis/proliferation in an animal; and for blocking the
CC interaction of caveolin with a protein in vivo. (II) may be useful in
CC treatment of inflammatory conditions such as osteoporosis, rheumatoid
CC arthritis, atherosclerosis, asthma and Alzheimer's disease. (I) and (II)
CC are also useful for treating pathological processes associated with a
CC pro-inflammatory response including allergies such as allergic rhinitis,
CC urticaria, anaphylaxis, dry sensitivity, food sensitivity, cutaneous
CC inflammation such as dermatitis, eczema, psoriasis contact dermatitis,
CC sunburn, aging, arthritis such as osteoarthritis, psoriatic arthritis,
CC lupus, spondylarthritis, and chronic obstruction pulmonary disease and
CC chronic inflammatory bowel disease. (I) and (II) are useful for replacing
CC corticosteroids useful for immunosuppression in transplant and cancer
CC patients. When administered along with one or more anti-inflammatory
CC agent (I) and (II) are useful for inhibiting tumour growth or malignant
CC neoplasm including cellular angiogenesis, proliferation, invasiveness,
CC and metastasis in biological systems. This sequence represents a fusion
CC peptide of the invention created from the fruit fly antennapedia
CC internalisation signal and control sequence Cav-X, based on the human
CC caveolin-1 scaffolding domain shown in AAU79340, residues 82-101.

CC XX
SQ Sequence 36 AA;

Query Match 67.6%; Score 100; DB 23; Length 36;
Best Local Similarity 69.2%; Pred. No. 9.9e-08;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 2 RQIKIWPNRRMKKKTALDASALQT 27
DB 1 RQIKIWPNRRMKKKGIDKAFPTT 26

RESULT 9
AAB13423 standard; peptide; 20 AA.
XX AAB13423;

XX 23-NOV-2000 (first entry)

XX Synthetic alpha smooth muscle actin inhibitor # 3.

XX alpha smooth muscle actin; alpha-SM; wound contraction;
XX hypertrophic scar; fibromatosis; Dupuytren disease; fibrotic condition;
XX lung fibrosis.

XX OS
XX Synthetic.

XX Key Location/Qualifiers
FH Modified-site 1 /note="N-terminal acetyl"

XX WO200038733-A1.

XX 06-JUL-2000.

XX 15-DEC-1999; 99WO-EP09964.

XX 24-DEC-1998; 98EP-0204396.

XX (UNIO) UCB-BIOPRODUCTS SA.

XX Gabbiani G, Scarso A;

XX WPI; 2000-452308/39.

XX A peptide product for prevention and treatment of a disease related to
XX alpha-SM actin expression comprises a tetrapeptide associated with a
XX chemical entity that is able to introduce the tetrapeptide into the
XX cell -

XX Claim 7; Page 23; 31pp; English.
XX The present invention relates to novel peptides comprising of a specific

CC tetrapeptide associated with an oligopeptide which allows the
CC introduction of the tetrapeptide into the target cell. The present
CC sequence is one such peptide. Residues 1 to 4 of the present sequence
CC correspond to the specific tetrapeptide, while residues 5 to 20
CC correspond to the oligopeptide. The specific tetrapeptide of the present
CC sequence interferes with alpha smooth muscle (alpha-SM) actin
CC organisation in stress fibers. The present sequence may be used in the
CC prevention and/or treatment of a disease related to alpha-SM actin
CC expression, e.g. wound contraction, hypertrophic scar, fibromatosis and
CC fibrotic conditions. The present sequence may also be used to treat
CC Dupuytren disease and lung fibrosis.

XX SQ Sequence 20 AA;

Query Match 66.2%; Score 98; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKIWPNRRMKKWK 17
DB 4 DRQIKIWPNRRMKKWK 20

RESULT 10
AAW1630 standard; peptide; 26 AA.
XX AAW1630;

XX 16-OCT-1997 (first entry)

XX Anti-apoptotic protein blocking peptide FP2.

XX Cell permeable; apoptosis; blocking; inhibition; tumour growth;
XX ex vivo purging; in vivo administration; Bcl-2.

XX OS
XX Synthetic.

XX Key Location/Qualifiers
FH Peptide 1..17
FT /label= sig_peptide

XX PN DE19526174-A1.

XX 23-JAN-1997.

XX 18-JUL-1995; 95DE-1026174.

XX 18-JUL-1995; 95DE-1026174.

XX (BRAC/) BRACH M.

XX (HERR/) HERMANN F.

XX (KIEH/) KIEHNTOFF M.

XX Brach M, Herrmann F, Kiehnkopf M;

XX WPI; 1997-088160/09.

XX Claim 6; Page 7; 7pp; German.

XX The present sequence is a cell permeable anti-apoptotic protein
XX blocking peptide, which can be used to inhibit tumour growth, e.g.
XX by ex vivo purging or (after stabilisation) in vivo
XX administration. The peptide preferably blocks Bcl-2, and comprises
XX a signal peptide mediating cell penetration and a functional
XX sequence corresponding to a Bcl-2 domain.

XX SQ Sequence 26 AA;
XX Query Match 66.2%; Score 98; DB 18; Length 26;

Best Local Similarity 89.5%; Pred. No. 1.4e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRBRMKKTA 19
:|||||
1 EROIKIWFQNRBRMKKTA 19

DB

RESULT 11

AAB80924
ID AAB80924 standard; Protein; 41 AA.

AC AAB80924;

DT 04-JUN-2001 (first entry)

DE Mixer SIM peptide.

XX Smad; Cytostatic; vulnery; cerebroprotective; immunosuppressive;
XX Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;
XX Smad interaction Motif; tissue repair; fibrotic condition;
XX immunosuppression; diabetic nephropathy; tumour.

OS Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note="Biotin.Aminohexanoic acid-R"

XX MO200114413-A2.

PD 01-MAR-2001.

XX 25-AUG-2000; 2000WO-GB03265.

XX 25-AUG-1999; 99GB-0020000.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

PI Germain SE, Hill CS, Howell MT;

XX WPI; 2001-265836/27.

PT Polypeptide capable of interacting with a Smad polypeptide, useful in
PT the treatment of cancer and for tissue remodelling or healing of a
PT wound, injury or surgery, comprises a Smad interaction Motif and is
PT less than 32 amino acids in length -

PS Claim 16; Page 140; 179pp; English.

XX The present invention relates to peptides capable of interacting with a
XX Smad protein, comprising a Smad interaction Motif (SIM; amino acid
XX sequence PP(T/N)K). The present sequence is one such Smad interacting
XX peptide. Smad proteins are a family of highly conserved, intracellular
XX proteins that signal cellular responses downstream of Transforming Growth
XX Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM
XX is thought to be necessary for interaction with the MH2 domain of Smad2.
XX The peptides of the present invention are useful in the manufacture of a
XX medicament for the treatment of a patient in need of modulation of
XX activin or TGF-beta signalling; cancer; a patient in need of reducing
XX extracellular matrix deposition, encouraging tissue repair and/or
XX regeneration, tissue remodelling or healing of a wound, injury or
XX surgery, or reducing scar tissue formation arising from injury to the
XX brain; a patient with or at risk of end-stage organ failure, pathologic
XX extracellular matrix accumulation, a fibrotic condition, disease states
XX associated with immunosuppression (such as different forms of malignancy,
XX chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour
XX growth, kidney damage (for e.g. obstructive neuropathy, IGA nephropathy
XX or non-inflammatory renal disease) or renal fibrosis.

XX Sequence 41 AA;

Query Match 66.2%; Score 98; DB 22; Length 41;

Best Local Similarity 85.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRBRMKKTA 21
:|||||
1 ROIKIWFQNRBRMKKTA 20

DB

RESULT 12

AAB80925

ID AAB80925 standard; Protein; 41 AA.

AC AAB80925;

DT 04-JUN-2001 (first entry)

DE Mixer SIM mutant peptide.

XX Smad; Cytostatic; vulnery; cerebroprotective; immunosuppressive;
XX Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;
XX Smad interaction Motif; tissue repair; fibrotic condition;
XX immunosuppression; diabetic nephropathy; tumour; mutein.

OS Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note="Biotin.Aminohexanoic acid-R"

FT Misc-difference 25 /note="Wild-type Pro replaced by Ala. Wild-type sequence
FT given in AAB80924."

FT Misc-difference 26 /note="Wild-type Pro replaced by Ala"

XX MO200114413-A2.

PD 01-MAR-2001.

XX 25-AUG-2000; 2000WO-GB03265.

XX 25-AUG-1999; 99GB-0020000.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

PI Germain SE, Hill CS, Howell MT;

XX WPI; 2001-265836/27.

PT Polypeptide capable of interacting with a Smad polypeptide, useful in
PT the treatment of cancer and for tissue remodelling or healing of a
PT wound, injury or surgery, comprises a Smad interaction Motif and is
PT less than 32 amino acids in length -

PS Example 2; Page 123; 179pp; English.

XX The present invention relates to peptides capable of interacting with a
XX Smad protein, comprising a Smad interaction Motif (SIM; amino acid
XX sequence PP(T/N)K). The present sequence is one such Smad interacting
XX peptide. Smad proteins are a family of highly conserved, intracellular
XX proteins that signal cellular responses downstream of Transforming Growth
XX Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM
XX is thought to be necessary for interaction with the MH2 domain of Smad2.
XX The peptides of the present invention are useful in the manufacture of a
XX medicament for the treatment of a patient in need of modulation of
XX activin or TGF-beta signalling; cancer; a patient in need of reducing
XX extracellular matrix deposition, encouraging tissue repair and/or
XX regeneration, tissue remodelling or healing of a wound, injury or
XX surgery, or reducing scar tissue formation arising from injury to the
XX brain; a patient with or at risk of end-stage organ failure, pathologic
XX extracellular matrix accumulation, a fibrotic condition, disease states
XX associated with immunosuppression (such as different forms of malignancy,
XX chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour
XX growth, kidney damage (for e.g. obstructive neuropathy, IGA nephropathy

CC or non-inflammatory renal disease) or renal fibrosis.

XX Sequence 41 AA;

Query Match 66.2%; Score 98; DB 22; Length 41;

Best Local Similarity 85.0%; Pred. No. 2.3e-07;

Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKIWFOQRMRKMKKTALD 21

DB 1 RQIKIWFOQRMRKMKKTALD 20

RESULT 13

AAW45976 standard; peptide; 21 AA.

AC AAW45976;

DT 01-JUL-1998 (first entry)

DE Cysteine protease inhibiting peptide for preventing cell death.

XX Neuronal cell death; neurodegenerative disorder; inhibition;

KM cysteine protease; cardiovascular; liver disease.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-3-nitro-2-pyridyl-sulphenyl-Arg"

PN W09735876-A1.

PD 02-OCT-1997.

PF 04-MAR-1997; 97MO-US04158.

PR 04-MAR-1996; 96US-0610220.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Troy CM;

DR WPI; 1997-489561/45.

PT New cysteine protease inhibiting peptide(s) for preventing cell

PT death - in cases of neurodegenerative, cardiovascular and liver

PT identifying enzyme inhibiting peptides

PS Claim 10; Page 68; 112pp; English.

XX This sequence represents a specifically claimed peptide of the formula:

CC V-(AA1)n-Cys(V')-(AA2)m-V' (I), in which n and m = 0-5, totalling 2-5;

CC if n = 1, AA1 = Ala; if n = 2, (AA1)n = Gln-Ala; and if n = 3 or more,

CC (AA1)n = (X)P-Gln-Ala; X = any amino acid; p = 1-3, depending on value

CC of n; if m = 1, AA2 = Arg; if m = 2, (AA2)n = Arg-Gly; if m = 3 or more,

CC (AA2)n = Arg-Gly-(X)q; q = 1-3, depending on value of m; V' and V'',

CC any or all of which may be absent, = agent on able to direct the compound

CC to a specific cell. The peptides are inhibitors of cysteine proteases,

CC specifically interleukin-1 beta converting enzyme (ICE). They inhibit

CC death of cells, particularly in humans, and can be used to treat

CC neurodegenerative diseases (e.g. ageing, Alzheimer's, Machado-Joseph,

CC Parkinson's or Huntington's diseases, multiple sclerosis, muscular

CC dystrophy, stroke), cardiovascular disease and liver disorders.

CC The peptides should be more specific than pseudosubstrate inhibitors.

XX Sequence 21 AA;

Query Match 64.2%; Score 95; DB 18; Length 21;

Best Local Similarity 94.4%; Pred. No. 3e-07;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RQIKIWFOQRMRKMKKTA 19

DB 1 RQIKIWFOQRMRKMKKTA 18

RESULT 14

AAW82957 standard; peptide; 24 AA.

AC AAW82957;

DT 04-FEB-1999 (first entry)

DE Oestrogen receptor activity inhibiting peptide #13.

XX Human; oestrogen receptor activity inhibitor; anti-oestrogen; diagnosis;

KM breast cancer; estrogen; tumour; phosphotyrosyl peptide;

XX malonyltirosyl peptide; steroid receptor co-activator-1.

OS Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 19 /note= "phosphotyrosine"

PN W09846250-A1.

PD 22-OCT-1998.

PF 14-APR-1998; 98MO-US07711.

PR 14-APR-1997; 97US-0043545.

PA (REGC) UNIV CALIFORNIA.

PI Pietras RJ;

DR WPI; 1998-594522/50.

PT New anti-oestrogen peptide compositions - comprise sequences based

PT on oestrogen receptor and steroid receptor co-activator-1 sequences,

PT used for treating cancers

PS Claim 11; Page 156; 182pp; English.

XX The present invention describes a composition comprising an isolated

CC oestrogen receptor activity inhibiting (anti-oestrogen) peptide. The

CC peptides used in the composition comprise sequences of human oestrogen

CC receptor (OR) surrounding Tyr537 and steroid receptor co-activator-1

CC (SRC-1). The peptide compositions, nucleic acids and vectors of the

CC polypeptide dimerisation in a cell and reduce the binding of SRC-1

CC to a specific cell. The peptides are inhibitors of cysteine proteases,

CC specifically interleukin-1 beta converting enzyme (ICE). They inhibit

CC death of cells, particularly in humans, and can be used to treat

CC neurodegenerative diseases (e.g. ageing, Alzheimer's, Machado-Joseph,

CC Parkinson's or Huntington's diseases, multiple sclerosis, muscular

CC dystrophy, stroke), cardiovascular disease and liver disorders.

CC The peptides should be more specific than pseudosubstrate inhibitors.

XX Sequence 24 AA;

Query Match 64.2%; Score 95; DB 19; Length 24;

Best Local Similarity 85.0%; Pred. No. 3.5e-07;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 15

ABP58107

ID ABP58107 standard; Peptide; 30 AA.

```

XX AC ABP58107;
XX DT 28-MAR-2003 (first entry)
XX DE Mouse TIRAP-Antennapedia fusion protein.
XX KW Toll/interleukin-1 receptor adapter protein; TIRAP; mouse;
XX KW inhibitor; Antennapedia; antiinflammatory.
XX OS Chimeric - Mus sp.
XX OS Chimeric - Drosophila sp.
XX FH Key Location/Qualifiers
XX FT Peptide 1..16
XX FT /note="Antennapedia peptide"
XX FT 17..30
XX FT /note="mouse TIRAP inhibitor peptide"
XX PN MO200290520-A2.
XX PD 14-NOV-2002.
XX PF 09-MAY-2002; 2002MO-US14915.
XX PR 09-MAY-2001; 2001US-289738P.
XX PR 09-MAY-2001; 2001US-289815P.
XX PR 29-AUG-2001; 2001US-289866P.
XX PR 19-MAR-2002; 2002US-0101398.
XX PA (UYVA ) UNIV YALE.
XX PI Medzhitov R, Hornig T, Barton G;
XX DR WPI; 2003-120542/11.
XX PT New toll/interleukin-1 receptor adapter protein (TIRAP) polynucleotides
XX PT and polypeptides, useful for treating a disease state associated with
XX PT TIRAP expression, e.g. inflammation, and for inducing and affecting
XX PT immune response
XX PS Disclosure; Page 74; 74pp; English.
XX CC The present sequence is that of a fusion protein comprising an
XX CC Antennapedia peptide and a mouse toll/interleukin-1 receptor
XX CC adapter protein (TIRAP) inhibitor polypeptide (see ABP58106) of
XX CC the invention. Antennapedia, derived from Drosophila, is a
XX CC cellular membrane transport protein and can be used to deliver
XX CC the TIRAP inhibitor across the cell membrane so that it becomes
XX CC therapeutically active within the cell. TIRAP is a component of the
XX CC Toll-like receptor 4 (TLR4) signalling pathway. It mediates MyD88
XX CC independent signalling in response to TLR4 ligation, and controls
XX CC dendritic cell maturation. Characterisation of TIRAP has led to
XX CC the discovery of compounds that inhibit both the MyD88 independent
XX CC pathway as well as the MyD88 dependent pathway of TLR4 by
XX CC inhibiting TIRAP polypeptide mediated signalling. Compounds that
XX CC inhibit TIRAP activity are useful for preventing or reducing in the
XX CC inflammation and septic shock, and especially for assisting in the
XX CC prevention of graft rejection, which occurs, at least in part,
XX CC because of cellular necrosis induced inflammation. The invention
XX CC provides TIRAP inhibitor polynucleotides (see ABY76259-62) and
XX CC polypeptides (see ABP58105-06). The TIRAP inhibitors can inhibit
XX CC both the MyD88 independent response, e.g. activation of NF-kappaB
XX CC and MAP kinases, and the MyD88 dependent response in cells
XX CC expressing TLR4.
XX SQ Sequence 30 AA;

```

DB 1 RQIKIWFOQRMRMKKQLRDAA 23

Search completed: February 18, 2004, 14:26:28
Job time : 106.269 secs

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OY Query Match 64.2%; Score 95; DB 24; Length 30;
Best Local Similarity 78.3%; Pred. NO. 4.5e-07;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
2 RQIKIWFOQRMRMKKQLRDAA 24

```

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 30.7632 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DRQIKWIFQNRMRKMKKALDMSWLQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	59.9	60	2	PC2399 antennapedia-like
2	97	59.9	60	2	PC2400 antennapedia-like
3	97	59.9	105	2	A27471 homeotic protein R
4	97	59.9	119	2	A03114 homeotic protein m
5	97	59.9	229	2	A28329 homeotic protein H
6	96	59.3	75	2	I51341 homeo box protein
7	95	58.6	66	2	S15536 homeotic protein H
8	95	58.6	81	2	B29585 homeotic protein H
9	95	58.6	96	2	A05266 homeotic protein H
10	95	58.6	97	2	C27176 homeotic protein H
11	95	58.6	224	2	S26400 homeotic protein H
12	95	58.6	224	2	A31324 homeotic protein H
13	94	58.0	33	2	S57235 antennapedia prote
14	94	58.0	42	2	I65241 homeotic protein H
15	94	58.0	45	2	PC1216 homeotic protein D
16	94	58.0	48	2	I51439 homeobox protein
17	94	58.0	66	2	S15538 homeotic protein H
18	94	58.0	71	2	JC1161 homeotic protein 3
19	94	58.0	71	2	A60084 homeotic protein H
20	94	58.0	74	2	D34510 homeotic protein H
21	94	58.0	75	2	S58852 homeotic protein S
22	94	58.0	76	2	C43559 homeotic protein R
23	94	58.0	78	2	I51342 homeo box protein
24	94	58.0	81	2	S47605 homeotic protein H
25	94	58.0	82	2	S08302 homeotic protein H
26	94	58.0	83	2	S47603 homeotic protein H
27	94	58.0	86	2	S50066 homeotic protein H
28	94	58.0	86	2	A34510 homeotic protein H
29	94	58.0	86	2	JT0489 homeotic protein Z

30	94	58.0	86	2	S08303 homeotic protein H
31	94	58.0	87	2	S00589 homeotic protein H
32	94	58.0	88	2	A03117 homeotic protein M
33	94	58.0	96	2	S08639 homeotic protein z
34	94	58.0	97	2	A24779 homeotic protein m
35	94	58.0	103	2	A32167 homeotic protein H
36	94	58.0	105	2	S47602 homeotic protein H
37	94	58.0	106	2	S36448 homeotic protein s
38	94	58.0	107	2	B61045 homeotic protein T
39	94	58.0	113	2	T10775 homeobox protein
40	94	58.0	118	2	A24777 homeotic protein H
41	94	58.0	118	2	UT0273 homeotic protein H
42	94	58.0	118	2	B24777 homeotic protein M
43	94	58.0	138	2	S20087 homeotic protein b
44	94	58.0	148	2	PC4071 homeobox A5 protel
45	94	58.0	153	1	WJHJ3C homeotic protein H

ALIGNMENTS

RESULT 1

PC2399 antennapedia-like homeotic protein AHox 2 - sea squirt (Styela clava) (fragment)

C/Species: Styela clava

C/Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jul-2000

C/Accession: PC2399

R/Ge, T./ Lee, H.; Tomlinson, C.R.

Gene 147, 219-222, 1994

A/Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela

A/Reference number: PC2399; PMID:95011617; PMID:7926803

A/Accession: PC2399

A/Molecule type: DNA

A/Residues: 1-60 <G>

A/Cross-references: GB:S73920; NID:5693714; PIDN:AA833061.2; PID:57387472

A/Note: The authors translated the codon ATT for residue 47 as Glu

C/Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/2-58/Domain: homeobox homology <Hox>

Query Match	59.9%	Score 97;	DB 2;	Length 60;
Best Local Similarity	94.1%	Pred. No. 1.5e-06;		
Matches 16;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DRQIKWIFQNRMRKMKK	17	
DB	42	DRQIKWIFQNRMRKMKK	58	

RESULT 2

PC2400 antennapedia-like homeotic protein AHox 3 - sea squirt (Styela plicata) (fragment)

C/Species: Styela plicata

C/Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 17-Oct-1997

C/Accession: PC2400

R/Ge, T./ Lee, H.; Tomlinson, C.R.

Gene 147, 219-222, 1994

A/Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela

A/Reference number: PC2399; PMID:95011617; PMID:7926803

A/Accession: PC2400

A/Molecule type: DNA

A/Residues: 1-60 <G>

A/Note: The authors translated the codon ATA for residue 47 as Glu

C/Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/2-58/Domain: homeobox homology <Hox>

Query Match	59.9%	Score 97;	DB 2;	Length 60;
Best Local Similarity	94.1%	Pred. No. 1.5e-06;		
Matches 16;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DRQIKWIFQNRMRKMKK	17	

Db 42 DRQIKWIFQNRMRKMKKTALDMSWLQT 58

RESULT 3

A27471
 A:Title: homeotic protein R5 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-May-1997
 C:Accession: A27471
 R:Palzon, M.; Sanderson, N.; Chung, S.Y.
 Gene 54, 23-32, 1987
 A:Title: Cloning and expression of rat homeo-box-containing sequences.
 A:Reference number: A91576; MUID:87277429; PMID:2886401
 A:Accession: A27471
 A:Molecule type: DNA
 A:Residues: 1-105 <PAL>
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:6-62/Domain: homeobox homology <HOX>

Query Match 59.9%; Score 97; DB 2; Length 105;
 Best Local Similarity 70.4%; Pred. No. 2.7e-06;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMRKMKKTALDMSWLQT 27
 :|||||
 Db 46 ERQIKWIFQNRMRKMKKKEKHDESOAPT 72

RESULT 4

A03314
 A:Title: homeotic protein m6 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Jul-1997
 C:Accession: A03314; S14043
 R:Colberg-Poley, A.M.; Voss, S.D.; Chowdhury, K.; Gruss, P.
 Nature 314, 713-718, 1985
 A:Title: Structural analysis of murine genes containing homeo box sequences and their
 A:Reference number: A03314; MUID:85188311; PMID:2886010
 A:Accession: A03314
 A:Molecule type: DNA
 A:Residues: 1-119 <COL>
 R:Beiler, G.; Bucan, M.; Francke, U.; Colberg-Poley, A.M.; Gruss, P.
 EMBO J. 5, 2209-2215, 1986
 A:Title: Sequential expression of murine homeo box genes during F9 EC cell differentiation
 A:Reference number: S13785; MUID:87053860; PMID:2877873
 A:Accession: S14043
 A:Molecule type: DNA
 A:Residues: 19-48, 'R', 51-87

 C:Genetics:
 A:Gene: m6
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:20-76/Domain: homeobox homology <HOX>

Query Match 59.9%; Score 97; DB 2; Length 119;
 Best Local Similarity 70.4%; Pred. No. 3.1e-06;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMRKMKKTALDMSWLQT 27
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 Db 60 ERQIKWIFQNRMRKMKKKEKHDESOAPT 86

RESULT 5

A28329
 A:Title: homeotic protein Hox A7 - mouse
 N:Alternate names: homeotic protein Hox 1.1; m6 homeotic protein
 C:Species: Mus musculus (house mouse)
 C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
 C:Accession: A28329; I49131
 R:Kessel, M.; Schultze, F.; Fildt, M.; Gruss, P.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5306-5310, 1987

A:Title: Primary structure and nuclear localization of a murine homeodomain protein.
 A:Reference number: A28329; MUID:87260976; PMID:2885847
 A:Accession: A28329
 A:Molecule type: mRNA
 A:Residues: 1-229 <KRS>

A:Cross-references: GB:M17192; NID:G193906; PIDN:AAA37833.1; PID:G309313
 R:Patikh, H.; Shan, S.; Hilt, D.; Peterkofsky, A.
 Gene 154, 237-242, 1995
 A:Title: Organization, sequence and regulation of expression of the murine Hoxa-7 gene.
 A:Reference number: I49131; MUID:95197009; PMID:7890170
 A:Accession: I49131
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-42, 'GAG', 46-229 <RES>
 A:Cross-references: EMBL:U15972; NID:G664757; PIDN:AAC52160.1; PID:G664758
 C:Genetics:
 A:Gene: Hoxa7
 A:Intron: 126/1
 C:Superfamily: homeotic protein Hox A7; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:130-186/Domain: homeobox homology <HOX>

Query Match 59.9%; Score 97; DB 2; Length 229;
 Best Local Similarity 70.4%; Pred. No. 6.2e-06;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMRKMKKTALDMSWLQT 27
 :|||||
 Db 170 ERQIKWIFQNRMRKMKKKEKHDESOAPT 196

RESULT 6

I51341
 A:Title: homeo box protein - Atlantic salmon (fragment)
 C:Species: Salmo salar (Atlantic salmon)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
 C:Accession: I51341
 R:Fjose, A.; Mølven, A.; Eiken, H.G.
 Gene 62, 141-152, 1988
 A:Title: Molecular cloning and characterization of homeobox-containing genes from Atlan
 A:Reference number: I51341; MUID:88226009; PMID:2897318
 A:Accession: I51341
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-75 <FJO>
 A:Cross-references: GB:M18903; NID:G213797; PIDN:AAA49559.1; PID:G213798
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:2-58/Domain: homeobox homology <HOX>

Query Match 59.3%; Score 96; DB 2; Length 75;
 Best Local Similarity 78.3%; Pred. No. 2.6e-06;
 Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMRKMKKTALDMS 23
 :|||||
 Db 42 ERQIKWIFQNRMRKMKKKEKHDE 64

RESULT 7

S15536
 A:Title: homeotic protein Hox A7 - human (fragment)
 N:Alternate names: homeotic protein Hox 1A
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997
 C:Accession: S15536
 R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; S
 Genome 31, 745-756, 1989
 A:Title: Organization of human class I homeobox genes.
 A:Reference number: S15036; MUID:90215256; PMID:2576652
 A:Accession: S15536
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA

A:Residues: 1-66 <BON>
C:Genetics:
A:Gene: GDB:HOXA7
A:Cross-references: GDB:120647; OMIM:142950
A:Map position: 7p15.3-7p15.3
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:2-58/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 66;
Best Local Similarity 81.0%; Pred. No. 3.1e-06;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DRQIKWPNRRMKKKTKTALD 21
DB 42 EROIKIWPNRRMKKKTKKDKD 62

RESULT 8
B29585
homeotic protein Hox 2.2 precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997
C:Accession: B29585
R:Lomal, P.; Arman, E.; Czosnek, H.; Ruddle, F.H.; Blatt, C.
DNA 6, 409-418, 1987
A:Title: New murine homeoboxes: structure, chromosomal assignment, and differential expr
A:Reference number: A29585; MUID:88054465; PMID:2890503
A:Accession: B29585
A:Molecule type: DNA
A:Residues: 1-81 <LON>
A:Cross-references: GB:M18167
A>Note: the authors translated the codon CAG for residue 69 as Glu
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:4-60/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 81;
Best Local Similarity 66.7%; Pred. No. 3.8e-06;
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWPNRRMKKKTKT--LDMSWLQTE 28
DB 44 EROIKIWPNRRMKKKESKLSASQLSAG 73

RESULT 9
A05266
homeotic protein Hox B6 - human (fragment)
N:Alternate names: homeotic protein Hox 2B; homeotic protein Hu2
C:Species: Homo sapiens (man)
C>Date: 03-Jun-1987 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997
C:Accession: A05266; S15537
R:Levine, M.; Rudin, G.M.; Tjian, R.
Cell 38, 667-673, 1984
A:Title: Human DNA sequences homologous to a protein coding region conserved between hom
A:Reference number: A05265; MUID:85024858; PMID:6091895
A:Accession: A05266
A:Molecule type: DNA
A:Residues: 1-96 <LEV>
A:Cross-references: EMBL:K02571
A>Note: this reading frame extends between two stop codons and does not begin with a sta
R:Bouchnell, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc
Genome 31, 745-756, 1989
A:Title: Organization of human class I homeobox genes.
A:Reference number: S15036; MUID:90215256; PMID:2576652
A:Accession: S15537
A:Molecule type: DNA
A:Residues: 18-19, 'R', 21-83 <BON>
C:Genetics:
A:Gene: GDB:HOXB6
A:Cross-references: GDB:120659; OMIM:142961
A:Map position: 17q21.3-17q21.3

C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:19-75/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 96;
Best Local Similarity 66.7%; Pred. No. 4.6e-06;
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWPNRRMKKKTKT--LDMSWLQTE 28
DB 59 EROIKIWPNRRMKKKESKLSASQLSAG 88

RESULT 10
C27176
homeotic protein Hox 2.2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Sep-1999
C:Accession: C27176
R:Hart, C.P.; Fainrod, A.; Ruddle, F.H.
Genomics 1, 182-195, 1987
A:Title: Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes: evolution
A:Reference number: A27176; MUID:88085193; PMID:2891608
A:Accession: C27176
A:Molecule type: DNA
A:Residues: 1-97 <HAR>
A:Cross-references: GB:M18401; NID:G193936; PID:MAC27130.1; PID:G3335322
C:Genetics:
A:Gene: Hox-2.2
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:20-76/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 97;
Best Local Similarity 66.7%; Pred. No. 4.7e-06;
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWPNRRMKKKTKT--LDMSWLQTE 28
DB 60 EROIKIWPNRRMKKKESKLSASQLSAG 89

RESULT 11
S26400
homeotic protein Hox 2.2 (variant 1) - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Nov-2000
C:Accession: S26400; S26401
R:Shen, W.; Demer, K.; Szymonitch-Bason, T.A.; Lawrence, H.J.; Largman, C.
Nucleic Acids Res. 19, 539-545, 1991
A:Title: Alternative splicing of the Hox 2.2 homeobox gene in human hematopoietic cell.
A:Reference number: S26400; MUID:91187672; PMID:1672751
A:Accession: S26400
A:Molecule type: DNA
A:Residues: 1-224 <SHE>
A:Cross-references: EMBL:X58431; NID:G32369; PID:CAA41335.1; PID:G32370
A:Experimental source: tissue-type placenta
A>Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue 60
A:Molecule type: DNA
A:Residues: 1-139, 'B', <SH2>
A:Cross-references: EMBL:X58431; NID:G32369; PID:CAA41336.1; PID:G32371
A:Experimental source: tissue-type placenta
A>Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue 60
C:Genetics:
A:Introns: 139/1
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regula
F:147-203/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 224;
Best Local Similarity 66.7%; Pred. No. 1.1e-05;

Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
 QY 1 DROIKIWFQNRMRMKKTA--LDMSWLTQTE 28
 :|||||
 Db 187 EROIKIWFQNRMRMKKESKTLASQLSAE 216

RESULT 12

A31324
 homeotic protein Hox 2.2 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 24-Sep-1999
 C/Accession: A31324
 R/Schuhardt, K.; Utecht, M.F.; Awgulewitsch, A.; Ruddle, F.H.
 Proc. Natl. Acad. Sci. U.S.A. 85, 5582-5586, 1988
 A/Title: Structure and expression of Hox-2.2, a murine homeobox-containing gene.
 A/Reference number: A31324; MUID:88289762; PMID:2899893
 A/Accession: A31324
 A/Molecule type: mRNA
 A/Residues: 1-224 <SCH>
 A/Cross-references: GB:U03782; NID:g193929; PIDN:AAA37843.1; PID:g387203
 C/Superfamily: unassigned homeobox proteins; homeobox homology
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:147-203/Domain: homeobox homology <Hox>

Query Match 58.6%; Score 95; DB 2; Length 224;
 Best Local Similarity 66.7%; Pred. No. 1.1e-05;
 Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DROIKIWFQNRMRMKKTA--LDMSWLTQTE 28
 :|||||
 Db 187 EROIKIWFQNRMRMKKESKTLASQLSAE 216

RESULT 13

SS7235
 antennapedia protein (clone p1105) - fruit fly (Drosophila pseudoobscura) (fragment)
 C/Species: Drosophila pseudoobscura
 C/Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 15-Oct-1999
 C/Accession: SS7235
 R/Randazzo, F.M.; Seeger, M.A.; Huss, C.A.; Sweeney, M.A.; Cecili, J.K.; Kaufman, T.C.
 Genetics 133, 319-330, 1993
 A/Title: Structural changes in the antennapedia complex of Drosophila pseudoobscura.
 A/Reference number: SS7224
 A/Molecule type: DNA
 A/Residues: 1-33 <RAN>
 A/Cross-references: EMBL:X77711
 C/Genetics:
 A/Gene: FLYBase:Antp
 A/Cross-references: FLYBase:FBgn0012693
 C/Superfamily: unassigned homeobox proteins; homeobox homology
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:1-22/Domain: homeobox homology (fragment) <Hox>

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 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMRMKK 17
 :|||||
 Db 6 EROIKIWFQNRMRMKK 22

RESULT 14

I65241
 homeotic protein Hox-A - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 15-Oct-1999
 C/Accession: I65241
 R/Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.
 Biochem. Genet. 33, 351-360, 1994
 A/Title: Cloning of rat homeobox genes.

A/Reference number: I52340; MUID:95217128; PMID:7702549
 A/Accession: I65241
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-42 <RES>
 A/Cross-references: GB:S76290; NID:g913077
 C/Genetics:
 A/Gene: Hox-A; Hox-1
 C/Superfamily: unassigned homeobox proteins; homeobox homology
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:1-40/Domain: homeobox homology (fragment) <Hox>

Query Match 58.0%; Score 94; DB 2; Length 42;
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 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMRMKK 17
 :|||||
 Db 24 EROIKIWFQNRMRMKK 40

RESULT 15

PC1216
 homeotic protein Dhhx1 - planarian (Dugesia tigritina) (fragment)
 C/Species: Dugesia tigritina
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Oct-1997
 C/Accession: PC1216
 R/Oliver, G.; Vispo, M.; Mallhos, A.; Martinez, C.; Sosa-Planned, B.; Fiehlitz, W.; Ehrl.
 Gene 121, 337-342, 1992
 A/Title: Homeoboxes in flatworms.
 A/Reference number: JCI386; MUID:93077050; PMID:1359988
 A/Accession: PC1216
 A/Molecule type: DNA
 A/Residues: 1-45 <OLI>
 A/Cross-references: EMBL:X66822
 C/Superfamily: unassigned homeobox proteins; homeobox homology
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:1-45/Domain: homeobox homology (fragment) <Hox>

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 Best Local Similarity 94.1%; Pred. No. 2.8e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMRMKK 17
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 Db 29 EROIKIWFQNRMRMKK 45

Search completed: February 18, 2004, 14:38:53
 Job time : 31.7632 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 77.9211 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DROIKIWFONRRMKKTALDMSWLQTE 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues
Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	28	10 US-09-847-940B-18	Sequence 18, Appl
2	162	100.0	28	11 US-09-847-946A-18	Sequence 18, Appl
3	134	82.7	28	10 US-09-847-940B-19	Sequence 19, Appl
4	134	82.7	28	11 US-09-847-946A-19	Sequence 19, Appl
5	105	64.8	18	11 US-09-847-946A-131	Sequence 131, Appl
6	101	62.3	36	9 US-09-731-023A-12	Sequence 12, Appl
7	101	62.3	36	12 US-10-358-365-12	Sequence 12, Appl
8	97	59.9	17	15 US-10-229-915-1	Sequence 1, Appl
9	97	59.9	34	15 US-10-161-499-79	Sequence 79, Appl
10	95	58.6	26	15 US-10-097-175-101	Sequence 101, Appl
11	95	58.6	21	8 US-09-610-220A-11	Sequence 11, Appl
12	95	58.6	21	9 US-09-150-623-11	Sequence 11, Appl
13	94	58.0	30	15 US-10-188-947-11	Sequence 11, Appl
14	94	58.0	64	15 US-10-118-079-44	Sequence 44, Appl
15	94	58.0	217	15 US-10-097-340-129	Sequence 129, Appl

16	94	58.0	233	12 US-10-420-940-4	Sequence 4, Appl
17	94	58.0	269	12 US-10-116-275-190	Sequence 190, Appl
18	94	58.0	295	15 US-10-118-079-4	Sequence 4, Appl
19	93.5	57.7	36	9 US-09-731-023A-11	Sequence 11, Appl
20	93.5	57.7	36	12 US-10-358-365-11	Sequence 11, Appl
21	93	57.4	22	12 US-10-359-226-50	Sequence 50, Appl
22	93	57.4	28	9 US-09-214-371-9	Sequence 9, Appl
23	93	57.4	115	9 US-09-925-299-1169	Sequence 1169, Appl
24	93	57.4	115	11 US-09-925-299-1169	Sequence 1169, Appl
25	92	56.8	16	8 US-08-610-220A-9	Sequence 9, Appl
26	92	56.8	16	9 US-09-214-371-43	Sequence 43, Appl
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29	92	56.8	16	9 US-09-731-023A-10	Sequence 10, Appl
30	92	56.8	16	9 US-09-854-204-1	Sequence 1, Appl
31	92	56.8	16	10 US-09-900-147-8	Sequence 8, Appl
32	92	56.8	16	10 US-09-792-480-29	Sequence 29, Appl
33	92	56.8	16	10 US-09-785-802A-2	Sequence 2, Appl
34	92	56.8	16	10 US-09-785-802A-5	Sequence 5, Appl
35	92	56.8	16	10 US-09-902-432-32	Sequence 32, Appl
36	92	56.8	16	10 US-09-953-031A-10	Sequence 10, Appl
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39	92	56.8	16	11 US-09-912-414-6	Sequence 6, Appl
40	92	56.8	16	11 US-09-775-052-54	Sequence 54, Appl
41	92	56.8	16	11 US-09-295-189-4	Sequence 4, Appl
42	92	56.8	16	11 US-09-965-876A-1	Sequence 1, Appl
43	92	56.8	16	12 US-10-017-672-11	Sequence 11, Appl
44	92	56.8	16	12 US-10-201-389A-14	Sequence 14, Appl
45	92	56.8	16	12 US-10-161-051-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-847-940B-18
; Sequence 18, Application US/09847940B
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PRI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD peptides
US-09-847-940B-18

Query Match 100.0%; Score 162; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DROIKIWFONRRMKKTALDMSWLQTE 28
DB 1 DROIKIWFONRRMKKTALDMSWLQTE 28
RESULT 2
US-09-847-946A-18
; Sequence 18, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

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APPLICANT: Ghosh, Sankar
APPLICANT: Flindeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-18
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Query Match          100.0%; Score 162; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 DROIKIFQNRMRMKKTALDMSWLQTE 28
Db 1 DROIKIFQNRMRMKKTALDMSWLQTE 28
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```
RESULT 3
US-09-847-940B-19
Sequence 19, Application US/9847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Sankar
APPLICANT: May, Michael J.
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-19
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Query Match          82.7%; Score 134; DB 10; Length 28;
Best Local Similarity 92.9%; Pred. No. 8e-10;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 1 DROIKIFQNRMRMKKTALDMSWLQTE 28
Db 1 DROIKIFQNRMRMKKTALDMSWLQTE 28
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RESULT 4
US-09-847-946A-19
Sequence 19, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Flindeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
```

```
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19
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Query Match          82.7%; Score 134; DB 11; Length 28;
Best Local Similarity 92.9%; Pred. No. 8e-10;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 1 DROIKIFQNRMRMKKTALDMSWLQTE 28
Db 1 DROIKIFQNRMRMKKTALDMSWLQTE 28
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RESULT 5
US-09-847-946A-131
Sequence 131, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Flindeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 131
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-131
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Query Match          64.8%; Score 105; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 11 RRRKKKKKTALDMSWLQTE 28
Db 1 RRRKKKKKTALDMSWLQTE 18
```

```
RESULT 6
US-09-731-023A-12
Sequence 12, Application US/09731023A
Patent No. US20020077283A1
GENERAL INFORMATION:
APPLICANT: Seesä, William
APPLICANT: Caveolin Peptides and Their Use as Therapeutics
FILE REFERENCE: 44574-5076-US
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/ CURRENT APPLICATION NUMBER: US/09/731.023A
/ CURRENT FILING DATE: 2000-12-07
/ PRIOR APPLICATION NUMBER: US 60/231,327
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
US-09-731-023A-12

Query Match          62.3%; Score 101; DB 9; Length 36;
Best Local Similarity 69.2%; Pred. No. 1.1e-05;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      2 ROIKIWFQNRMRMKKKTALDMSWLOT 27
Db      1 ROIKIWFQNRMRMKKKGIDKAFPTT 26

RESULT 7
US-10-358-365-12
/ Sequence 12, Application US/10358365
/ Publication No. US20030165510A1
/ GENERAL INFORMATION:
/ APPLICANT: Segee, William
/ TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
/ FILE REFERENCE: 44574-5076-US
/ CURRENT APPLICATION NUMBER: US/10/358,365
/ CURRENT FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: US 09/731,023
/ PRIOR FILING DATE: 2000-12-07
/ PRIOR APPLICATION NUMBER: US 60/231,327
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
US-10-358-365-12

Query Match          62.3%; Score 101; DB 12; Length 36;
Best Local Similarity 69.2%; Pred. No. 1.1e-05;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      2 ROIKIWFQNRMRMKKKTALDMSWLOT 27
Db      1 ROIKIWFQNRMRMKKKGIDKAFPTT 26

RESULT 8
US-10-229-915-1
/ Sequence 1, Application US/10229915
/ Publication No. US20030083262A1
/ GENERAL INFORMATION:
/ APPLICANT: Lazarus, Douglas
/ APPLICANT: Hamdy, Gerhard
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
/ TITLE OF INVENTION: DISORDERS
/ FILE REFERENCE: PPI-127
/ CURRENT APPLICATION NUMBER: US/10/229,915
/ CURRENT FILING DATE: 2002-08-27
/ PRIOR APPLICATION NUMBER: US 60/316,328
/ PRIOR FILING DATE: 2001-08-30
/ NUMBER OF SEQ ID NOS: 39
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/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: anti-inflammatory compound
US-10-229-915-1

Query Match          60.5%; Score 98; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DROIKIWFQNRMRMKK 17
Db      1 DROIKIWFQNRMRMKK 17

RESULT 9
US-10-161-499-79
/ Sequence 79, Application US/10161499
/ Publication No. US20030044427A1
/ GENERAL INFORMATION:
/ APPLICANT: Howley, Peter M.
/ APPLICANT: Benson, John
/ APPLICANT: Kasukawa, Hiroaki
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
/ TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
/ FILE REFERENCE: HMV-041.01
/ CURRENT APPLICATION NUMBER: US/10/161,499
/ CURRENT FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US/09/347,504
/ PRIOR FILING DATE: 1999-07-02
/ NUMBER OF SEQ ID NOS: 79
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 79
/ LENGTH: 34
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-161-499-79

Query Match          59.9%; Score 97; DB 15; Length 34;
Best Local Similarity 64.3%; Pred. No. 3.3e-05;
Matches 18; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy      1 DROIKIWFQNRMRMKKKTALDMSWLOT 28
Db      1 EROIKIWFQNRMRMKKKG--WKMRLE 26

RESULT 10
US-10-097-175-101
/ Sequence 101, Application US/10097175
/ Publication No. US20030045680A1
/ GENERAL INFORMATION:
/ APPLICANT: JOYAL, JOHN L.
/ APPLICANT: MUELLER, JOHN
/ APPLICANT: OZA, VIBHA B.
/ APPLICANT: FINDEIS, MARK A.
/ TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
/ FILE REFERENCE: PPI-110
/ CURRENT APPLICATION NUMBER: US/10/097,175
/ CURRENT FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: 60/275,240
/ PRIOR FILING DATE: 2001-03-12
/ PRIOR APPLICATION NUMBER: 60/352,399
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 101
/ LENGTH: 26
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
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FEATURE:
OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-101

Query Match 59.3%; Score 96; DB 15; Length 26;
Best Local Similarity 77.3%; Pred. No. 3,4e-05;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRMRKMKKTA 19
DB 1 ROIKIWFQNRMRKMKKTA 18

RESULT 11
US-08-610-220A-11
Sequence 11, Application US/08610220A
Publication No. US2003009638A1
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/610,220A
FILING DATE: MAR-04-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 48332/JPW/JML
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-610-220A-11

Query Match 58.6%; Score 95; DB 8; Length 21;
Best Local Similarity 94.4%; Pred. No. 3,7e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRMRKMKKTA 19
DB 1 ROIKIWFQNRMRKMKKTA 18

RESULT 12
US-09-150-623-11
Sequence 11, Application US/09150623
Patent No. US20020044931A1
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/150,623
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/610,220
FILING DATE: MAR-04-1996
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-150-623-11

Query Match 58.6%; Score 95; DB 9; Length 21;
Best Local Similarity 94.4%; Pred. No. 3,7e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRMRKMKKTA 19
DB 1 ROIKIWFQNRMRKMKKTA 18

RESULT 13
US-10-188-947-11
Sequence 11, Application US/10188947
Publication No. US2003002393A1
GENERAL INFORMATION:
APPLICANT: MEDHITOV, Ruslan
APPLICANT: HORNIG, Tiffany
APPLICANT: BARTON, Gregory
TITLE OF INVENTION: TOLL/INTERLEUKIN-1 RECEPTOR ADAPTER PROTEIN (TIRAP)
FILE REFERENCE: 044574-5101US
CURRENT APPLICATION NUMBER: US/10/188,947
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/289,738
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/289,815
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/289,866
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent version 3.1
SEQ ID NO 11
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: TIRAP/Antennapedia fusion protein
NAME/KEY: MISC FEATURE
OTHER INFORMATION: TIRAP/Antennapedia fusion protein
US-10-188-947-11

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Query Match      58.0%; Score 94; DB 15; Length 30;
Best Local Similarity 89.5%; Pred. No. 6.8e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 ROIKIWFQNRMRMKKTAL 20
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Db      1 ROIKIWFQNRMRMKKQL 19

RESULT 14
US-10-118-079-44
; Sequence 44, Application US/10118079
; Publication No. US20030103957A1
; GENERAL INFORMATION:
; APPLICANT: MCKERRACHER, LISA
; TITLE OF INVENTION: FUSION PROTEINS
; FILE REFERENCE: 06746-004-US-03
; CURRENT APPLICATION NUMBER: US/10/118,079
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: CA 2,367,636
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: CA 2,362,004
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: CA 2,342,970
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent version 3.1
; SEQ ID NO 44
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of Antennapedia from C3APL
US-10-118-079-44

Query Match      58.0%; Score 94; DB 15; Length 64;
Best Local Similarity 94.1%; Pred. No. 0.00013;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DROIKIWFQNRMRMKWK 17
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Db      46 EROIKIWFQNRMRMKWK 62

RESULT 15
US-10-097-340-129
; Sequence 129, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNANAPAPU
; APPLICANT: Sebaetian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIRBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumel ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
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; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-129

Query Match      58.0%; Score 94; DB 15; Length 217;
Best Local Similarity 94.1%; Pred. No. 0.0004;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DROIKIWFQNRMRMKWK 17
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Db      178 EROIKIWFQNRMRMKWK 194
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Search completed: February 18, 2004, 15:42:02
Job time : 78.9766 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 / Search time 106.289 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162
Sequence: 1 DRQIKWPNRRMKKLTALDWSLQTE 28

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	28	23	ABR08740
2	162	100.0	28	23	AA448523
3	162	100.0	28	24	ABU08434
4	134	82.7	28	23	ABR08741
5	134	82.7	28	23	AA448524
6	134	82.7	28	24	ABU08435
7	105	64.8	18	23	AA448628
8	105	64.8	18	23	AA448629
9	101	62.3	36	23	AAU79345

10	100	61.7	41	22	ABR0924
11	100	61.7	41	22	ABR0925
12	98	60.5	20	21	AA13423
13	98	60.5	26	18	AA11630
14	97	59.9	34	21	AA17919
15	96	59.3	26	24	AAE31836
16	95.5	59.0	42	23	ABP53779
17	95	58.6	21	18	AA45976
18	95	58.6	24	19	AA482957
19	95	58.6	36	21	AA178416
20	95	58.6	230	21	AA158610
21	94	58.0	27	18	AA11629
22	94	58.0	27	20	AA127444
23	94	58.0	27	23	ABR83151
24	94	58.0	30	24	ABP58107
25	94	58.0	60	20	AA142291
26	94	58.0	60	20	AA127403
27	94	58.0	60	20	AA104364
28	94	58.0	60	23	ABR84470
29	94	58.0	61	22	AAE00811
30	94	58.0	64	24	ABE32060
31	94	58.0	128	24	ABR99729
32	94	58.0	217	22	AAE10922
33	94	58.0	217	23	ABG96337
34	94	58.0	295	24	AAE32047
35	94	58.0	378	22	ABR72035
36	94	58.0	417	22	ABR57755
37	94	58.0	589	22	ABR58929
38	93.5	57.7	36	23	AAU79344
39	93	57.4	22	20	AA191049
40	93	57.4	22	21	AAE27063
41	93	57.4	106	21	AAE21030
42	93	57.4	115	21	AAE53629
43	93	57.4	220	22	AA441487
44	93	57.4	236	22	AA139701
45	93	57.4	243	19	AA448885

ALIGNMENTS

RESULT 1					
ID	ABR08740	standard; peptide; 28 AA.			
XX	XX				
AC	ABR08740;				
XX	XX				
DT	14-JUN-2002	(first entry)			
XX	XX				
DE	IKKbeta NEMO binding domain peptide SEQ ID NO 18.				
XX	XX				
XX	XX				
KW	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;				
KW	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;				
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;				
KW	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;				
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;				
KW	corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;				
KW	osteopathic; cytostatic; nocotropic; neuroprotective; anti-HIV; human;				
KW	antiarteriosclerotic; virucide; antiasthmatic; antiallergic;				
KW	dermatological; antibacterial; antiparasitic; antirheumatic;				
KW	antiarthritic; osteopathic; antitumor.				
OS	Homo sapiens.				
PN	WO200183547-A2.				
XX	XX				
PD	08-NOV-2001.				
XX	XX				
PF	02-MAY-2001; 2001WO-US40654.				
XX	XX				
PR	02-MAY-2000; 2000US-201261P.				
XX	XX				
PR	22-AUG-2000; 2000US-0643260.				
XX	XX				

Mixer SIM peptide.
Mixer SIM mutant p
Synthetic alpha sm
Anti-apoptotic pro
Human papillomavir
Androgen receptor
Antennapedia helix
Antennapedia helix
Cysteine protease
Oestrogen receptor
Drosophila antenna
Protein regulating
Anti-apoptotic pro
Antennapedia inter
Transduction domai
Mouse TIRAP-Antenn
Drosophila antenna
D. melanogaster PA
Drosophila antenna
S. cerevisiae Antp
D. melanogaster an
Antennapedia C3APL
Amino acid sequenc
Human HOXB7 varian
Human ovarian canc
Clostridium Botuli
Drosophila melanog
Drosophila melanog
Drosophila melanog
Antennapedia-caveo
Internalization be
Beta-catenin deriv
Human nucleic acid
Human colon cancer
Human polypeptide
Human polypeptide
Amino acid sequenc

PA (UYVA) UNIV YALE.
 XX May MJ, Ghosh S;
 XX WPI; 2002-179350/23.
 DR
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 PS Claim 23, Fig 5, 82pp, English.
 XX
 XX The invention relates to modulating NF-kappaB (NF-KB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (AB08725-AB08742) comprising at least one NEMO binding domain
 CC (AB077313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-KB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of I-kappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-KB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of the NEMO
 CC binding domain of IKKbeta.
 XX
 SO Sequence 28 AA;
 Query Match 100.0%; Score 162; DB 23; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.9e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFONRRMKKKTALDMSWLQTE 28
 DB 1 DROIKIWFONRRMKKKTALDMSWLQTE 28

RESULT 2
 AAM48523 standard; Peptide; 28 AA.
 ID AAM48523
 AC AAM48523;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX
 XX NBD peptide SEQ ID NO 18.
 DB
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; anti-psoriatic; neurotropic;
 KM antineumatic; antidiabetic; osteopathic; antibacterial; virocidic;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KM cytokine; NFkappaB; IkkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX MO200183554-A2.
 XX
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRABCTIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Fandels MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Example 5, Fig 5, 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48620-AM48645), comprising a membrane translocation domain
 CC (AAM48620-AM48627 or AAM48646-AM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antidiabetic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antiatherosclerotic, virocidic and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SO Sequence 28 AA;
 Query Match 100.0%; Score 162; DB 23; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.9e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFONRRMKKKTALDMSWLQTE 28
 DB 1 DROIKIWFONRRMKKKTALDMSWLQTE 28

RESULT 3
 ABU08434 standard; peptide; 28 AA.
 ID ABU08434
 AC ABU08434;
 XX
 XX 12-JUN-2003 (first entry)
 DT
 XX

DE Wild-type human NEMO binding site (NBD) peptide.
 XX
 XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cystostatic; nocotropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antineumatic; antirheumatic.
 XX
 OS Homo sapiens.
 XX
 PN US2002156000-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 02-MAY-2001; 2001US-0847940.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (MAYM/) MAY M J.
 XX (GHOS/) GHOSH S.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2003-209142/20.
 XX
 PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX
 XX Claim 35; Page 22; 47pp; English.
 XX
 PS The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. The present sequence represents
 CC an antiinflammatory compound of the invention.
 CC
 SQ Sequence 28 AA;
 XX
 XX
 Query Match 100.0%; Score 162; DB 24; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.9e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DROIKIPFORRMKMKKTKALDMSGLQTE 28
 DB 1 DROIKIPFORRMKMKKTKALDMSGLQTE 28
 AC ABB08741 standard; peptide; 28 AA.
 XX ABB08741;
 AC
 XX 14-JUN-2002 (first entry)
 XX
 DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 19.
 XX

KW IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; nocotropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; anti-allergic;
 KW dermatological; antibacterial; antiparasitic; antineumatic;
 KW antirheumatic; osteopathic; antitumor; mutant; mutein.
 XX
 OS Homo sapiens.
 XX
 PN Synthetic.
 XX
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 22
 FT
 FT Misc-difference 24 /note= "Wildtype Trp substituted by Ala"
 FT
 FT Misc-difference 24 /note= "Wildtype Trp substituted by Ala"
 XX
 PN WO200183547-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US40654.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYTA) UYTA YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2002-179350/23.
 XX
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 XX Claim 23; Fig 5; 82pp; English.
 XX
 PS The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB077313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyvalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC

CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC binding domain of IKKbeta.

SO Sequence 28 AA:

Query Match 82.7%; Score 134; DB 23; Length 28;
Best Local Similarity 92.9%; Pred. No. 4.3e-11;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRRMKWTKTALDMSWLTQTE 28
1 DRQIKIWFQNRRMKWTKTALDMSWLTQTE 28

RESULT 5

AA048524 standard; Peptide; 28 AA.

AC AA048524;

DT 20-MAR-2002 (first entry)

DE NBD peptide SEQ ID NO 19.

XX Antiinflammatory; antiaesthetic; cytoskeletal; antipsoriatic; nootropic;
XX Antineumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX Immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX Antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

PA (PRAE-) PRAECIS PHARM INC.

PA (UYTA) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;

PI WPI; 2002-121889/16.

PT Novel antiinflammatory compound comprising membrane translocation

PT domain fused to NEMO binding sequence, useful for blocking nuclear

PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis

PT

PS Example 5; Fig 5; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
XX AA048528-AA048645), comprising a membrane translocation domain
XX (AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15
XX amino acid residues, fused to a NEMO binding sequence
XX (AA048525-AA048619). The antiinflammatory compounds have antiaesthetic,
XX cytoskeletal, antipsoriatic, antineumatic, antiarthritic, osteopathic,
XX antibacterial, immunosuppressive, dermatological, neuroprotective,
XX nootropic, antiatherosclerotic, virucide and antiallergic activity. The
XX compounds act as selective inhibitors of cytokine-mediated NF-kappaB
XX activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
XX the NEMO binding domain that results in inhibition of IkappaB kinase
XX activation and subsequent decreased phosphorylation of IkappaB. The
XX compounds are useful for treating inflammatory disorders, e.g. asthma,

CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.

SO Sequence 28 AA:

Query Match 82.7%; Score 134; DB 23; Length 28;
Best Local Similarity 92.9%; Pred. No. 4.3e-11;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRRMKWTKTALDMSWLTQTE 28
1 DRQIKIWFQNRRMKWTKTALDMSWLTQTE 28

RESULT 6

AB008435 standard; peptide; 28 AA.

AC AB008435;

DT 12-JUN-2003 (first entry)

DE Human mutant NEMO binding site (NBD) peptide.

XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
XX IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
XX nuclear factor-kappaB induction; inflammatory disorder;
XX autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
XX atherosclerosis; viral infection; Ataxia telangiectasia;
XX transplantation detection; immunosuppressive; osteopathic;
XX cytoskeletal; nootropic; neuroprotective; antiatherosclerotic; virucide;
XX vasotropic; antineumatic; antiarthritic; mutant; mutein.

OS Homo sapiens.

PN US2002156000-A1.

PD 24-OCT-2002.

PF 02-MAY-2001; 2001US-0847940.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

PA (MAYW/) MAY M J.

PA (GHOS/) GHOSH S.

PI May MJ, Ghosh S;

PI WPI; 2003-209142/20.

PT Novel antiinflammatory peptide compounds comprising NEMO binding

PT domain, useful for modulating NF-kappaB induction in a cell and for

PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,

PT psoriasis, vasculitis

PS Claim 22; Fig 5A; 47pp; English.

XX The present invention relates to antiinflammatory compounds comprising
XX NEMO binding domain (NBD) peptides. The NEMO binding domains are
XX found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
XX (IKKalpha) proteins. The antiinflammatory compounds of the invention
XX are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
XX in a cell, where the compounds are capable of blocking the interaction
XX between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The

CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplacental detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. The present sequence represents
 CC a human mutant NBD peptide.
 XX
 SQ Sequence 28 AA;
 Query Match 82.7%; Score 134; DB 24; Length 28;
 Best Local Similarity 92.9%; Pred. No. 4.3e-11;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DRQIKIWFQNRNRMKKKTALDWSWLTQTE 28
 DB 1 DRQIKIWFQNRNRMKKKTALDASALQTE 28
 RESULT 7
 AAM48628 AAM48628 standard; Peptide; 18 AA.
 XX
 AC AAM48628;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 131.
 XX
 KM Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 OS Synthetic.
 XX
 PN MO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 Claim 12; Page 62; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective, the
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 18 AA;
 Query Match 64.8%; Score 105; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RRMKKKTALDWSWLTQTE 28
 DB 1 RRMKKKTALDWSWLTQTE 18
 RESULT 8
 AAM48629 AAM48629 standard; Peptide; 18 AA.
 XX
 AC AAM48629;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 132.
 XX
 KM Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 OS Synthetic.
 XX
 PN MO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 Claim 12; Page 63; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM4620-AAM4827 or AAM4846-AAM4851) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
 CC cytoskeletal, antipneumatic, antirheumatic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antihypertensive, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of I-kappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of I-kappaB kinase
 CC activation and subsequent decreased phosphorylation of I-kappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 SQ Sequence 18 AA:
 Query Match 64.8%; Score 105; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RRMKKKTALDMSWLTQTE 28
 Db 1 RRMKKKTALDMSWLTQTE 18
 RESULT 9
 AAV79345
 ID AAV79345 standard; Peptide: 36 AA.
 AC AAV79345;
 XX
 DT 02-JUN-2002 (first entry)
 XX
 DE Antennapedia-caveolin-X fusion peptide.
 XX
 KW Caveolin; scaffolding domain; endothelial nitric oxide synthase; eNOS;
 KW vasodilation inhibitor; inflammation inhibitor; tumour cell angiogenesis;
 KW tumour cell proliferation; osteoporosis; arthritis; atherosclerosis;
 KW asthma; Alzheimer's disease; allergy; allergic rhinitis; urticaria;
 KW anaphylaxis; dry sensitivity; food sensitivity; dermatitis; eczema;
 KW psoriasis; sunburn; aging; osteoarthritis; psoriatic arthritis; lupus;
 KW spondylarthritis; chronic obstruction pulmonary disease; cancer; Cav;
 KW chronic inflammatory bowel disease; tumour growth; malignant neoplasm;
 KW human; fruit fly; antennapedia internalisation signal.
 XX
 OS Drosophila melanogaster.
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..16
 FT /label= Antennapedia internalisation signal
 FT /note= "Specifically claimed in claim 9"
 FT Misc-difference 17..32
 FT /label= Cav-X
 FT /note= "Control peptide based on a human caveolin-1
 FT scaffolding domain shown in AAV79340 residues
 FT 82-101"
 XX
 PN WO200220766-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US42069.
 XX
 PR 08-SEP-2000; 2000US-231327P.

PR 07-DEC-2000; 2000US-0731023.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI Sessa WC;
 XX
 DR WPI; 2002-329877/36.
 XX
 PT New peptide having caveolin scaffolding domain, useful for modulating
 PT activity of endothelial nitric oxide synthase and inhibiting
 PT inflammation and tumour cell angiogenesis proliferation -
 XX
 PS Claim 16; Page 72; 73pp; English.
 XX
 CC The invention describes an isolated caveolin scaffolding domain peptide
 CC (I). A fusion peptide (II) containing (I) and at least a membrane
 CC translocation sequence is useful for down regulating endothelial nitric
 CC oxide synthase (eNOS) activity in a cell, resulting in blockage of
 CC vasodilation. (II) is therefore useful for inhibiting inflammation and
 CC tumour cell angiogenesis/proliferation in an animal; and for blocking the
 CC interaction of caveolin with a protein in vivo. (II) may be useful in
 CC treatment of inflammatory conditions such as osteoporosis, rheumatoid
 CC arthritis, atherosclerosis, asthma and Alzheimer's disease. (I) and (II)
 CC are also useful for treating pathological processes associated with a
 CC pro-inflammatory response including allergies such as allergic rhinitis,
 CC urticaria, anaphylaxis, dry sensitivity, food sensitivity, cutaneous
 CC inflammation such as dermatitis, eczema, psoriasis contact dermatitis,
 CC sunburn, aging, arthritis such as osteoarthritis, psoriatic arthritis,
 CC lupus, spondylarthritis, and chronic obstruction pulmonary disease and
 CC chronic inflammatory bowel disease. (I) and (II) are useful for replacing
 CC corticosteroids useful for immunosuppression in transplant and cancer
 CC patients. When administered along with one or more anti-inflammatory
 CC agent (I) and (II) are useful for inhibiting tumour growth or malignant
 CC neoplasm including cellular angiogenesis, proliferation, invasiveness,
 CC and metastasis in biological systems. This sequence represents a fusion
 CC peptide of the invention created from the fruit fly antennapedia
 CC internalisation signal and control sequence Cav-X, based on the human
 CC caveolin-1 scaffolding domain shown in AAV79340, residues 82-101.
 CC
 SQ Sequence 36 AA;
 Query Match 62.3%; Score 101; DB 23; Length 36;
 Best Local Similarity 69.2%; Pred. No. 1.4e-06;
 Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 2 RQIKIFQNRBMKKKTALDMSWLTQT 27
 Db 1 RQIKIFQNRBMKKKTALDMSWLTQT 26
 RESULT 10
 ID AAB80924
 AAB80924 standard; Protein: 41 AA.
 AC AAB80924;
 XX
 DT 04-JUN-2001 (first entry)
 XX
 DE Mixer SIM peptide.
 XX
 KW Smad; Cytostatic; vulnerary; cerebroprotective; immunosuppressive;
 KW Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;
 KW Smad interaction Motif; tissue repair; fibrotic condition;
 KW immunosuppression; diabetic nephropathy; tumour.
 XX
 OS Unidentified.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Biotin.Aminohexanoic acid-R"
 XX
 PN WO200114413-A2.
 XX

PD 01-MAR-2001.
 XX
 PF 25-AUG-2000; 2000WO-GB03265.
 XX
 PR 25-AUG-1999; 99GB-0020000.
 XX
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 XX
 PI Germain SE, Hill CS, Howell MT;
 XX
 DR WPI; 2001-265836/27.
 XX
 PT Polypeptide capable of interacting with a Smad polypeptide, useful in
 PT the treatment of cancer and for tissue remodeling or healing of a
 PT wound, injury or surgery, comprises a Smad interaction Motif and is
 PT less than 32 amino acids in length -
 XX
 PS Claim 16; Page 140; 179pp; English.
 XX
 CC The present invention relates to peptides capable of interacting with a
 CC Smad protein, comprising a Smad interaction Motif (SIM; amino acid
 CC sequence PP(T/N)K). The present sequence is one such Smad interacting
 CC peptide. Smad proteins are a family of highly conserved, intracellular
 CC proteins that signal cellular responses downstream of Transforming Growth
 CC Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM
 CC is thought to be necessary for interaction with the WH2 domain of Smad2.
 CC The peptides of the present invention are useful in the manufacture of a
 CC medicament for the treatment of a patient in need of modulation of
 CC activation or TGF-beta signaling; cancer; a patient in need of reducing
 CC extracellular matrix deposition, encouraging tissue repair and/or
 CC regeneration, tissue remodeling or healing of a wound, injury or
 CC surgery, or reducing scar tissue formation arising from injury to the
 CC brain; a patient with or at risk of end-stage organ failure, pathologic
 CC extracellular matrix accumulation, a fibrotic condition, disease states
 CC associated with immunosuppression (such as different forms of malignancy,
 CC chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour
 CC growth, kidney damage (for e.g. obstructive neuropathy, Iga nephropathy
 CC or non-inflammatory renal disease) or renal fibrosis.
 CC
 XX
 SQ Sequence 41 AA;
 Query Match 61.7%; Score 100; DB 22; Length 41;
 Best Local Similarity 77.3%; Pred. No. 2.2e-06;
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 ROIKIWFOVRBMKKKLTALDWS 23
 Db 1 ROIKIWFOVRBMKKKLTALDWFN 22
 RESULT 11
 AAB80925
 ID AAB80925 standard; Protein; 41 AA.
 AC AAB80925;
 XX
 DT 04-JUN-2001 (first entry)
 XX
 DE Mixer SIM mutant peptide.
 XX
 KW Smad; Cytostatic; vulnary; cerebroprotective; immunosuppressive;
 KW Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;
 KW Smad interaction Motif; tissue repair; fibrotic condition;
 KW immunosuppression; diabetic nephropathy; tumour; mutuin.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT Misc-difference 25 /note= "Biotin.Aminohexanoic acid-R"
 FT /note= "Wild-type Pro replaced by Ala. Wild-type sequence
 FT given in AAB80924."

FT Misc-difference 26 /note= "Wild-type Pro replaced by Ala"
 FT
 XX
 PN WO200114413-A2.
 XX
 PD 01-MAR-2001.
 XX
 PF 25-AUG-2000; 2000WO-GB03265.
 XX
 PR 25-AUG-1999; 99GB-0020000.
 XX
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 XX
 PI Germain SE, Hill CS, Howell MT;
 XX
 DR WPI; 2001-265836/27.
 XX
 PT Polypeptide capable of interacting with a Smad polypeptide, useful in
 PT the treatment of cancer and for tissue remodeling or healing of a
 PT wound, injury or surgery, comprises a Smad interaction Motif and is
 PT less than 32 amino acids in length -
 XX
 PS Example 2; Page 123; 179pp; English.
 XX
 CC The present invention relates to peptides capable of interacting with a
 CC Smad protein, comprising a Smad interaction Motif (SIM; amino acid
 CC sequence PP(T/N)K). The present sequence is one such Smad interacting
 CC peptide. Smad proteins are a family of highly conserved, intracellular
 CC proteins that signal cellular responses downstream of Transforming Growth
 CC Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM
 CC is thought to be necessary for interaction with the WH2 domain of Smad2.
 CC The peptides of the present invention are useful in the manufacture of a
 CC medicament for the treatment of a patient in need of modulation of
 CC activation or TGF-beta signaling; cancer; a patient in need of reducing
 CC extracellular matrix deposition, encouraging tissue repair and/or
 CC regeneration, tissue remodeling or healing of a wound, injury or
 CC surgery, or reducing scar tissue formation arising from injury to the
 CC brain; a patient with or at risk of end-stage organ failure, pathologic
 CC extracellular matrix accumulation, a fibrotic condition, disease states
 CC associated with immunosuppression (such as different forms of malignancy,
 CC chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour
 CC growth, kidney damage (for e.g. obstructive neuropathy, Iga nephropathy
 CC or non-inflammatory renal disease) or renal fibrosis.
 CC
 XX
 SQ Sequence 41 AA;
 Query Match 61.7%; Score 100; DB 22; Length 41;
 Best Local Similarity 77.3%; Pred. No. 2.2e-06;
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 ROIKIWFOVRBMKKKLTALDWS 23
 Db 1 ROIKIWFOVRBMKKKLTALDWFN 22
 RESULT 12
 AAB13423
 ID AAB13423 standard; peptide; 20 AA.
 AC AAB13423;
 XX
 DT 23-NOV-2000 (first entry)
 XX
 DE Synthetic alpha smooth muscle actin inhibitor # 3.
 XX
 KW Alpha smooth muscle actin; alpha-SM; wound contraction;
 KW hypertrophic scar; fibromatosis; Dupuytren disease; fibrotic condition;
 KW lung fibrosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1

```

FT      /note="N-terminal acetyl"
XX      WO200008733-A1.
XX      06-JUL-2000.
XX      15-DEC-1999; 99WO-EP09964.
XX      24-DEC-1998; 98EP-0204396.
XX      (UNIO ) UCB-BIOPRODUCTS SA.
XX      Gabblant G, Scarso A;
XX      WPI, 2000-452308/39.
XX      A peptidic product for prevention and treatment of a disease related to
XX      alpha-SM actin expression comprises a tetrapeptide associated with a
XX      chemical entity that is able to introduce the tetrapeptide into the
XX      cell -
XX      Claim 7; Page 23; 31pp; English.
XX      The present invention relates to novel peptides comprising of a specific
XX      tetrapeptide associated with an oligopeptide which allows the
XX      introduction of the tetrapeptide into the target cell. The present
XX      sequence is one such peptide. Residues 1 to 4 of the present sequence
XX      correspond to the specific tetrapeptide, while residues 5 to 20
XX      correspond to the oligopeptide. The specific tetrapeptide of the present
XX      sequence interferes with alpha smooth muscle (alpha-SM) actin
XX      organisation in stress fibers. The present sequence may be used in the
XX      prevention and/or treatment of a disease related to alpha-SM actin
XX      expression, e.g. wound contraction, hypertrophic scars, fibromatosis and
XX      fibrotic conditions. The present sequence may also be used to treat
XX      Dupuyren disease and lung fibrosis.
XX      Sequence 20 AA;
SQ      Query Match 60.5%; Score 98; DB 21; Length 20;
        Best Local Similarity 100.0%; Pred. No. 1.9e-06;
        Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 DRQIKWIFQNRBMKMKK 17
        : |||||
        4 DRQIKWIFQNRBMKMKK 20
DB      RESULT 13
        AAM11630
        ID AAM11630 standard; peptide; 26 AA.
        XX
        AC AAM11630;
        XX
        DT 16-OCT-1997 (first entry)
        XX
        DE Anti-apoptotic protein blocking peptide FP2.
        XX
        KM Cell permeable; apoptocosis; blocking; inhibition; tumour growth;
        KM ex vivo purging; in vivo administration; Bcl-2.
        XX
        OS Synthetic.
        XX
        FH Key Location/Qualifiers
        FT Peptide 1..17
        PT Peptide /label= sig_peptide
        XX
        PN DB19526174-A1.
        XX
        PD 23-JAN-1997.
        XX
        PE 18-JUL-1995; 95DE-1026174.
        XX
        PR 18-JUL-1995; 95DE-1026174.

```

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XX      (BRAC/) BRACH M.
XX      PA (HERR/) HERRMANN F.
XX      PA (KIER/) KIERHNTOPF M.
XX      PI Brach M, Herrmann F, Kierhntopf M;
XX      WPI, 1997-088160/09.
XX      Peptide(s) that block anti-apoptotic proteins - useful for
XX      inhibiting tumour growth
XX      Claim 6; Page 7; 7pp; German.
XX      The present sequence is a cell permeable anti-apoptotic protein
XX      blocking peptide, which can be used to inhibit tumour growth, e.g.
XX      by ex vivo purging or (after stabilisation) in vivo
XX      administration. The peptide preferably blocks Bcl-2, and comprises
XX      a signal peptide mediating cell penetration and a functional
XX      sequence corresponding to a Bcl-2 domain.
XX      Sequence 26 AA;
SQ      Query Match 60.5%; Score 98; DB 18; Length 26;
        Best Local Similarity 89.5%; Pred. No. 2.5e-06;
        Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY      1 DRQIKWIFQNRBMKMKKTA 19
        : |||||
        1 BRQIKWIFQNRBMKMKKAA 19
DB      RESULT 14
        AAY79919
        ID AAY79919 standard; Peptide; 34 AA.
        XX
        AC AAY79919;
        XX
        DT 10-MAY-2000 (first entry)
        XX
        DE Human papillomavirus 16 E2 fusion peptide Ant-WP.
        XX
        KM Papillomavirus; PV; infection; cell proliferation; E2; peptidomimetic;
        KM E1; antiviral; virucide; cytostatic; antiproliferative; dermatological;
        KM preneoplastic lesion; neoplastic lesion; cutaneous lesion; wart;
        KM epidermodysplasia verruciformis; anorectal carcinoma.
        XX
        OS Human papillomavirus.
        OS Synthetic.
        XX
        PN WO200001720-A2.
        XX
        PD 13-JAN-2000.
        XX
        PE 02-JUL-1999; 99WO-US15144.
        XX
        PR 02-JUL-1998; 98US-0091661.
        XX
        PA (HARD ) HARVARD COLLEGE.
        XX
        PI Howley P, Benson J, Kasukawa H;
        XX
        DR WPI, 2000-171001/15.
        XX
        PT Use of papillomavirus E2 protein peptidomimetics for treating
        PT papillomavirus-infected cells and papillomavirus-induced conditions in
        PT mammals by inhibiting E1-E2 interaction
        XX
        PS Disclosure; P43 13; 110pp; English.
        XX
        CC The present invention describes the use of a small organic compound (A)
        CC which competitively inhibits interaction of a papillomavirus (PV) E2
        CC protein with a PV E1 protein for treating a cell infected with PV or a

```

CC mammal with a PV-induced condition. (A) has antiviral, virucide,
CC cytotoxic, antiproliferative and dermatological activities. Methods
CC from the present invention can be used to treat PV-induced conditions
CC including growth of PV preneoplastic and neoplastic lesions, cutaneous
CC lesions chosen from warts and other benign cutaneous lesions, plantar
CC warts (verruca plantaris), common warts (verruca plana), Butcher's
CC common warts, flat warts, genital warts (condyloma acuminatum) and
CC epidermodysplasia verruciformis, laryngeal, oral, pharyngeal,
CC esophageal and other upper airway papilloma or vaginal, cervical,
CC vulvar, penile and anorectal carcinoma. The B2 inhibitors may also be
CC used to treat epithelial and internal fibropapillomas in animals.
CC The present sequence represents a peptide sequence used in the
CC exemplification of the present invention.

XX Sequence 34 AA;

Query Match 59.9%; Score 97; DB 21; Length 34;
Best Local Similarity 64.3%; Pred. No. 4.5e-06;
Matches 18; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
QY 1 DRQIKIWFQNRMRMKKKTALDWSMLQTE 28
:|||||:|||||:|:|
DB 1 ERQIKIWFQNRMRMKKKG--WKHWRLE 26

RESULT 15

AAE31836
ID AAE31836 standard; peptide; 26 AA.

XX AAE31836;

XX 07-MAR-2003 (first entry)

XX Androgen receptor binding peptide #87.

XX Androgen receptor; androgen-associated disorder; prostate cancer; acne;
XX benign prostatic hypertrophy; hirsutism; androgen insensitivity syndrome;
XX male pattern baldness; Stein-Leventhal syndrome; infertility; cytotoxic;
XX X-linked spinal bulbar muscular atrophy; anti-seborrheic; dermatological;
XX depilatory; androgen receptor binding peptide.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"
FT 26
FT Modified-site /note= "C-terminal amide"

XX WO200272612-A2.

XX 19-SEP-2002.

XX 12-MAR-2002; 2002WO-US07487.

XX 12-MAR-2001; 2001US-275240P.

XX 28-JAN-2002; 2002US-352399P.

XX (PRAE-) PRAECIS PHARM INC.

XX Joyal JL, Mueller J, Oza VB, Findels MA,

XX WPI, 2003-067363/06.

XX New peptide modulators of androgen receptor, useful for treating
XX androgen-associated disorder, e.g. prostate cancer, particularly
XX hormonally refractive prostate cancer, colon cancer, lung cancer, acne,
XX or hirsutism -

XX Example; Page 30; 68pp; English.

XX The present invention relates to novel peptide modulators of androgen
XX receptor. The peptides of the invention are useful for treating androgen-

CC associated disorders such as prostate cancer, particularly hormonally
CC refractive prostate cancer, colon cancer, lung cancer, benign prostatic
CC hypertrophy, acne, hirsutism, male pattern baldness, Stein-Leventhal
CC syndrome, androgen insensitivity syndrome, infertility, endometrial
CC cancer and X-linked spinal bulbar muscular atrophy. The present sequence
CC is an androgen receptor binding peptide.

XX Sequence 26 AA;

Query Match 59.3%; Score 96; DB 24; Length 26;
Best Local Similarity 77.3%; Pred. No. 4.6e-06;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 RQIKIWFQNRMRMKKKTALDWS 23
:|||||:|||||:|:|
DB 1 RQIKIWFQNRMRMKKKTALDWS 22

Search completed: February 18, 2004, 14:26:27
Job time : 107.289 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 32.9737 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162
Sequence: 1 DRQIKIWFQNRMRKKTALDMSWLQTE 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97.9	59.9	34	4	US-09-347-504-79
2	95.6	58.6	24	4	US-09-419-826-34
3	94.0	58.0	27	4	US-09-040-725A-2
4	94.0	58.0	61	2	US-08-202-044-3
5	94.0	58.0	61	3	US-08-751-344B-3
6	94.0	58.0	61	3	US-08-751-344B-6
7	94.0	58.0	61	3	US-08-751-344B-9
8	93.4	57.4	22	4	US-09-057-363C-50
9	93.4	57.4	27	3	US-09-051-934-51
10	93.4	57.4	27	3	US-09-051-934-52
11	93.4	57.4	61	3	US-08-751-344B-7
12	92.6	56.6	16	2	US-08-928-958-7
13	92.6	56.6	16	2	US-08-810-540-3
14	92.6	56.6	16	2	US-08-810-540-6
15	92.6	56.6	16	2	US-09-072-429-7
16	92.6	56.6	16	3	US-08-964-302A-6
17	92.6	56.6	16	3	US-09-116-294-4
18	92.6	56.6	16	3	US-08-964-614A-4
19	92.6	56.6	16	3	US-08-849-486-1
20	92.6	56.6	16	3	US-08-849-486-4
21	92.6	56.6	16	3	US-09-208-966-54
22	92.6	56.6	16	3	US-09-308-935-8
23	92.6	56.6	16	3	US-09-441-416A-6
24	92.6	56.6	16	4	US-09-296-089-33
25	92.6	56.6	16	4	US-09-419-826-35
26	92.6	56.6	16	4	US-09-302-305C-10
27	92.6	56.6	16	4	US-09-346-847-1

28	92	56.8	16	4	US-09-346-847-25	Sequence 25, Appl
29	92	56.8	16	4	US-09-057-363C-47	Sequence 47, Appl
30	92	56.8	16	4	US-09-043-560B-3	Sequence 3, Appl
31	92	56.8	17	4	US-09-346-847-17	Sequence 17, Appl
32	92	56.8	17	4	US-09-346-847-20	Sequence 20, Appl
33	92	56.8	17	4	US-09-346-847-22	Sequence 22, Appl
34	92	56.8	17	4	US-09-346-847-27	Sequence 27, Appl
35	92	56.8	18	3	US-08-838-545-20	Sequence 20, Appl
36	92	56.8	18	3	US-09-349-533-20	Sequence 20, Appl
37	92	56.8	19	4	US-09-346-847-23	Sequence 23, Appl
38	92	56.8	19	4	US-09-658-517C-7	Sequence 7, Appl
39	92	56.8	20	4	US-09-468-772-3	Sequence 3, Appl
40	92	56.8	20	4	US-09-346-847-16	Sequence 16, Appl
41	92	56.8	20	4	US-09-346-847-18	Sequence 18, Appl
42	92	56.8	20	4	US-09-346-847-30	Sequence 30, Appl
43	92	56.8	20	4	US-09-658-517C-8	Sequence 8, Appl
44	92	56.8	22	4	US-09-346-847-28	Sequence 28, Appl
45	92	54.9	42	3	US-08-751-344B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-347-504-79
; Sequence 79, Application US/09347504
; Patent No. 6399075
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; TITLE OF INVENTION: KASUKAWA, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/09/347,504
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-504-79

Query Match 59.9%; Score 97; DB 4; Length 34;
Best Local Similarity 64.3%; Pred. No. 1.9e-06;
Matches 18; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Cy 1 DRQIKIWFQNRMRKKTALDMSWLQTE 28
Db 1 DRQIKIWFQNRMRKKTALDMSWLQTE 26

RESULT 2
US-09-419-826-34
; Sequence 34, Application US/09419826
; Patent No. 6306832
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDE ANTISTROGEN COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR TREATING BREAST CANCER
; NUMBER OF SEQUENCES: 39
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/419,826
; FILING DATE: 14-OCT-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/07711
; FILING DATE: 14-APR-1998

APPLICATION NUMBER: US 60/043,545
FILING DATE: 14-APR-1997
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 19
OTHER INFORMATION: /note= "X = Phosphotyrosine"
US-09-419-826-34

Query Match 58.6%; Score 94; DB 4; Length 24;
Best Local Similarity 89.5%; Pred. No. 2,4e-06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRMKKTALD 21
DB 1 RQIKWIFQNRMRMKKELXD 20

RESULT 3
US-09-040-725A-2
Sequence 2, Application US/09040725A
Patent No. 6399584
GENERAL INFORMATION:
APPLICANT: Institut Curie
APPLICANT: CNRS
APPLICANT: Arpin, Monique
APPLICANT: Crepaldi, Tiziana
APPLICANT: Gautreau, Alexis
APPLICANT: Louvard, Daniel
TITLE OF INVENTION: Pharmaceutical composition containing ezrin mutated
TITLE OF INVENTION: on tyrosine 353
FILE REFERENCE: 39108200100
CURRENT APPLICATION NUMBER: US/09/040.725A
CURRENT FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (22)
OTHER INFORMATION: Xaa = tyrosine or a phosphorylated tyrosine
US-09-040-725A-2

Query Match 58.0%; Score 94; DB 4; Length 27;
Best Local Similarity 89.5%; Pred. No. 3,6e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRMKKTAL 20
DB 1 RQIKWIFQNRMRMKKRL 19

RESULT 4
US-08-202-044-3
Sequence 3, Application US/08202044
Patent No. 5858973
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square

CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,044
FILING DATE: 23-FEB-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: MGH-124XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-202-044-3

Query Match 58.0%; Score 94; DB 2; Length 61;
Best Local Similarity 94.1%; Pred. No. 8,4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKWIFQNRMRMKK 17
DB 43 EROIKWIFQNRMRMKK 59

RESULT 5
US-08-751-344B-3
Sequence 3, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-NOV-6210960-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-751-344B-3

Query Match 58.0%; Score 94; DB 3; Length 61;
Best Local Similarity 94.1%; Pred. No. 8.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRKMKKK 17
:|||||
DB 43 ERQIKIWFQNRKMKKK 59

RESULT 6
US-08-751-344B-6
Sequence 6, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-751-344B-6

Query Match 58.0%; Score 94; DB 3; Length 61;
Best Local Similarity 94.1%; Pred. No. 8.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRQIKIWFQNRKMKKK 17

DB 43 ERQIKIWFQNRKMKKK 59
:|||||

RESULT 7
US-08-751-344B-9
Sequence 9, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-751-344B-9

Query Match 58.0%; Score 94; DB 3; Length 61;
Best Local Similarity 94.1%; Pred. No. 8.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRKMKKK 17
:|||||
DB 43 ERQIKIWFQNRKMKKK 59

RESULT 8
US-09-057-363C-50
Sequence 50, Application US/09057363C
Patent No. 6551994
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle

```
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,363C
FILING DATE: 08-Apr-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Christensen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 100086.406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-057-363C-50

Query Match          57.4%; Score 93; DB 3; Length 22;
Best Local Similarity 94.1%; Pred. No. 3.9e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFONRKMKKK 17
Db 6 NRQIKWFONRKMKKK 22

RESULT 9
US-09-051-934-51
Sequence 51, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide inhibitors of a phosphotyrosine-binding domain
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 27
TYPE: PRT
ORGANISM: phosphotyrosine binding domain
US-09-051-934-51

Query Match          57.4%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. No. 4.9e-06;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWFONRKMKKTLAD 21
Db 1 RQIKWFONRKMKKGLIE 20

RESULT 10
US-09-051-934-52
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Sequence 52, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide inhibitors of a phosphotyrosine-binding domain
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52
LENGTH: 27
TYPE: PRT
ORGANISM: phosphotyrosine binding domain
FEATURE:
NAME/KEY: MOD RES
LOCATION: [24]
OTHER INFORMATION: Phosphorylated at Tyr
US-09-051-934-52

Query Match          57.4%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. No. 4.9e-06;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWFONRKMKKTLAD 21
Db 1 RQIKWFONRKMKKGLIE 20

RESULT 11
US-08-751-344B-7
Sequence 7, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
FILE REFERENCE:
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-NOV-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-7

Query Match 57.4%; Score 93; DB 3; Length 61;
Best Local Similarity 88.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIFONRRMKKK 17
DB 43 ERQVKIFONRRMKKK 59

RESULT 12

US-08-928-958-7
Sequence 7, Application US/08928958
Patent No. 5877282
GENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
APPLICANT: CLEVELAND, JEFFREY S.
APPLICANT: BLAKE, JAMES
APPLICANT: HAFER, OMAR K.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
TITLE OF INVENTION: TRANSLLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026978
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 345-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-928-958-7

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ROIKIFONRRMKKK 17
DB 1 ROIKIFONRRMKKK 16

RESULT 13
US-08-810-540-3
Sequence 3, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-3

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ROIKIFONRRMKKK 17
DB 1 ROIKIFONRRMKKK 16

RESULT 14
US-08-810-540-6
Sequence 6, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-391-0526
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-6

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ROIKWFONRBMKWK 17
DB 1 ROIKWFONRBMKWK 16

RESULT 15

US-09-072-429-7
Sequence 7, Application US/09072429
Patent No. 5962415
GENERAL INFORMATION:
APPLICANT: Nadler, Steven G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN
TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,429
FILING DATE: 04-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Klein, Christopher A.
REGISTRATION NUMBER: 34,363
REFERENCE/DOCKET NUMBER: C00141b
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 252-3714
TELEFAX: (609) 252-4526
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-072-429-7

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ROIKWFONRBMKWK 17
DB 1 ROIKWFONRBMKWK 16

Search completed: February 18, 2004, 14:41:52
Job time : 33.9737 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignment)
41.814 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41

Sequence: 1 IDMEWL 6

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	41	100.0	6	23	AAW48522
3	41	100.0	6	23	AAW48542
4	41	100.0	6	23	AAW48614
5	41	100.0	6	24	ABU08432
6	41	100.0	7	23	AAW48618
7	41	100.0	8	23	AAW48611
8	41	100.0	8	23	AAW48619
9	41	100.0	9	23	AAW48610

10	41	100.0	9	23	AAW48613	Anti-inflammatory
11	41	100.0	9	23	AAW48616	Anti-inflammatory
12	41	100.0	9	23	AAW48617	Anti-inflammatory
13	41	100.0	10	23	AAW48612	Anti-inflammatory
14	41	100.0	10	23	AAW48615	Anti-inflammatory
15	41	100.0	11	23	AAW48609	Anti-inflammatory
16	41	100.0	11	23	ABW77307	Human IKKbeta muta
17	38	92.7	12	21	AAW07057	Human IKKbeta muta
18	38	92.7	24	22	AAU56674	Proteinlactone
19	37	90.2	20	23	AAU90327	Insulin/insulin-11
20	37	90.2	70	22	ABG49130	Human liver peptid
21	37	90.2	70	22	AAW67482	Human bone marrow
22	37	90.2	70	22	AAW27770	Peptide #1807 enco
23	37	90.2	70	23	ABG37095	Human peptide enco
24	37	90.2	210	20	AAW28793	Schizosaccharomyce
25	37	90.2	354	24	ABJ37451	Benzodiazepines bi
26	37	90.2	379	22	AAW96114	Putative P. abyssi
27	37	90.2	408	22	AAW96440	Putative P. abyssi
28	37	90.2	692	22	AAU04851	Micromonospora eve
29	37	90.2	1291	22	ABW71544	Drosophila melanog
30	36	87.8	6	23	ABW08725	IKKbeta NEMO bindi
31	36	87.8	6	23	AAW48530	Anti-inflammatory
32	36	87.8	6	23	AAW48655	NBD mutant peptide
33	36	87.8	6	24	ABU08418	Human NEMO binding
34	36	87.8	7	23	AAW48534	Anti-inflammatory
35	36	87.8	8	23	AAW48527	Anti-inflammatory
36	36	87.8	8	23	AAW48535	Anti-inflammatory
37	36	87.8	9	20	AAW96182	IKK-alpha polypept
38	36	87.8	9	23	AAW48526	Anti-inflammatory
39	36	87.8	9	23	AAW48529	Anti-inflammatory
40	36	87.8	9	23	AAW48532	Anti-inflammatory
41	36	87.8	9	23	AAW48533	Anti-inflammatory
42	36	87.8	10	23	ABW77313	IKKbeta NEMO bindi
43	36	87.8	10	23	AAW48528	Anti-inflammatory
44	36	87.8	10	23	AAW48531	Anti-inflammatory
45	36	87.8	11	23	ABW77311	Human NBD peptide

ALIGNMENTS

RESULT 1
ABB08739
ID ABB08739 standard; peptide; 6 AA.

AC ABB08739;
DT 14-JUN-2002 (first entry)

Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 17.

IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; leukocyte; inflammation; E-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive; osteopathic; cyclostatic; nootropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virocidic; antiaspartic; antiallergic; dermatological; antibacterial; antipneumatic; antirheumatic; antichronic; osteopathic; antitumor; mutant; mutatin.

OS Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
Misc-difference /note= "Wildtype Ser substituted by Glu"

WO200183547-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US40654.
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYTA) UNITV YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprising contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 PS Claim 23; Page 45; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB077313). The compound has access through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of I-kappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC polyarthritis. Also for Crohn's disease, ulcerative colitis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 QY 1 LDMEWL 6
 DB 1 LDMEWL 6
 Query Match 100.0%; Score 41; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 2
 AAM48522
 ID AAM48522 standard; Peptide: 6 AA.
 XX
 AC AAM48522;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DB NBD mutant peptide SEQ ID NO 17.

XX
 XX Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; vitruclide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; I-kappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECTIS PHARM INC.
 PA (UYTA) UNITV YALE.
 XX
 PI May MJ, Ghosh S, Fandels MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Example 6; Page 48; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48620-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, vitruclide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of I-kappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of I-kappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease, atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 QY 1 LDMEWL 6
 DB 1 LDMEWL 6
 Query Match 100.0%; Score 41; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 AAM48542
 ID AAM48542 standard; Peptide: 6 AA.

XX AA48542;
AC
XX
XX 20-MAR-2002 (first entry)
DE Anti-inflammatory peptide SEQ ID NO 45.
XX
XX Antiinflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;
XX antiinflammatory; antiaesthetic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX 02-MAY-2000; 2000US-201261P.
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
PI
XX MPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX
XX Claim 6; Page 61; 88pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
CC AA48628-AA48645), comprising a membrane translocation domain
CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AA48525-AA48619). The antiinflammatory compounds have antiaesthetic,
CC cyostatic, antipsoriatic, antirheumatic, antiallergic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX Sequence 6 AA;
SO

Query Match 100.0%; Score 41; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LDWEML 6
||||||

DB 1 LDWEML 6
RESULT 4
XX AA48614
XX ID AA48614 standard; Peptide; 6 AA.
XX
XX AA48614;
AC
XX
XX 20-MAR-2002 (first entry)
DE Anti-inflammatory peptide SEQ ID NO 117.
XX
XX Antiinflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;
XX antiinflammatory; antiaesthetic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX 02-MAY-2000; 2000US-201261P.
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
PI
XX MPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX
XX Claim 6; Page 62; 88pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
CC AA48628-AA48645), comprising a membrane translocation domain
CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AA48525-AA48619). The antiinflammatory compounds have antiaesthetic,
CC cyostatic, antipsoriatic, antirheumatic, antiallergic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX Sequence 6 AA;
SO

Query Match 100.0%; Score 41; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMEWL 6
 |||||
 Db 1 LDMEWL 6

RESULT 5
 ABU08432 ID ABU08432 standard; peptide: 6 AA.

XX AC ABU08432;
 XX DT 12-JUN-2003 (first entry)
 XX XX

DE Human NEMO binding site (NBD) mutant peptide #15.

XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW translocation detection; immunosuppressive; osteopathic;
 KW cyostatic; neutrotrophic; antiatherosclerotic; virucide;
 KW vasotrophic; antirheumatic; antiarthritic; mutant; muteln.

XX OS Homo sapiens.
 OS Synthetic.

PN US2002156000-A1.

PD 24-OCT-2002.

PF 02-MAY-2001; 2001US-0847940.

XX 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (MAYM/) MAY M J.

PA (GHOSH/) GHOSH S.

PI May MJ, Ghosh S;

XX WPI; 2003-209142/20.

PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT creating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -

PS Claim 22; Page 17; 47pp; English.

XX The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplant rejection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.

Sequence 6 AA;
 Query Match 100.0%; Score 41; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMEWL 6
 |||||
 Db 1 LDMEWL 6

RESULT 6
 AAM48618 ID AAM48618 standard; peptide: 7 AA.

XX AC AAM48618;

XX DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 121.

XX Antiinflammatory; antiasthmatic; cyostatic; antiporiatic; neutrotrophic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neutrotrophic; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NPkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAEIS PHARM INC.

PA (UYVA) UNIV YALE.

PI May MJ, Ghosh S, Finkel MA, Phillips K;

XX WPI; 2002-121889/16.

PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for creating asthma, lung inflammation,
 PT psoriasis -

PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antiporiatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neutrotrophic,
 CC neutrotrophic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IKKbeta. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, utticaria, anaphylaxis.

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 41; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LDWEML 6
 Db 1 LDWEML 6
 RESULT 7
 ID AAM48611 standard; Peptide; 8 AA.
 XX AAM48611;
 AC
 XX 20-MAR-2002 (first entry)
 DT
 XX
 DE Anti-inflammatory peptide SEQ ID NO 114.
 KM Antinflammatory; antiaesthetic; cyostatic; antiporiatic; nootropic;
 KM antithematic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findels MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 PT Novel antinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antinflammatory compound (especially
 CC AAM48628-AAM48651), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiaesthetic,
 CC cyostatic, antiporiatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis; multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 41; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LDWEML 6
 Db 3 LDWEML 8
 RESULT 8
 ID AAM48619 standard; Peptide; 8 AA.
 AC AAM48619;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 122.
 KM Antinflammatory; antiaesthetic; cyostatic; antiporiatic; nootropic;
 KM antithematic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findels MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 PT Novel antinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiaesthetic,
 CC cyostatic, antiporiatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated Nf-kappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis,
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
SQ Sequence 8 AA;
Query Match 100.0%; Score 41; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWEWL 6
DB 1 LDWEWL 6
RESULT 9
AA48610
ID AA48610 standard; Peptide; 9 AA.
XX
AC AA48610;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 113.
XX
KW Antinflammatory; antiasthmatic; cytosolic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; Nf-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
XX
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis
XX
PS Claim 6; Page 62; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AA48658-AA48645), comprising a membrane translocation domain

CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
CC cytosolic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virocidic and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated Nf-kappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis,
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
SQ Sequence 9 AA;
Query Match 100.0%; Score 41; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWEWL 6
DB 1 LDWEWL 6
RESULT 10
AA48613
ID AA48613 standard; Peptide; 9 AA.
XX
AC AA48613;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 116.
XX
KW Antinflammatory; antiasthmatic; cytosolic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; Nf-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
XX
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis

PR 22-AUG-2000, 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI, 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PT
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 SQ Sequence 9 AA;
 QY
 Query Match 100.0%; Score 41; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 LDWEML 6
 2 LDWEML 7
 RESULT 13
 AAM48612
 ID AAM48612 standard; Peptide; 10 AA.
 XX
 AC AAM48612;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 115.
 XX
 KM Antinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; nootropic;
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 KM
 OS Synthetic.
 XX
 XX
 PN WO200183554-A2.

XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001, 2001WO-US14346.
 XX
 PR 02-MAY-2000, 2000US-201261P.
 XX 22-AUG-2000, 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI, 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PT
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
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 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 SQ Sequence 10 AA;
 QY
 Query Match 100.0%; Score 41; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 4.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 LDWEML 6
 2 LDWEML 7
 RESULT 14
 AAM48615
 ID AAM48615 standard; Peptide; 10 AA.
 XX
 AC AAM48615;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 118.
 XX
 KM Antinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; nootropic;
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;

KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX 02-MAY-2000; 2000US-201261P.
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S, Findels MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
XX psoriasis -
XX
XX Claim 6; Page 62; 88pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
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CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 41; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMEWL 6
| | | | |
| | | | |
Db 3 LDMEWL 8
| | | | |
| | | | |
RESULT 15
AAM48609
ID AAM48609 standard; Peptide; 11 AA.
XX
XX AAM48609;
AC
XX
XX 20-MAR-2002 (first entry)
DT
XX Anti-inflammatory peptide SEQ ID NO 112.
XX
XX Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;
KM

KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM autoimmune disorder; multiple sclerosis; transplant rejection;
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX 02-MAY-2000; 2000US-201261P.
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S, Findels MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
XX psoriasis -
XX
XX Claim 6; Page 62; 88pp; English.
XX
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CC activation and subsequent decreased phosphorylation of IkappaB. The
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CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX Sequence 11 AA;
SQ
Query Match 100.0%; Score 41; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMEWL 6
| | | | |
| | | | |
Db 3 LDMEWL 8
| | | | |
| | | | |

Search completed: February 18, 2004, 14:26:26
Job time : 22.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-16
Sequence: 1 LDMAWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	173	16	Q8E5U2
2	40	100.0	173	16	Q8E5U2
3	40	100.0	173	16	Q8E5U2
4	38	95.0	173	16	Q8E5U2
5	37	92.5	173	16	Q8E5U2
6	37	92.5	173	16	Q8E5U2
7	37	92.5	173	16	Q8E5U2
8	36	90.0	173	16	Q8E5U2
9	36	90.0	173	16	Q8E5U2
10	36	90.0	173	16	Q8E5U2
11	36	90.0	173	16	Q8E5U2
12	36	90.0	173	16	Q8E5U2
13	36	90.0	173	16	Q8E5U2
14	36	90.0	173	16	Q8E5U2
15	36	90.0	173	16	Q8E5U2
16	36	90.0	173	16	Q8E5U2

17	36	90.0	524	10	Q42700
18	36	90.0	1044	10	Q9FEB1
19	36	90.0	1083	13	Q90W08
20	36	90.0	1083	13	Q8AXU2
21	36	90.0	1100	13	Q90W09
22	36	90.0	1127	13	Q9W615
23	36	90.0	1212	16	Q9HX70
24	36	90.0	1575	2	P94904
25	35	87.5	162	16	Q53756
26	35	87.5	204	16	Q9KER2
27	35	87.5	282	16	Q8D354
28	35	87.5	288	2	Q8V714
29	35	87.5	299	16	Q9H218
30	35	87.5	308	2	Q8KX52
31	35	87.5	311	16	Q92W07
32	35	87.5	313	2	Q8VU06
33	35	87.5	318	16	Q8ZC58
34	35	87.5	329	16	Q8XV84
35	35	87.5	331	16	P94904
36	35	87.5	337	16	Q8UB44
37	35	87.5	341	16	Q8G3A8
38	35	87.5	344	16	Q8YEH7
39	35	87.5	353	16	Q9A7R0
40	35	87.5	385	16	Q92U27
41	35	87.5	393	16	Q87ZL1
42	35	87.5	394	10	Q9M0Y4
43	35	87.5	418	10	Q944N8
44	35	87.5	418	10	Q9M0Y3
45	35	87.5	439	2	Q93Q61

ALIGNMENTS

RESULT 1	Q8E5U2	PRELIMINARY:	PRT:	173 AA.
AC	Q8E5U2	01-MAR-2003 (TRENBLREL. 23, Created)		
DT	01-MAR-2003 (TRENBLREL. 23, Last sequence update)			
DT	01-MAR-2003 (TRENBLREL. 23, Last annotation update)			
DE	Hypothetical protein.			
GN	GBS0887.			
OS	Streptococcus agalactiae (serotype III).			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=216495;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NEW316 / Serotype III;			
RX	MEDLINE=22242508; PubMed=12354221;			
RA	Glaser P., Ruenlokk C., Buchrieser C., Chevalier F., Frangeul L.,			
RA	Madek T., Zouine M., Couve E., Lallou L., Poyart C., Titeu-Cuot P.,			
RA	Kunst F.;			
RT	"Genome sequence of Streptococcus agalactiae, a pathogen causing			
RT	invasive neonatal disease.";			
RT	Mol. Microbiol. 45:1499-1513(2002).			
DR	EMBL; AL766847; CAD46531.1; -.			
KW	Sageliet; gbs0887; -.			
DR	Hypothetical protein; Complete proteome.			
SQ	SEQUENCE 173 AA; 20135 MW; F5F3404F0224CD1 CRC64;			
QY	Query Match	100.0%; Score 40; DB 16; Length 173;		
DB	Best local similarity	100.0%; Pred. No. 48;		
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
	1 LDMAWL 6			
	125 LDMAWL 130			
RESULT 2	Q8E065			

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ID Q9E065 PRELIMINARY; PRT; 173 AA.
AC Q9E065;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Acetyltransferase, GNAI family.
GN SAG0870.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCB1_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RC MEDLINE=22222988; PubMed=12200547;
RA Tetteijn H., Maingnan I.T., Cieslewicz M.J., Bisen J.A., Peterson S.,
RA Wessels M.R., Pulgen I.T., Nelson K.E., Margalit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Ralume D., Fedorova N.B., Scanlan D., Khouli H., Mulligan S.,
RA Carey H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Jacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rapunoli R., Telford J.L., Kaepfer D.L., Grandi G.,
RA Frazer C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014231; AAM9756.1; -.
DR TIGR; SAG0870; -.
KW Transferrase; Complete proteome.
SQ SEQUENCE 173 AA; 20135 MW; 0081677125975921 CRC64;

Query Match 100.0%; Score 40; DB 16; Length 173;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
Db 125 LDMAML 130

RESULT 3
ID Q9X6C6 PRELIMINARY; PRT; 645 AA.
AC Q9X6C6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-galactosidase.
GN BGA7.
OS Thermus brockianus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCB1_TaxID=56956;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IT1360;
RC MEDLINE=99402735; PubMed=10473401;
RA "Cloning of the gene encoding a novel thermostable alpha-galactosidase
RA from Thermus brockianus IT1360.";
RT Appl. Environ. Microbiol. 65:3955-3963(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IT1360;
RC MEDLINE=20203878; PubMed=10741834;
RA Fildjoneson O., Matzlawick H., Mattes R.;
RT "The structure of the alpha-galactosidase gene loci in Thermus
RT brockianus IT1360 and Thermus thermophilus TH125.";
RL Extremophiles 4:23-33(2000).
DR EMBL; AF135398; AAD3667.1; -.
DR InterPro; IPR001554; Glyco_hydro_14.
DR InterPro; IPR003476; Glyco_hydro_42.

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DR Pfam; PF01373; Glyco_hydro_14; 1.
DR Pfam; PF02449; Glyco_hydro_42; 1.
SQ SEQUENCE 645 AA; 73420 MW; C79A9BIC0020BC40 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 645;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
Db 48 LDMAML 53

RESULT 4
ID Q96XZ8 PRELIMINARY; PRT; 396 AA.
AC Q96XZ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative anaerobic glycerol-3-phosphate dehydrogenase subunit C.
GN ST2369.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCB1_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX PubMed=11572479; Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RX Kawarabayashi Y., Baba S.-I., Anka A., Kosugi H., Hosoyama A., Fukui S.,
RX Sekine M., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Kato Y.,
RX Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kuchida N., Oguchi A.,
RX Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RX Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000989; BAB67479.1; -.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR004017; DUF224.
DR Pfam; PF02754; DUF224; 2.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 396 AA; 45359 MW; 15301A2AF22DC9F CRC64;

Query Match 95.0%; Score 38; DB 17; Length 396;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
Db 94 LDMAML 99

RESULT 5
ID Q95KV1 PRELIMINARY; PRT; 740 AA.
AC Q95KV1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ikb kinase-alpha.
GN BIKKALPHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCB1_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC Rottenberg S., Dobbelaere D.A.B., Heusler V.T.;

```

RT "Identification and characterisation of the bovine IKB kinases (IKKs)
 RT alpha, beta and gamma." to the EMBL/GenBank/DBJ databases.
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AJ414555; CAC93686.1; -
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SMO0220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 740 AA; 84343 MW; 01903BE1F44D176 CRC64;
 SQ

Query Match 92.5%; Score 37; DB 6; Length 740;
 Best Local Similarity 83.3%; Pred. No. 5.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMAML 6
 |||:|
 Db 733 LDMAML 738

RESULT 6
 Q8CBT3 PRELIMINARY; PRT; 745 AA.
 ID Q8CBT3;
 AC Q8CBT3;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Conserved helix-loop-helix ubiquitous kinase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=urinary bladder;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RANTOM Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK035326; BAC29034.1; -
 SQ SEQUENCE 745 AA; 84770 MW; 48C9B01C17A61184 CRC64;
 SQ

Query Match 92.5%; Score 37; DB 11; Length 745;
 Best Local Similarity 83.3%; Pred. No. 5.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMAML 6
 |||:|
 Db 738 LDMAML 743

RESULT 7
 Q95KVO PRELIMINARY; PRT; 756 AA.
 ID Q95KVO;
 AC Q95KVO;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE IKB kinase-beta.
 GN BIKKBEA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Rottendy S.; Dobbelaere D.A.E.; Heusler V.T.;
 RT "Identification and characterisation of the bovine IKB kinases (IKKs)
 RT alpha, beta and gamma." to the EMBL/GenBank/DBJ databases.
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AJ414556; CAC93687.1; -
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;
 SQ

Query Match 92.5%; Score 37; DB 6; Length 756;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMAML 6
 |||:|
 Db 737 LDMAML 742

RESULT 8
 Q9QRU7 PRELIMINARY; PRT; 27 AA.
 ID Q9QRU7;
 AC Q9QRU7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE E2 glycoprotein hypervariable region (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B-AS;
 RA Yeh C.-T.;
 RT "Replication of hepatitis C virus in the acetic mononuclear cells and
 RT development of distinct quasispecies in the acetic fluid."
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF109742; AAD51573.1; -
 DR F0N_TER 1
 FT NON_TER 1
 SQ SEQUENCE 27 AA; 2964 MW; 8A68DCDC25CE4FAB CRC64;
 SQ

Query Match 90.0%; Score 36; DB 12; Length 27;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMAML 6
 |||:|
 Db 12 DMAML 16

RESULT 9
 Q9QRU6 PRELIMINARY; PRT; 27 AA.
 ID Q9QRU6;
 AC Q9QRU6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE E2 glycoprotein hypervariable region (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=MO;
 RA Yeh C.-T.;
 RT "Replication of hepatitis C virus in the ascitic mononuclear cells and development of distinct quasi-species in the ascitic fluid.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF109743; AAD51574.1; -.
 FT NON_TER 1 1
 FT NON_TER 27 27
 SQ SEQUENCE 27 AA; 2964 MW; 8A68DCDC25CE4FAB CRC64;
 Query Match 90.0%; Score 36; DB 12; Length 27;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWAML 6
 Db 12 DWAML 16

RESULT 10
 Q96ZU3 PRELIMINARY; PRT; 207 AA.
 AC Q96ZU3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cheapsin B-like protease (Fragment).
 OS Trypanosoma rangeli.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 ON NCBI_TaxID=5698;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SC 58;
 RA Nobrega O.T., Teixeira A.R.L., Campbell D.A., Santana J.M.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF400046; AAK65411.1; -.
 DR MEROPS; C01.098; -.
 DR InterPro; IPR000668; Peptidase_C1.
 DR InterPro; IPR00169; SHPOT_acs1te.
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR PRINTS; PR00705; PAPAIN.
 DR ProDom; PD000158; Peptidase_C1; 1.
 DR SMART; SM00645; Pept_C1; 1.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 KM Hydrolyase; Protease; Thiol protease.
 FT NON_TER 1 1
 FT NON_TER 207 207
 SQ SEQUENCE 207 AA; 22968 MW; 7AF0D95D5F81C5B CRC64;
 Query Match 90.0%; Score 36; DB 5; Length 207;
 Best Local Similarity 100.0%; Pred. No. 2,3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWAML 6
 Db 71 DWAML 75

RESULT 11
 Q9V227 PRELIMINARY; PRT; 215 AA.
 AC Q9V227;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Purine phosphoribosyltransferase.
 OS GPTA OR PAB2405.
 ON Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 ON NCBI_TaxID=29292;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GES / Orsay;
 RA Hellig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ248283; CAB49171.1; -.
 DR HSSP; Q2697; 10K3.
 DR InterPro; IPR000836; PRTtransferase.
 DR Pfam; PF00156; Pribosyltran; 1.
 KM Glycosyltransferase; Transferase; Complete proteome.
 SQ SEQUENCE 215 AA; 24832 MW; A58D71EBBD5FD723 CRC64;
 Query Match 90.0%; Score 36; DB 17; Length 215;
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAML 6
 Db 141 LDWAML 146

RESULT 12
 O07806 PRELIMINARY; PRT; 251 AA.
 AC O07806;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Phosphotransferase (Aminoglycoside 3'-phosphotransferase).
 GN RV3817 OR MTCY409.13C OR MT3925.1.
 ON Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 ON NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Biglietier K., Gas S., Barry C.B. III, Tekle F., Badcock K., Baeham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S., Hornsby F., Jagsels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborn J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
 RL Nature 393:537-544 (1998).
 RT [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A., Bishai W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z97186; CAB10016.1; -.
 DR EMBL; AE007186; AAK48292.1; -.
 DR TIGR; MT3925; -.
 DR Tuberculisc; RV3817; -.
 DR InterPro; IPR002575; APH.
 DR Pfam; PF01636; APH; 1.
 KM Transferase; Complete proteome.
 SQ SEQUENCE 251 AA; 27241 MW; 52807FDA006A21B3 CRC64;
 Query Match 90.0%; Score 36; DB 16; Length 251;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNAME 6
DB 86 DNAME 90

RESULT 13

Q91719 PRELIMINARY; PRT; 304 AA.
AC Q91719;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Probable cytochrome c oxidase assembly factor.
GN PA013.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltz L., Tolentino B., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Spencer S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Coulter D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RT Nature 406:959-964(2000).
DR EMBL; AE004449; AAC03503.1; -;
DR InterPro; IPR006369; Cyoe_Ctab.
DR InterPro; IPR000537; UblA-
DR TIGRPFAM; TIGR01473; Cyoe_Ctab; 1.
DR PROSITE; PS00943; UblA; 1.
KW Complete proteome.

Query Match 90.0%; Score 36; DB 16; Length 304;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNAME 5
DB 259 LDNAME 263

RESULT 14

Q8UBG8 PRELIMINARY; PRT; 316 AA.
AC Q8UBG8;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE ABC transporter, membrane spanning protein.
GN ATU3048 OR AGR L 3514.
OS Aerobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN
RP SEQUENCE FROM N.A.
RP MEDLINE=21608550; PubMed=11743193;
RX Wood D.W., Secubal J.C., Kaul R., Monks D.E., Kiraajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.B., Almeida N.F.Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. St.,
RA Chapman P., Clendenning J., Decherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-C., McClelland E., Palmeri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-X., Dolan M.,
RA Chunmley F., Tingey S.V., Tomb S.-F., Gordon M.F., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RT Science 294:2317-2323(2001).

Q91719 PRELIMINARY; PRT; 444 AA.
AC Q91719;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative integral membrane sugar transporter.
GN CZA382.17C.
OS Amycolatopsis orientalis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.
OX NCBI_TaxID=31958;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Leonard N., Harris B.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Leonard N., Jones M., Jones S., Solenberg P.;
RT "Sequencing and analysis of genes involved in the biosynthesis of a
RT vancomycin group antibiotic.";
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; AL076635; CAB45038.1; -;
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transp.
DR Pfam; PF00083; sugar_tr; 1.
DR PROSITE; PS00850; MFS; 1.
KW Sugar transport; Transmembrane.

RESULT 15

Q91719 PRELIMINARY; PRT; 444 AA.
AC Q91719;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative integral membrane sugar transporter.
GN CZA382.17C.
OS Amycolatopsis orientalis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.
OX NCBI_TaxID=31958;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Leonard N., Harris B.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Leonard N., Jones M., Jones S., Solenberg P.;
RT "Sequencing and analysis of genes involved in the biosynthesis of a
RT vancomycin group antibiotic.";
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; AL076635; CAB45038.1; -;
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transp.
DR Pfam; PF00083; sugar_tr; 1.
DR PROSITE; PS00850; MFS; 1.
KW Sugar transport; Transmembrane.

SEQ SEQUENCE 444 AA; 48039 MM; 51ACE2D9EB121EDA CRC64;

Query Match 90.0%; Score 36; DB 2; Length 444;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAW 5

DB 194 LDWAW 198

Search completed: February 18, 2004, 14:35:58
Job time : 18.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds

(without alignments)
(75.239 Million cell updates/sec)

Title: US-09-643-260-16

Perfect score: 40

Sequence: 1 LDMAWL 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	6	10 US-09-847-940B-16	Sequence 16, Appl
2	40	100.0	6	11 US-09-847-946A-16	Sequence 16, Appl
3	40	100.0	6	11 US-09-847-946A-44	Sequence 44, Appl
4	40	100.0	6	11 US-09-847-946A-106	Sequence 106, Appl
5	40	100.0	7	11 US-09-847-946A-110	Sequence 110, Appl
6	40	100.0	8	11 US-09-847-946A-103	Sequence 103, Appl
7	40	100.0	8	11 US-09-847-946A-111	Sequence 111, Appl
8	40	100.0	9	11 US-09-847-946A-102	Sequence 102, Appl
9	40	100.0	9	11 US-09-847-946A-105	Sequence 105, Appl
10	40	100.0	9	11 US-09-847-946A-108	Sequence 108, Appl
11	40	100.0	9	11 US-09-847-946A-109	Sequence 109, Appl
12	40	100.0	10	11 US-09-847-946A-104	Sequence 104, Appl
13	40	100.0	10	11 US-09-847-946A-107	Sequence 107, Appl
14	40	100.0	11	11 US-09-847-946A-101	Sequence 101, Appl
15	37	92.5	6	10 US-09-847-940B-2	Sequence 2, Appl

15	37	92.5	6	11	US-09-847-946A-2	Sequence 2, Appl
17	37	92.5	6	11	US-09-847-946A-33	Sequence 33, Appl
18	37	92.5	7	11	US-09-847-946A-37	Sequence 37, Appl
19	37	92.5	8	11	US-09-847-946A-30	Sequence 30, Appl
20	37	92.5	8	11	US-09-847-946A-38	Sequence 38, Appl
21	37	92.5	9	11	US-09-847-946A-29	Sequence 29, Appl
22	37	92.5	9	11	US-09-847-946A-32	Sequence 32, Appl
23	37	92.5	9	11	US-09-847-946A-35	Sequence 35, Appl
24	37	92.5	10	11	US-09-847-946A-36	Sequence 36, Appl
25	37	92.5	10	11	US-09-847-946A-31	Sequence 31, Appl
26	37	92.5	11	11	US-09-847-946A-34	Sequence 34, Appl
27	37	92.5	11	11	US-09-847-946A-28	Sequence 28, Appl
28	37	92.5	11	11	US-09-847-946A-132	Sequence 132, Appl
29	37	92.5	11	11	US-09-847-946A-140	Sequence 140, Appl
30	37	92.5	13	11	US-09-847-946A-143	Sequence 143, Appl
31	37	92.5	13	11	US-09-847-946A-144	Sequence 144, Appl
32	37	92.5	13	11	US-09-847-946A-145	Sequence 145, Appl
33	37	92.5	13	11	US-09-847-946A-148	Sequence 148, Appl
34	37	92.5	17	11	US-09-847-946A-141	Sequence 141, Appl
35	37	92.5	17	11	US-09-847-946A-142	Sequence 142, Appl
36	37	92.5	17	11	US-09-847-946A-146	Sequence 146, Appl
37	37	92.5	17	11	US-09-847-946A-147	Sequence 147, Appl
38	37	92.5	18	11	US-09-847-946A-131	Sequence 131, Appl
39	37	92.5	18	11	US-09-847-946A-135	Sequence 135, Appl
40	37	92.5	18	11	US-09-847-946A-136	Sequence 136, Appl
41	37	92.5	22	11	US-09-847-946A-133	Sequence 133, Appl
42	37	92.5	22	11	US-09-847-946A-134	Sequence 134, Appl
43	37	92.5	22	11	US-09-847-946A-137	Sequence 137, Appl
44	37	92.5	22	11	US-09-847-946A-138	Sequence 138, Appl
45	37	92.5	22	11	US-09-847-946A-139	Sequence 139, Appl

ALIGNMENTS

RESULT 1
US-09-847-940B-16
Sequence 16, Application US/09847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPL-117CP
CURRENT APPLICATION NUMBER: US/09/847.940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-16

Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LDMAWL 6
Db 1 LDMAWL 6

RESULT 2
US-09-847-946A-16
Sequence 16, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J

```
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-16
```

```
Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 LDMAWL 6
        |||||
Db      1 LDMAWL 6
```

```
RESULT 3
US-09-847-946A-44
Sequence 44, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-44
```

```
Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 LDMAWL 6
        |||||
Db      1 LDMAWL 6
```

```
RESULT 4
US-09-847-946A-106
Sequence 106, Application US/09847946A
Publication No. US20030054999A1
```

```
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 106
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-106
```

```
Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 LDMAWL 6
        |||||
Db      1 LDMAWL 6
```

```
RESULT 5
US-09-847-946A-110
Sequence 110, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 110
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-110
```

```
Query Match          100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 LDMAWL 6
        |||||
Db      1 LDMAWL 6
```

```
RESULT 6
```

```
US-09-847-946A-103
; Sequence 103, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Finkelstein, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-103

Query Match          100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
DB 3 LDWAWL 8

RESULT 7
US-09-847-946A-111
; Sequence 111, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Finkelstein, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-111

Query Match          100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
DB 1 LDWAWL 6
```

```
RESULT 8
US-09-847-946A-102
; Sequence 102, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Finkelstein, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-102

Query Match          100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
DB 1 LDWAWL 6

RESULT 9
US-09-847-946A-105
; Sequence 105, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Finkelstein, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-105

Query Match          100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 LDMAML 6
Db 1 LDMAML 6

RESULT 10

US-09-847-946A-108
; Sequence 108, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-108

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAML 6
Db 3 LDMAML 8

RESULT 11

US-09-847-946A-109
; Sequence 109, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-109

Query Match 100.0%; Score 40; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDMAML 6
Db 2 LDMAML 7

RESULT 12

US-09-847-946A-104
; Sequence 104, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-104

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAML 6
Db 2 LDMAML 7

RESULT 13

US-09-847-946A-107
; Sequence 107, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-107

US-09-847-946A-107

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAML 6
DB 3 LDWAML 8

RESULT 14

US-09-847-946A-101
; Sequence 101, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Flindeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NEMO binding
US-09-847-946A-101

Query Match 100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAML 6
DB 3 LDWAML 8

RESULT 15

US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-2

Query Match 92.5%; Score 37; DB 10; Length 6;

Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAML 6
DB 1 LDMSWL 6

Search completed: February 18, 2004, 15:42:01
Job time: 17.7529 secs

PF	02-MAY-2001; 2001MO-US40654.
XX	
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(UYVA) UNIV YALE.
XX	
PI	May MJ, Ghosh S;
XX	
DR	WPI: 2002-1179350/23.
XX	
PT	Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT	inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT	cell with an anti-inflammatory compound comprising at least one NEMO
PT	binding domain -
PS	
PS	Claim 23; Page 45; 82pp; English.
XX	
XX	The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
XX	comprises contacting a cell with an anti-inflammatory compound
CC	(ABB087125-ABB08742) comprising at least one NEMO binding domain
CC	(ABB077113). The compound has acts through selective inhibition of
CC	cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC	with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC	interaction results in inhibition of IKKbeta kinase activation and
CC	subsequent decreased phosphorylation of I-kappaB. The compound may also
CC	act (directly or indirectly) by blocking the recruitment of leukocytes
CC	into sites of acute and chronic inflammation, by down-regulating the
CC	expression of E-selectin on leukocytes or by blocking osteoclast
CC	differentiation. The compound is useful in treating NF-kB mediated
CC	conditions, where the condition is an inflammatory disorder, an
CC	autoimmune disease, transplant rejection, osteoporosis, cancer,
CC	Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC	telangiectasias. The inflammatory disorder is asthma, allergies,
CC	urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC	rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC	bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC	burns. The inflammatory disorder may also be dermatitis, eczema,
CC	psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC	spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC	polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC	cryoglobulinemia or multiple sclerosis. For chronic viral infections
CC	caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC	diseases include HIV and influenza. The compound may also be useful for
CC	treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC	sunburn or aging. The compound may be used to replace corticosteroids in
CC	any application in which corticosteroids are used, including
CC	immunosuppression in transplants and cancer therapy. Also for identifying
CC	antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC	The compound may be administered alone or in combination with other known
CC	anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC	binding domain of IKKbeta.
XX	
XX	
SQ	Sequence 6 AA;
XX	
QY	1 LDMAWL 6
DB	1 LDMAWL 6
XX	
RESULT 2	
AA	AA048521
XX	AA048521 standard; peptide; 6 AA.
XX	AA048521;
XX	20-MAR-2002 (first entry)
XX	
DE	NBD mutant peptide SEQ ID NO 16.

XX Antinflammatory; antiaesthetic; cytosratic; antipsoriatic; nootropic;
 XX antirheumatic; antiarthritic; osteopathic; antibacterial; vitruide;
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 XX autoimmune disorder; multiple sclerosis; transplant rejection;
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 OS Synthetic.
 XX WO200183554-A2.
 PN 08-NOV-2001.
 XX
 PD 02-MAY-2001; 2001WO-US14346.
 XX
 PF 02-MAY-2000; 2000US-201261P.
 PR 22-NOV-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECTIS PHARM INC.
 XX (UTYA) UNIV YALE.
 XX
 P1 May MJ, Ghosh S, Findels MA, Phillips K;
 DR WPI; 2002-12189/16.
 XX
 PT Novel antinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Example 6; Page 48; 88pp; English.
 XX
 CC The invention relates to an antinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiaesthetic,
 CC cytosratic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antietherosclerotic, vitruide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 SQ Sequence 6 AA;
 OY
 DB 1 LDMAWL 6
 1 LDMAWL 6
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 AAM48541
 ID AAM48541 standard; Peptide; 6 AA.

XX AAM48541;
AC 20-MAR-2002 (first entry)
XX
XX
DE Anti-inflammatory peptide SEQ ID NO 44.
XX
XX
XX Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;
XX antiinflammatory; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
XX WO200183554-A2.
XX
XX PD 08-NOV-2001.
XX
XX PF 02-MAY-2001; 2001WO-US14346.
XX
XX PR 02-MAY-2000; 2000US-201261P.
XX PR 22-AUG-2000; 2000US-0643260.
XX
XX PA (PRAE-) PRAECIS PHARM INC.
XX PA (UYA) UNIV YALE.
XX
XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX DR Novel antiinflammatory compound comprising membrane translocation
XX domain fused to NEMO binding sequence, useful for blocking nuclear
XX factor kappaB activation, and for treating asthma, lung inflammation,
XX psoriasis -
XX
XX PS Claim 6; Page 61; 88pp; English.
XX
XX CC The invention relates to an antiinflammatory compound (especially,
XX AAM48628-AAM48645), comprising a membrane translocation domain
XX (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
XX amino acid residues, fused to a NEMO binding sequence
XX (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
XX cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
XX antibacterial, immunosuppressive, dermatological, neuroprotective,
XX nootropic, antiatherosclerotic, virucide and antiallergic activity. The
XX compounds act as selective inhibitors of cytokine-mediated NFkappaB
XX activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
XX the NEMO binding domain that results in inhibition of IKKbeta kinase
XX activation and subsequent decreased phosphorylation of IkappaB. The
XX compounds are useful for treating inflammatory disorders, e.g. asthma,
XX lung inflammation or cancer, psoriasis, rheumatoid arthritis,
XX osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
XX bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
XX granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
XX Alzheimer's disease; atherosclerosis; viral infections; and ataxia
XX telangiectasia. The compounds are also useful for treating
XX pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
XX drug or food sensitivity, eczema, dermatitis, sunburn, aging and
XX arthritis.
XX
XX SO Sequence 6 AA;
Query Match 100.0%; Score 40; DB 23; Length 6;
Best local similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 LDMAWL 6
RESULT 4
AAM48603
ID AAM48603 standard; Peptide; 6 AA.
XX
XX AAM48603;
XX
XX 20-MAR-2002 (first entry)
XX
XX DE Anti-inflammatory peptide SEQ ID NO 106.
XX
XX
XX Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;
XX antiinflammatory; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX OS Synthetic.
XX WO200183554-A2.
XX
XX PN 08-NOV-2001.
XX
XX PD 02-MAY-2001; 2001WO-US14346.
XX
XX PF 02-MAY-2000; 2000US-201261P.
XX PR 22-AUG-2000; 2000US-0643260.
XX
XX PA (PRAE-) PRAECIS PHARM INC.
XX PA (UYA) UNIV YALE.
XX
XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX DR Novel antiinflammatory compound comprising membrane translocation
XX domain fused to NEMO binding sequence, useful for blocking nuclear
XX factor kappaB activation, and for treating asthma, lung inflammation,
XX psoriasis -
XX
XX PS Claim 6; Page 62; 88pp; English.
XX
XX CC The invention relates to an antiinflammatory compound (especially
XX AAM48628-AAM48645), comprising a membrane translocation domain
XX (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
XX amino acid residues, fused to a NEMO binding sequence
XX (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
XX cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
XX antibacterial, immunosuppressive, dermatological, neuroprotective,
XX nootropic, antiatherosclerotic, virucide and antiallergic activity. The
XX compounds act as selective inhibitors of cytokine-mediated NFkappaB
XX activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
XX the NEMO binding domain that results in inhibition of IKKbeta kinase
XX activation and subsequent decreased phosphorylation of IkappaB. The
XX compounds are useful for treating inflammatory disorders, e.g. asthma,
XX lung inflammation or cancer, psoriasis, rheumatoid arthritis,
XX osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
XX bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
XX granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
XX Alzheimer's disease; atherosclerosis; viral infections; and ataxia
XX telangiectasia. The compounds are also useful for treating
XX pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
XX drug or food sensitivity, eczema, dermatitis, sunburn, aging and
XX arthritis.
XX
XX SO Sequence 6 AA;

Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 LDMAML 6
 1 LDMAML 6

RESULT 5
 ABU08431
 ID ABU08431 standard; peptide; 6 AA.
 XX
 AC ABU08431;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human NEMO binding site (NBD) mutant peptide #14.
 XX
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytotoxic; neutrotropic; neuroprotective; antiatherosclerotic; virucide;
 KW vabotropic; antirheumatic; antiarthritic; mutant; mutain.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2002156000-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 02-MAY-2001; 2001US-0847940.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2003-209142/20.
 XX
 PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX
 PS Claim 22; Page 17; 47pp; English.
 XX
 CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 CC
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 40; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 LDMAML 6
 1 LDMAML 6

RESULT 6
 AAM48607
 ID AAM48607 standard; peptide; 7 AA.
 XX
 AC AAM48607;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 110.
 XX
 KW Antiinflammatory; antiaesthetic; cytotoxic; antiporiatic; neutrotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 OS
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Finkels MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytotoxic, antiporiatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neutrotropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC granulitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis, transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 40; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAWL 6
 Db 1 LDMAWL 6

RESULT 7
 AAM48600 standard; Peptide; 8 AA.
 XX
 AC AAM48600;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 103.
 XX
 KM Antiinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; nootropic;
 KM antineumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; Nfkappab; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findels MA, Phillips K;
 XX
 DR WPI, 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappab activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytoskeletal, antipsoriatic, antineumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated Nfkappab
 CC activation by blocking interaction of Ikappab kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of Ikappab. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAWL 6
 Db 3 LDMAWL 8

RESULT 8
 AAM48608 standard; Peptide; 8 AA.
 XX
 AC AAM48608;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 111.
 XX
 KM Antiinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; nootropic;
 KM antineumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; Nfkappab; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findels MA, Phillips K;
 XX
 DR WPI, 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappab activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytoskeletal, antipsoriatic, antineumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated Nf-kappaB
CC activation by blocking interaction of I-kappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of I-kappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.

CC
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 40; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAWL 6
Db 1 LDMAWL 6

RESULT 9
AAM48599
ID AAM48599 standard; Peptide; 9 AA.
XX
AC AAM48599;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 102.
XX
KW Anti-inflammatory; antiallergic; cytoprotective; antiparasitic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; Nf-kappaB; I-kappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
XX
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI, 2002-121889/16.
XX
PT Novel anti-inflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis
XX
XX
PS Claim 6, Page 62; 88pp; English.
XX
CC The invention relates to an anti-inflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiallergic,
CC cytoprotective, antiparasitic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated Nf-kappaB
CC activation by blocking interaction of I-kappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of I-kappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.

CC
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAWL 6
Db 1 LDMAWL 6

RESULT 10
AAM48602
ID AAM48602 standard; Peptide; 9 AA.
XX
AC AAM48602;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 105.
XX
KW Anti-inflammatory; antiallergic; cytoprotective; antiparasitic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; Nf-kappaB; I-kappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
XX
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
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PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI, 2002-121889/16.
XX
PT Novel anti-inflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis

PT psoriasis -
XX
XX Claim 6; Page 62; 88pp; English.
XX
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CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytoskeletal, antiproliferative, antirheumatic, antiarthritic, osteoparathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neurotropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursts; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMANL 6
DB 1 LDMANL 6
RESULT 11
AAM48605
ID AAM48605 standard; Peptide; 9 AA.
XX
XX AAM48605;
AC
XX
XX 20-MAR-2002 (first entry)
DT
XX
DE Anti-inflammatory peptide SEQ ID NO 108.
XX
XX Anti-inflammatory; antiasthmatic; cytoskeletal; antiproliferative; neurotropic;
XX anti-rheumatic; antiarthritic; osteoparathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
OS
XX
PN WO200183554-A2.
XX
XX 08-NOV-2001.
PD
XX
XX 02-MAY-2001; 2001WO-US14346.
PF
XX
XX 02-MAY-2000; 2000US-201261P.
PR
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S, Finkelstein MA, Phillips K,
PI

XX
DR WPI; 2002-121889/16.
XX
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX Claim 6; Page 62; 88pp; English.
XX
XX
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CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytoskeletal, antiproliferative, antirheumatic, antiarthritic, osteoparathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neurotropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursts; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMANL 6
DB 3 LDMANL 8
RESULT 12
AAM48606
ID AAM48606 standard; Peptide; 9 AA.
XX
XX AAM48606;
AC
XX
XX 20-MAR-2002 (first entry)
DT
XX
DE Anti-inflammatory peptide SEQ ID NO 109.
XX
XX Anti-inflammatory; antiasthmatic; cytoskeletal; antiproliferative; neurotropic;
XX anti-rheumatic; antiarthritic; osteoparathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
OS
XX
PN WO200183554-A2.
XX
XX 08-NOV-2001.
PD
XX
XX 02-MAY-2001; 2001WO-US14346.
PF
XX 02-MAY-2000; 2000US-201261P.
PR

PR	22-AUG-2000; 2000US-0643260.
XX	(PRAE-) PRAECIS PHARM INC.
PA	(UYIA) UNIT YALE.
XX	
PI	May MJ, Ghosh S, Findels MA, Phillips K;
XX	WPI; 2002-121889/16.
DR	
XX	
PT	Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis -
PS	Claim 6; Page 62; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAW48620-AAW48645), comprising a membrane translocation domain
CC	(AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAW48525-AAW48619). The antiinflammatory compounds have antiasthmatic,
CC	cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteoprotic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective, the
CC	nocrotic, antidiabetic, vitamin D and anti-allergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappa
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	gastrointestinal, autoimmune diseases such as lupus, polyarthritis, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
XX	Sequence 9 AA;
SO	
Query Match	100.0%; Score 40; DB 23; Length 9;
Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Matches 6;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 LDWAWL 6
Db	2 LDWAWL 7
RESULT 13	
AAW48601	
ID	AAW48601 standard; Peptide; 10 AA.
XX	
XX	AAW48601;
XX	
DT	20-MAR-2002 (first entry)
DE	Anti-inflammatory peptide SEQ ID NO 104.
XX	
KW	Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nocrotic;
KW	antirheumatic; antiarthritic; osteoprotic; antibacterial; vitamin D;
KW	immunosuppressive; dermatological; neuroprotective; antidiabetic;
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	
OS	Synthetic.
XX	
PN	WO200183554-A2.

XX 08-NOV-2001.
PD
XX
XX 02-MAY-2001, 2001MO-US14346.
PF
XX
XX 02-MAY-2000, 2000US-201261P.
PR
XX 22-AUG-2000, 2000US-0643260.
PR
XX
XX (PRAE-) PRAEIS PHARM INC.
PA
XX (UYA) UNIV YALB.
PI
XX May MJ, Ghosh S, Findeis MA, Phillips K,
XX
XX WPI, 2002-121869/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX
PS Claim 6, Page 62, 88pp; English.
PS
XX
XX The invention relates to an antiinflammatory compound (especially
CC AA448628-AA448651), comprising a membrane translocation domain
CC (AA448620-AA448627 or AA448646-AA448651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AA448525-AA448619). The antiinflammatory compounds have antiasthmatic,
CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteoprotective,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neurotropic, antiallergic, antineoplastic, virocidic and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
XX
XX Sequence 10 AA;
SQ
XX
XX Query Match 100.0%; Score 40; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 2,7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMAWL 6
|||
|||
Db 2 LDMAWL 7
|||
|||
RESULT 14
AA448604
ID AA448604 standard; Peptide; 10 AA.
XX
XX AA448604;
AC
XX
XX 20-MAR-2002 (first entry)
DT
XX
XX Anti-inflammatory peptide SEQ ID NO 107.
XX
XX Antiinflammatory; antiasthmatic; cytoskeletal; antipsoriatic, neurotropic;
XX antiinflammatory; antiarthritic; osteoprotective; antibacterial; virocidic;
XX immunosuppressive; dermatological; neuroprotective; antiallergic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX

KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 XX
 PN
 PD 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Finkel MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PS
 PS Claim 6; Page 62; 88pp; English.
 CC The invention relates to an antiinflammatory compound (especially
 CC (AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 CC
 SQ Sequence 10 AA;
 XX
 XX
 Query Match 100.0%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.7; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 1 LDMAML 6
 |||||
 Db 3 LDMAML 8
 |||||
 RESULT 15
 AAM48598
 ID AAM48598 standard; Peptide; 11 AA.
 XX
 AC AAM48598;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX
 DE Anti-inflammatory peptide SEQ ID NO 101.
 XX
 KM Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;

KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 XX
 PN
 PD 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Finkel MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PS
 PS Claim 6; Page 62; 88pp; English.
 CC The invention relates to an antiinflammatory compound (especially
 CC (AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 CC
 SQ Sequence 11 AA;
 XX
 XX
 Query Match 100.0%; Score 40; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMAML 6
 |||||
 Db 3 LDMAML 8
 |||||

Search completed: February 18, 2004, 14:26:26
 Job time : 23.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-15

Sequence: 1 LDMSTL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPREMBL.23.*
1: sp_Archaea.*
2: sp_Bacteria.*
3: sp_Fungi.*
4: sp_Human.*
5: sp_Invertebrate.*
6: sp_Mammal.*
7: sp_Mhc.*
8: sp_Organella.*
9: sp_Phage.*
10: sp_Plant.*
11: sp_Rodent.*
12: sp_Virus.*
13: sp_Vertebrate.*
14: sp_Unclassified.*
15: sp_Virus.*
16: sp_Bacteriophage.*
17: sp_Archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	939	16	Q8YGR3
2	36	100.0	1466	3	Q42930
3	34	94.4	317	16	Q8FMV4
4	34	94.4	369	17	Q58160
5	33	91.7	542	3	Q60113
6	32	88.9	75	10	Q94HM4
7	32	88.9	136	16	P72919
8	32	88.9	142	6	Q8HYV0
9	32	88.9	153	16	P73698
10	32	88.9	172	16	Q9RYF2
11	32	88.9	221	10	Q9S403
12	32	88.9	229	17	Q8ZYL1
13	32	88.9	262	10	Q9FNU0
14	32	88.9	278	10	Q9LUT6
15	32	88.9	308	3	Q12010
16	32	88.9	319	5	Q9NEV3

17	32	88.9	337	4	Q95RE6
18	32	88.9	362	5	Q4634
19	32	88.9	393	16	Q9ZKA8
20	32	88.9	409	4	Q8N6M5
21	32	88.9	412	10	Q8RYL7
22	32	88.9	429	12	Q65111
23	32	88.9	438	16	Q8RHMS
24	32	88.9	450	16	Q99R10
25	32	88.9	450	16	Q8NUV5
26	32	88.9	451	16	Q91151
27	32	88.9	455	16	Q8CN46
28	32	88.9	480	16	Q67595
29	32	88.9	497	10	Q9LZ84
30	32	88.9	497	10	Q94EY8
31	32	88.9	505	16	Q8PAX6
32	32	88.9	542	17	Q30147
33	32	88.9	555	16	Q8PMN9
34	32	88.9	561	16	Q9HTJ2
35	32	88.9	567	16	Q8ZGM0
36	32	88.9	573	16	Q8YX11
37	32	88.9	599	10	Q8FHV3
38	32	88.9	620	11	Q8B0G4
39	32	88.9	647	2	Q8YVMS
40	32	88.9	673	4	Q8RTT9
41	32	88.9	708	5	Q9W0D8
42	32	88.9	738	11	Q8VE80
43	32	88.9	793	5	Q9VYV0
44	32	88.9	828	3	Q74240
45	32	88.9	839	10	Q9M0G3

ALIGNMENTS

RESULT 1

Q8YGR3 PRELIMINARY: PRT; 939 AA.
Q8YGR3
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein AL3756.
ANABAENA SP. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
[1]
SEQUENCE FROM N.A.
MEDLINE:21695285; PubMed:11759840;
Kaneke T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iritugu M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120."
DNA Rep. 8:205-213(2001).
EMBL: AP003594; BAB75455.1;
Hypothetical protein; Complete proteome.
SEQUENCE 939 AA; 10423 MW; 8FE0AYCAC1759AS CRC64;

Query Match 100.0%; Score 36; DB 16; Length 939;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSTL 6
|||||
Db 648 LDMSTL 653

RESULT 2
Q42930 PRELIMINARY: PRT; 1466 AA.

No art

AC 042930;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative membrane glycoprotein, possible vacuolar protein sorting
 DE /targeting.
 GN SPBC16C6.06.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 NC NCB1_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972h-;
 RA Punnett B., Goffeau A., Wood V., Lyne M., Barrell B.G.,
 RA Rajadream M.A.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL021767; CA16914.1; -;
 DR GeneDB_Spombe; SPBC16C6.06; -;
 DR InterPro; IPR002860; GH_BNR.
 DR InterPro; IPR006581; VPS10.
 DR Pfam; PF02012; BNR; 12.
 DR SMART; SM00602; VPS10; 2.
 SQ SEQUENCE 1466 AA; 16501 MW; CB315E0F7688D79 CRC64;

Query Match 100.0%; Score 36; DB 3; Length 1466;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6
 Db 1046 LDMSYL 1051

RESULT 3
 ID 08PMV4 PRELIMINARY; PRT; 317 AA.
 AC 08PMV4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Conserved hypothetical protein.
 GN CE2395.
 OS Corynebacterium efficiens.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 NC NCB1_TaxID=152794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Y8-314 / AJ 12310 / DSM 44549 / JCM 11189;
 RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
 RA Ikeyo K., Suzuki M., Maehata J., Itoh T., Yamagishi A., Nishio Y.,
 RA Ueda Y., Sugimoto S.;
 RT "The entire genomic sequence of Corynebacterium efficiens Y8-314.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005222; BAC19205.1; -;
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 317 AA; 33135 MW; 3805BDE05030A81C CRC64;

Query Match 94.4%; Score 34; DB 16; Length 317;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6
 Db 114 LDMSYL 119

RESULT 4
 ID 058160 PRELIMINARY; PRT; 389 AA.
 AC 058160;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein PH0423.
 GN PH0423.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 NC NCB1_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kuhsida N., Oguchi A.,
 RA Aoki K.-I., Yoshitawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 DR EMBL; AP000002; BAA29509.1; -;
 DR InterPro; IPR002814; NTP_transf.
 DR Pfam; PF01909; NTP_transf_2; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 389 AA; 46335 MW; 81F32C817B1A53D4 CRC64;

Query Match 94.4%; Score 34; DB 17; Length 389;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6
 Db 139 LDMSYL 144

RESULT 5
 ID 060113 PRELIMINARY; PRT; 542 AA.
 AC 060113;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Amino acid permease.
 GN SPBC15C4.04C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 NC NCB1_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972h-;
 RA Lyne M., Rajadream M.A., Barrell B.G., Xiang Z., Aves S.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL023290; CA18895.1; -;
 DR GeneDB_Spombe; SPBC15C4.04C; -;
 DR InterPro; IPR002293; AA/rel_permease1.
 DR InterPro; IPR004840; AAC_permease.
 DR InterPro; IPR004756; AA_permease.
 DR InterPro; IPR004841; Permease.
 DR Pfam; PF00324; aa_permeases; 1.
 DR TIGRFAMs; TIGR00907; ZA0304; 1.
 DR PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
 SQ SEQUENCE 542 AA; 59726 MW; 17D9B15C0429468 CRC64;

Query Match 91.7%; Score 33; DB 3; Length 542;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6
 Db 114 LDMSYL 119

Db 436 LDMSYV 441

RESULT 6

Q94HM4 PRELIMINARY; PRT; 75 AA.
 ID 094HM4
 AC 094HM4
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 GN T4M14.6
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Town C.D., Haas B.J., Wu D., Maitl R., Hannick L.I., Chan A.P.,
 RA Tallon L.J., Rooney T., Utteback T.R., Vanaken S.E., Feldblyum T.V.,
 RA White O., Fraser C.M.;
 RT Arabidopsis thaliana chromosome 1 BAC T4M14 genomic sequence.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; ACC27036; AAK62781.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 75 AA; 8834 MW; B34EB28B5C41EBB5 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 75;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5
 |||||
 Db 12 LDMSY 16

RESULT 7

P72919 PRELIMINARY; PRT; 136 AA.
 ID P72919
 AC P72919
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein slr1082.
 GN SLR1082.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OC NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugiyama M., Sasegawa S., Kimura T.,
 RA Hosouchi T., Matsumoto A., Muraki A., Nakazaki N., Nakano K., Okumura S.,
 RA Shimizu S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D90901; BAA16936.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 136 AA; 15774 MW; E80414D06029605E CRC64;

Query Match 88.9%; Score 32; DB 16; Length 136;

Best Local Similarity 83.3%; Pred. No. 2e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6
 |||||
 Db 42 LDMSYL 47

RESULT 8

Q8HYV0 PRELIMINARY; PRT; 142 AA.
 ID Q8HYV0
 AC Q8HYV0
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Glycogen synthase (Fragment).
 GN GYS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA te Pas M.F., Leenhouters J.I., Knol E.F., Booit M., Pliem J.,
 RA van der Lende T.;
 RT "Marker polymorphism in the porcine muscle glycogen synthase (glycogen
 RT synthase 1).";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ507152; CAD47844.1; -
 FT NON_TER 1 142
 FT NON_TER 142 142
 SQ SEQUENCE 142 AA; 15951 MW; C02BAD285F8A7E CRC64;

Query Match 88.9%; Score 32; DB 6; Length 142;

Best Local Similarity 83.3%; Pred. No. 2.1e+02; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSYL 6
 |||||
 Db 83 LDMSYL 88

RESULT 9

P73698 PRELIMINARY; PRT; 153 AA.
 ID P73698
 AC P73698
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein slr1813.
 GN SLR1813.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OC NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugiyama M., Sasegawa S., Kimura T.,
 RA Hosouchi T., Matsumoto A., Muraki A., Nakazaki N., Nakano K., Okumura S.,
 RA Shimizu S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D90908; BAA17745.1; -
 DR InterPro; IPR002636; DUF29.
 DR Pfam; PF01724; DUF29; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 153 AA; 18387 MW; 6B54BB36EDCB9AFL CRC64;

Query Match 88.9%; Score 32; DB 16; Length 153;

Best Local Similarity 83.3%; Pred. No. 2.2e+02; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSYL 6
 |||||
 Db 36 LDMSYL 41

RESULT 10

Q9RYF2 PRELIMINARY; PRT; 172 AA.

AC Q9RYF2, 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein DRA0366.

GN DRA0366.

OS Deinococcus radiodurans.

OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;

OC Deinococcaceae; Deinococcus.

OX NCBI_TaxID=1299;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RI;

RX MEDLINE=20036896; PubMed=10567266;

RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,

RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,

RA Moffat K.S., Qin H., Jiang L., Pamphile W., Croebly M., Shen M.,

RA Vamathevan J.J., Lam P., McDonald L., Uterback T., Zalewski C.,

RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,

RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,

RA Fraser C.M.;

RT "Genome sequence of the radioreistant bacterium Deinococcus

RT radiodurans RI."

RL Science 286:1571-1577(1999).

DR EMBL; AB01863; AAF12501.1; -.

KM Hypothetical protein; Complete proteome.

SO SEQUENCE 172 AA; 19874 MW; CCF8D41ADCF7DC0 CRC64;

Query Match 88.9%; Score 32; DB 16; Length 172;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5

Db 96 LDMSY 100

RESULT 11

Q9SJ03 PRELIMINARY; PRT; 221 AA.

AC Q9SJ03, 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Atg936550 protein.

GN Atg936550.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=20083487; PubMed=10617197;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

RA Buel J.C., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

RA Cronin L.A., Shen M., Vankam S.E., Umayam L., Tallon L.J., Gail J.E.,

RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

RA Copeland G.P., Freus D., Nierman W.C., White O., Eisen J.A.,

RA Salzberg S.L., Fraser C.M., Venter J.C.;

RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis

thaliana."

RL Nature 402:761-768(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RA Lin X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC006919; AAD24637.1; -.

SO SEQUENCE 221 AA; 25043 MW; D3037BC4CC103990 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 221;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5

Db 208 LDMSY 212

RESULT 12

Q8ZYI1 PRELIMINARY; PRT; 229 AA.

AC Q8ZYI1, 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Molybdenum cofactor biosynthesis protein D/E.

GN PAB0727.

OS Pyrobaculum aerophilum.

OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;

OC Pyrobaculaceae; Pyrobaculum.

OX NCBI_TaxID=13773;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=IM2 / ATCC 51768 / DSM 7523;

RX PubMed=11792869;

RA Filtz-Gibson S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,

RA Miller J.H.;

RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum

RT aerophilum."

RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

DR EMBL; AB009782; AAL62982.1; -.

DR InterPro; IPR003448; Mb_biosynth_MoAB.

DR InterPro; IPR003749; THIS.

DR Pfam; PF02391; MoAB; 1.

DR Pfam; PF02597; THIS; 1.

KM Complete proteome.

SO SEQUENCE 229 AA; 25544 MW; 11B06C8F85982EA CRC64;

Query Match 88.9%; Score 32; DB 17; Length 229;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5

Db 60 LDMSY 64

RESULT 13

Q9FNJ0 PRELIMINARY; PRT; 262 AA.

AC Q9FNJ0, 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Genomic DNA, chromosome 5, p1 clone:MDJ22.

OS Arabidopsis thaliana (Mouse-ear cress)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RX MEDLINE=98069011; PubMed=9405937;

RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asanizu E., Miyajima N.,

RA Tabata S.;

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RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
RT Sequence features of the regions of 1,044,062 bp covered by thirteen
RT physically assigned P1 clones."
DL DNA Ref. 4:291-300(1997).
DR EMBL; AB006699; BAB1677.1; -.
DR InterPro; IPR006566; PBD.
DR SMART; SM00579; PBD; 1.
SQ SEQUENCE 262 AA; 30706 MW; CE1SDDB92CD3CCB9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 10; Length 262;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSYL 6
DB 46 DMSYL 50

RESULT 14
Q9LUT6 PRELIMINARY; PRT; 278 AA.
AC Q9LUT6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE Gb|AAD32889.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Sato S.; Nakamura Y.; Kaneko T.; Kato T.; Asamizu E.; Tabata S.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones."
DL DNA Ref. 7:131-135(2000).
DR EMBL; AB022216; BAB02739.1; -.
SQ SEQUENCE 278 AA; 31217 MW; A16AE1E0910484B2 CRC64;

Query Match
Best Local Similarity 88.9%; Score 32; DB 10; Length 278;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5
DB 217 LDMSY 221

RESULT 15
Q12010 PRELIMINARY; PRT; 308 AA.
AC Q12010;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Chromosome XV reading frame ORF YOL092W.
GN YOL092W.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycas.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Zumeitein E.; Pearson B.M.; Kalogeropoulos A.; Schweitzer M.;

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RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=96021609; PubMed=8533473;
RA Zumeitein E.; Pearson B.M.; Kalogeropoulos A.; Schweitzer M.;
RT "A 29.425 kb segment on the left arm of Yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames."
RL Yeast 11:975-986(1995).
DR EMBL; 274834; CAA99104.1; -.
DR EMBL; X83121; CAA58187.1; -.
DR SGD; S0005452; YOL092W.
DR InterPro; IPR006603; CTNS.
DR SMART; SM00679; CTNS; 2.
SQ SEQUENCE 308 AA; 34872 MW; 38EB1645FA034812 CRC64;

Query Match
Best Local Similarity 88.9%; Score 32; DB 3; Length 308;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSYL 6
DB 267 LDMSYL 272

Search completed: February 18, 2004, 14:35:57
Job time : 19.3684 secs

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6
|||||
Db 1046 LDMSYL 1051

RESULT 3
ydas protein - Escherichia coli (strain K-12)
H64885
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: H64885
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
A.; Rose, D.J.; Mau, B.; Shaoh, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64885
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <BLAT>
A:Cross-references: GB:AE000233; GB:U00096; NID:G1787613; PIDN:AAC74439.1; PID:G1787620;
C:Experimental source: strain K-12, substrain M61655
C:Genetics:
A:Gene: ydas

Query Match 94.4%; Score 34; DB 2; Length 98;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6
|||||
Db 67 LDMSYL 72

RESULT 4
H71152
hypothetical protein PH0423 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: H71152
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Sekit
M.; Ohnuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: H71152
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-389 <KAN>
A:Cross-references: GB:AF000002; NID:G3236129; PIDN:BAA29509.1; PID:G3256826
A:Experimental source: strain OT3
A>Note: this accession replaces an interim accession for a sequence replaced by Genbank
C:Genetics:
A:Gene: PH0423
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0423

Query Match 94.4%; Score 34; DB 2; Length 389;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6
|||||
Db 139 LDMSYL 144

RESULT 5
H69798
conserved hypothetical protein yecK - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: H69798

R:Kunet, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bert
C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; C
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Erington, J.; Faderl, C.; Ferrari, E
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fume, S.; Galazzi, A.; Gall
tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidos, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maude, S.; Maue
Y., M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlo
A:Authors: Schleich, S.; Schreier, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Ser
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tozato, V.; Uchiyam
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A:Authors: Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A:Reference number: A63580; MUID:98044033; PMID:9384377
A:Accession: H69798
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-330 <KUN>
A:Cross-references: GB:299107; GB:AL009126; NID:G2632866; PIDN:CAB12540.1; PID:G263303
A:Experimental source: strain 168
C:Genetics:
A:Gene: yecK
C:Superfamily: hypothetical protein yed

Query Match 91.7%; Score 33; DB 1; Length 330;
Best Local Similarity 83.3%; Pred. No. 97;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6
|||||
Db 239 LDMSYL 244

RESULT 6
T39474
amino acid permease - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T39474
R:Lyne, M.; Rejandram, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.
submitted to the EMBL Data Library, May 1998
A:Reference number: Z21857
A:Accession: T39474
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-542 <LYN>
A:Cross-references: EMBL:AL023290; PIDN:CA18895.1; GSPDB:GN00067; SPDB:SPBC15C4.04C
A:Experimental source: strain 972h-; cosmid cl5C4
C:Genetics:
A:Gene: SPDB:SPBC15C4.04C
A:Map position: 2
C:Superfamily: choline transport protein

Query Match 91.7%; Score 33; DB 2; Length 542;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6
|||||
Db 436 LDMSYL 441

RESULT 7
S74785
hypothetical protein slr1082 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C:Accession: S74785
R:Kaneko, T.; Sato, S.; Kocani, H.; Tanaka, A.; Asamitsu, E.; Nakamura, Y.; Miyajima, N
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yaeu

DNA Ref. 3, 109-136, 1996
 A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S74785
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-136 <KAN>
 A/Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAAL6936.1; PID:g165201
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C/Superfamily: *Synechocystis* hypothetical protein slr0489

Query Match 88.9%; Score 32; DB 2; Length 136;
 Best Local Similarity 83.3%; Pred. No. 59;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6
 |||||
 Db 42 LDMSFL 47

RESULT 8
 S77187
 hypothetical protein slr1813 - *Synechocystis* sp. (strain PCC 6803)
 C/Species: *Synechocystis* sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 C/Accession: S77187
 R/Kanehiko, T.; Sato, S.; Kozani, H.; Tanaka, A.; Asamiu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Ref. 3, 109-136, 1996
 A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S77187
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-153 <KAN>
 A/Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAAL7745.1; PID:g165282
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C/Superfamily: hypothetical protein slr1203

Query Match 88.9%; Score 32; DB 2; Length 153;
 Best Local Similarity 83.3%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSYL 6
 |||||
 Db 36 LDMEYL 41

RESULT 9
 A75592
 hypothetical protein - *Deinococcus radiodurans* (strain R1)
 C/Species: *Deinococcus radiodurans*
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
 C/Accession: A75592
 R/White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Usterback, T.; Zalewski, C.; Ma, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A>Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: A75592
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-172 <WHI>
 A/Cross-references: GB:AB001863; GB:AE001825; NID:g6460670; PIDN:AAFL3501.1; PID:g646079
 A/Experimental source: strain R1
 C/Genetics:
 A/Map position: 2
 C/Superfamily: *Deinococcus radiodurans* hypothetical protein DRA0366

Query Match 88.9%; Score 32; DB 2; Length 172;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 5
 |||||
 Db 96 LDMSY 100

RESULT 10
 H84781
 hypothetical protein At2g36550 (imported) - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C/Accession: H84781
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentli, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A/Reference number: A84420; MUID:20083487; PMID:10617197
 A/Accession: H84781
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-221 <STO>
 A/Cross-references: GB:AE002093; NID:g4581153; PIDN:AAD24637.1; GSPDB:GN00139
 C/Genetics:
 A/Map position: 2

Query Match 88.9%; Score 32; DB 2; Length 221;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 5
 |||||
 Db 208 LDMSY 212

RESULT 11
 T40878
 probable FAD synthetase - fission yeast (*Schizosaccharomyces pombe*)
 C/Species: *Schizosaccharomyces pombe*
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C/Accession: T40878
 R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harte, D.
 submitted to the EMBL Data Library, September 1998
 A/Reference number: Z21954
 A/Accession: T40878
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-265 <WOO>
 A/Cross-references: EMBL:AL031764; PIDN:CAN21108.1; GSPDB:GN00068; SPDB:SPCC1235.04C
 A/Experimental source: strain 972h-; cosmid c1235
 C/Genetics:
 A/Map position: 3
 A/Introns: 46/2; 182/3

Query Match 88.9%; Score 32; DB 2; Length 265;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 5
 |||||
 Db 173 LDMSY 177

RESULT 12
 S57377
 probable membrane protein YOL092w - yeast (*Saccharomyces cerevisiae*)
 N/Alternate names: hypothetical protein O0929; protein YBR17w homolog

C/Species: *Saccharomyces cerevisiae*
 C/Date: 28-Oct-1999 #sequence_revision 03-Nov-1995 #text_change 19-Apr-2002
 C/Accession: S57377; S6786; S50413
 R/Zumstede, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
 Yeast 11, 975-986, 1995
 A/Title: A 29.425 kb segment on the left arm of yeast chromosome XV contains more than 6
 A/Reference number: S57374; MUID:96021609; PMID:8533473
 A/Accession: S57377
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-308 <ZMW>
 A/Cross-references: EMBL:X83121, NID:G600461, PIDN:CA58187.1, PID:G600466
 R/Zumstede, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
 submitted to the Protein Sequence Database, July 1996
 A/Reference number: S66775
 A/Accession: S66786
 A/Molecule type: DNA
 A/Residues: 1-308 <ZMW>
 A/Cross-references: EMBL:Z74834, NID:G141937, PID:G141938; MIPS:YOL092W
 A/Experimental source: strain S288C
 C/Genetics:
 A/Cross-references: SGD:S0005452
 A/Map position: 15L
 C/Superfamily: *Saccharomyces* probable membrane protein YBR147W
 C/Keywords: transmembrane protein
 F/14-30/Domain: transmembrane #status predicted <TM1>
 F/45-61/Domain: transmembrane #status predicted <TM2>
 F/73-89/Domain: transmembrane #status predicted <TM3>
 F/168-184/Domain: transmembrane #status predicted <TM4>
 F/248-265/Domain: transmembrane #status predicted <TM5>
 F/278-294/Domain: transmembrane #status predicted <TM6>

Query Match 88.9%; Score 32; DB 2; Length 308;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSYL 6
 DB 267 LDMSYL 272

RESULT 13
 132659
 hypothetical protein F16B4.2 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 R/Davidson, S.; Wohldmann, P.; Bauer, C.; O'Neal, D.
 submitted to the EMBL Data Library, December 1997
 A/Description: The sequence of C. elegans cosmid F16B4.
 A/Reference number: Z21208
 A/Accession: T32659
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-362 <DNA>
 A/Cross-references: EMBL:AF039048, PIDN:AA94233.1, GSPDB:GN00023, CESP:F16B4.2
 A/Experimental source: strain Bristol N2; clone F16B4
 C/Genetics:
 A/Map position: 5
 A/Introns: 48/2; 112/2; 160/3; 255/3; 291/2; 333/3

Query Match 88.9%; Score 32; DB 2; Length 362;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6
 DB 26 LDMSYL 31

RESULT 14
 T45032

hypothetical protein Y398B.f [imported] - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C/Accession: T45032
 R/Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berke, M.; Bonfield, J.; Burton
 Raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Jon
 B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifkin, L.; Roopre, A.; Saunders, D.
 Nature 368, 32-38, 1994
 A/Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonhammer, E.;
 Cock, L.; Wilkinson-Spratt, J.; Wohldmann, P.
 A/Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
 A/Reference number: S43531; MUID:94150718; PMID:7906398
 A/Accession: T45032
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-392 <NTL>
 A/Cross-references: EMBL:AL132895, NID:G6434440, PIDN:CAB60911.1, PID:G6434446
 A/Experimental source: clone Y398B
 C/Genetics:
 A/Map position: 3
 A/Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3
 A/Note: Y398B.f

Query Match 88.9%; Score 32; DB 2; Length 392;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSYL 6
 DB 289 DMSYL 293

RESULT 15
 B71857
 probable lipopolysaccharide biosynthesis protein - *Helicobacter pylori* (strain J99)
 C/Species: *Helicobacter pylori*
 A/Variety: strain J99
 C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
 C/Accession: B71857
 R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.
 ; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.
 Nature 397, 176-180, 1999
 A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric pa
 A/Reference number: A71800; MUID:99120557; PMID:9923682
 A/Accession: B71857
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-393 <ARN>
 A/Cross-references: GB:AE001531, GB:AE001439, NID:G4155617, PIDN:ADD06611.1, PID:G4155
 A/Experimental source: strain J99
 C/Genetics:
 A/Map position: 3
 A/Introns: 48/2; 112/2; 160/3; 255/3; 291/2; 333/3

Query Match 88.9%; Score 32; DB 2; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSYL 6
 DB 284 DMSYL 288

Search completed: February 18, 2004, 14:38:51
 Job time : 7.5921 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(Without alignment)
35.929 Million cell updates/sec

Title: US-09-643-260-15

Sequence: 1 LDMSYL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Issued Patent AA: *
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/1aa/PCUS_COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	829	US-09-252-991A-27150	Sequence 27150, A
2	32	88.9	462	US-09-134-001C-4300	Sequence 4300, Ap
3	32	88.9	597	US-09-252-991A-17139	Sequence 17139, A
4	32	88.9	651	US-09-107-532A-4902	Sequence 4902, Ap
5	32	88.9	706	US-08-484-105-16	Sequence 16, Appl
6	32	88.9	706	US-08-484-105-16	Sequence 16, Appl
7	32	88.9	911	US-08-596-985-2	Sequence 2, Appl
8	31	86.1	745	US-08-887-518-3	Sequence 3, Appl
9	31	86.1	745	US-08-887-518-3	Sequence 3, Appl
10	31	86.1	745	US-08-890-853-4	Sequence 4, Appl
11	31	86.1	745	US-09-032-475-3	Sequence 3, Appl
12	31	86.1	745	US-09-032-475-3	Sequence 3, Appl
13	31	86.1	745	US-09-099-125A-4	Sequence 4, Appl
14	31	86.1	745	US-09-099-125A-4	Sequence 4, Appl
15	31	86.1	745	US-09-032-476-4	Sequence 4, Appl
16	31	86.1	745	US-08-890-854-4	Sequence 4, Appl
17	31	86.1	745	US-09-023-324-4	Sequence 4, Appl
18	31	86.1	745	US-09-168-629-2	Sequence 2, Appl
19	31	86.1	745	US-08-910-820-10	Sequence 10, Appl
20	31	86.1	745	US-08-810-131A-2	Sequence 2, Appl
21	31	86.1	745	US-09-109-986-4	Sequence 4, Appl
22	31	86.1	745	US-09-844-908-10	Sequence 10, Appl
23	31	86.1	745	US-09-868-758-3	Sequence 3, Appl
24	31	86.1	756	US-08-867-518-4	Sequence 4, Appl
25	31	86.1	756	US-09-023-321-4	Sequence 4, Appl
26	31	86.1	756	US-08-890-853-2	Sequence 2, Appl
27	31	86.1	756	US-09-032-475-4	Sequence 4, Appl

28	31	86.1	756	2	US-09-099-124A-2	Sequence 2, Appl
29	31	86.1	756	3	US-09-032-476-2	Sequence 2, Appl
30	31	86.1	756	3	US-08-890-854-2	Sequence 2, Appl
31	31	86.1	756	3	US-09-023-324-2	Sequence 2, Appl
32	31	86.1	756	3	US-09-168-629-15	Sequence 15, Appl
33	31	86.1	756	3	US-08-910-820-9	Sequence 9, Appl
34	31	86.1	756	4	US-09-109-986-2	Sequence 2, Appl
35	31	86.1	756	4	US-09-844-908-9	Sequence 9, Appl
36	31	86.1	756	4	US-08-868-758-4	Sequence 4, Appl
37	31	86.1	756	4	US-07-756-250-16	Sequence 16, Appl
38	31	86.1	996	4	US-09-417-197-123	Sequence 123, App
39	31	86.1	997	4	US-09-417-197-123	Sequence 121, App
40	30	83.3	122	4	US-08-936-165A-397	Sequence 397, App
41	30	83.3	363	1	US-07-681-704A-2	Sequence 2, Appl
42	30	83.3	417	3	US-08-640-906-4	Sequence 4, Appl
43	30	83.3	417	3	US-08-640-906-4	Sequence 18, Appl
44	30	83.3	417	4	US-09-395-936-4	Sequence 4, Appl
45	30	83.3	417	4	US-09-395-936-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-252-991A-27150
Sequence 27150, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US-60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US-60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27150
LENGTH: 829
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27150

Query Match 100.0%; Score 36; DB 4; Length 829;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6
|||||
Db 486 LDMSYL 491

RESULT 2
US-09-134-001C-4300
Sequence 4300, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US-60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US-60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4300
LENGTH: 462
TYPE: PRT

ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4300

Query Match 88.9%; Score 32; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5
|||
Db 159 LDMSY 163

RESULT 3
US-09-252-991A-17139
Sequence 17139, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17139
LENGTH: 597
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17139

Query Match 88.9%; Score 32; DB 4; Length 597;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSYL 6
|||
Db 153 DMSYL 157

RESULT 4
US-09-107-532A-4902
Sequence 4902, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSER: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER READABLE FORM:
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4902:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...651
SEQUENCE DESCRIPTION: SEQ ID NO: 4902:
US-09-107-532A-4902

Query Match 88.9%; Score 32; DB 4; Length 651;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5
|||
Db 360 LDMSY 364

RESULT 5
US-08-484-105-16
Sequence 16, Application US/08484105
Patent No. 5589341
GENERAL INFORMATION:
APPLICANT: STILLMAN, Bruce
APPLICANT: BELL, Stephen P
APPLICANT: KOBAYASHI, Ryuji
APPLICANT: RINE, Jasper
APPLICANT: FOSS, Margit
APPLICANT: McNALLY, Francis J
APPLICANT: LAURENSEN, Patricia
APPLICANT: HERSKOWITZ, Ira
APPLICANT: LI, Joachim J
APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: FLIER, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,105
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Atton
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/BAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:

LENGTH: 706 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-105-16

Query Match 88.9%; Score 32; DB 1; Length 706;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 5
Db 193 LDMSY 197

RESULT 6
US-08-484-106-16
Sequence 16, Application US/08484106
Patent No. 5614618
GENERAL INFORMATION:
APPLICANT: STILLMAN, Bruce
APPLICANT: BELL, Stephen P
APPLICANT: KOBAYASHI, Ryuji
APPLICANT: RINE, Jaeger
APPLICANT: FOSS, Margit
APPLICANT: MCNALLY, Francis J
APPLICANT: LAURENSEN, Patricia
APPLICANT: HERSKOWITZ, Ira
APPLICANT: LI, Joachim J
APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,106
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oseman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-106-16

Query Match 88.9%; Score 32; DB 1; Length 706;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 5
Db 193 LDMSY 197

RESULT 7
US-08-596-985-2
Sequence 2, Application US/08596985
Patent No. 5736374
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Hucul, John A.
APPLICANT: Ward, Michael
TITLE OF INVENTION: Increased Production of
BETA-galactosidase in Aspergillus oryzae
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,985
FILING DATE: 05-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/267,631
FILING DATE: 29-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Horn, Margaret A
REGISTRATION NUMBER: 33,401
REFERENCE/DOCKET NUMBER: GC250
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7536
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-596-985-2

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Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSYL 6
Db 675 LDMSYL 680

RESULT 8
US-08-887-518-3
Sequence 3, Application US/08887518
Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6
Db 738 LDMSWL 743

RESULT 9
US-09-023-321-3
Sequence 3, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6
Db 738 LDMSWL 743

RESULT 10
US-08-890-853-4
Sequence 4, Application US/08890853
Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Moronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6
Db 738 LDMSWL 743

RESULT 11
US-09-032-475-3
Sequence 3, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4

;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
;; STREET: 268 BUSH STREET, SUITE 3200
;; CITY: SAN FRANCISCO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94104
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
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;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/887,518
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-008
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
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;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
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;; US-09-032-475-3
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Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSTL 6
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RESULT 12
US-09-099-125A-4
;; Sequence 4, Application US/09099125A
;; Patent No. 5916760
;; GENERAL INFORMATION:
;; APPLICANT: Goeddel, David V.
;; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
;; STREET: 268 BUSH STREET, SUITE 3200
;; CITY: SAN FRANCISCO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94104
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;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
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;; APPLICATION NUMBER: US/09/099,125A
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/890,853
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-006-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
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;; MOLECULE TYPE: peptide
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;; US-09-099-124A-4
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Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSTL 6
Db 738 LDMSTL 743

;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-006-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
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;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
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;; US-09-099-125A-4
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Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSTL 6
Db 738 LDMSTL 743
;;
RESULT 13
US-09-099-124A-4
;; Sequence 4, Application US/09099124A
;; Patent No. 5939302
;; GENERAL INFORMATION:
;; APPLICANT: Goeddel, David V.
;; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
;; STREET: 268 BUSH STREET, SUITE 3200
;; CITY: SAN FRANCISCO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94104
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;; COMPUTER READABLE FORM:
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;; FILING DATE:
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/890,853
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-006-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
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Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSTL 6
Db 738 LDMSTL 743

Db 738 LDMSWL 743

RESULT 14

US-09-032-476-4
Sequence 4, Application US/09032476

Patent No. 6235492

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Cao, Zhaoan

APPLICANT: R. gnier, Catherine

TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/890,854

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-032-476-4

QY 1 LDMSYL 6
Db 738 LDMSWL 743

RESULT 15

US-08-890-854-4

Sequence 4, Application US/08890854

Patent No. 6235512

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Cao, Zhaoan

APPLICANT: R. gnier, Catherine

TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-890-854-4

QY 1 LDMSYL 6
Db 738 LDMSWL 743

Query Match 86.1%; Score 31; DB 3; Length 745;

Best Local Similarity 83.3%; Pred. No. 7.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: February 18, 2004, 14:41:51
Job time : 8.06579 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-15

Perfect score: 36
Sequence: 1 LDMSYL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	32	88.9	27	11	US-09-305-735-385
8	32	88.9	27	12	US-09-818-683-385
9	32	88.9	376	12	US-10-369-493-12565
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11	32	88.9	445	15	US-10-156-761-8567
12	32	88.9	525	12	US-10-369-493-267
13	32	88.9	542	12	US-10-369-493-913
14	32	88.9	560	12	US-10-369-493-13768
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28 <td>31 <td>86.1</td> <td>9</td> <td>11</td> <td>US-09-847-946A-32</td> <td>Sequence 36, Appl</td> </td>	31 <td>86.1</td> <td>9</td> <td>11</td> <td>US-09-847-946A-32</td> <td>Sequence 36, Appl</td>	86.1	9	11	US-09-847-946A-32	Sequence 36, Appl
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30 <td>31 <td>86.1</td> <td>9</td> <td>11</td> <td>US-09-847-946A-36</td> <td>Sequence 34, Appl</td> </td>	31 <td>86.1</td> <td>9</td> <td>11</td> <td>US-09-847-946A-36</td> <td>Sequence 34, Appl</td>	86.1	9	11	US-09-847-946A-36	Sequence 34, Appl
31 <td>31 <td>86.1</td> <td>10</td> <td>11</td> <td>US-09-847-946A-31</td> <td>Sequence 28, Appl</td> </td>	31 <td>86.1</td> <td>10</td> <td>11</td> <td>US-09-847-946A-31</td> <td>Sequence 28, Appl</td>	86.1	10	11	US-09-847-946A-31	Sequence 28, Appl
32 <td>31 <td>86.1</td> <td>10</td> <td>11</td> <td>US-09-847-946A-34</td> <td>Sequence 137, App</td> </td>	31 <td>86.1</td> <td>10</td> <td>11</td> <td>US-09-847-946A-34</td> <td>Sequence 137, App</td>	86.1	10	11	US-09-847-946A-34	Sequence 137, App
33 <td>31 <td>86.1</td> <td>11</td> <td>11</td> <td>US-09-847-946A-28</td> <td>Sequence 140, App</td> </td>	31 <td>86.1</td> <td>11</td> <td>11</td> <td>US-09-847-946A-28</td> <td>Sequence 140, App</td>	86.1	11	11	US-09-847-946A-28	Sequence 140, App
34 <td>31 <td>86.1</td> <td>11</td> <td>11</td> <td>US-09-847-946A-132</td> <td>Sequence 141, App</td> </td>	31 <td>86.1</td> <td>11</td> <td>11</td> <td>US-09-847-946A-132</td> <td>Sequence 141, App</td>	86.1	11	11	US-09-847-946A-132	Sequence 141, App
35 <td>31 <td>86.1</td> <td>11</td> <td>11</td> <td>US-09-847-946A-140</td> <td>Sequence 142, App</td> </td>	31 <td>86.1</td> <td>11</td> <td>11</td> <td>US-09-847-946A-140</td> <td>Sequence 142, App</td>	86.1	11	11	US-09-847-946A-140	Sequence 142, App
36 <td>31 <td>86.1</td> <td>13</td> <td>11</td> <td>US-09-847-946A-143</td> <td>Sequence 143, App</td> </td>	31 <td>86.1</td> <td>13</td> <td>11</td> <td>US-09-847-946A-143</td> <td>Sequence 143, App</td>	86.1	13	11	US-09-847-946A-143	Sequence 143, App
37 <td>31 <td>86.1</td> <td>13</td> <td>11</td> <td>US-09-847-946A-144</td> <td>Sequence 144, App</td> </td>	31 <td>86.1</td> <td>13</td> <td>11</td> <td>US-09-847-946A-144</td> <td>Sequence 144, App</td>	86.1	13	11	US-09-847-946A-144	Sequence 144, App
38 <td>31 <td>86.1</td> <td>13</td> <td>11</td> <td>US-09-847-946A-145</td> <td>Sequence 145, App</td> </td>	31 <td>86.1</td> <td>13</td> <td>11</td> <td>US-09-847-946A-145</td> <td>Sequence 145, App</td>	86.1	13	11	US-09-847-946A-145	Sequence 145, App
39 <td>31 <td>86.1</td> <td>13</td> <td>11</td> <td>US-09-847-946A-148</td> <td>Sequence 146, App</td> </td>	31 <td>86.1</td> <td>13</td> <td>11</td> <td>US-09-847-946A-148</td> <td>Sequence 146, App</td>	86.1	13	11	US-09-847-946A-148	Sequence 146, App
40 <td>31 <td>86.1</td> <td>17</td> <td>11</td> <td>US-09-847-946A-141</td> <td>Sequence 147, App</td> </td>	31 <td>86.1</td> <td>17</td> <td>11</td> <td>US-09-847-946A-141</td> <td>Sequence 147, App</td>	86.1	17	11	US-09-847-946A-141	Sequence 147, App
41 <td>31 <td>86.1</td> <td>17</td> <td>11</td> <td>US-09-847-946A-142</td> <td>Sequence 135, App</td> </td>	31 <td>86.1</td> <td>17</td> <td>11</td> <td>US-09-847-946A-142</td> <td>Sequence 135, App</td>	86.1	17	11	US-09-847-946A-142	Sequence 135, App
42 <td>31 <td>86.1</td> <td>17</td> <td>11</td> <td>US-09-847-946A-146</td> <td></td> </td>	31 <td>86.1</td> <td>17</td> <td>11</td> <td>US-09-847-946A-146</td> <td></td>	86.1	17	11	US-09-847-946A-146	
43 <td>31 <td>86.1</td> <td>17</td> <td>11</td> <td>US-09-847-946A-147</td> <td></td> </td>	31 <td>86.1</td> <td>17</td> <td>11</td> <td>US-09-847-946A-147</td> <td></td>	86.1	17	11	US-09-847-946A-147	
44 <td>31 <td>86.1</td> <td>18</td> <td>11</td> <td>US-09-847-946A-131</td> <td></td> </td>	31 <td>86.1</td> <td>18</td> <td>11</td> <td>US-09-847-946A-131</td> <td></td>	86.1	18	11	US-09-847-946A-131	
45 <td>31 <td>86.1</td> <td>18</td> <td>11</td> <td>US-09-847-946A-135</td> <td></td> </td>	31 <td>86.1</td> <td>18</td> <td>11</td> <td>US-09-847-946A-135</td> <td></td>	86.1	18	11	US-09-847-946A-135	

ALIGNMENTS

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RESULT 1
US-09-847-940B-15
; Sequence 15, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; TYPE: PRT
; LENGTH: 6
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-15
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Query Match      100.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSYL 6
      |||||
Db      1 LDMSYL 6

RESULT 2
US-09-847-946A-15
; Sequence 15, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
```

```
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hamnig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-15
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Query Match
Best Local Similarity 100.0%; Score 36; DB 11; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDMSYL 6
DB 1 LDMSYL 6
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RESULT 3
US-10-287-274-432
Sequence 432, Application US/10287274
Publication No. US20030181408A1
GENERAL INFORMATION:
APPLICANT: Foreysth, R. Allym
APPLICANT: Ohlsen, Karl
APPLICANT: Zykkind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREOF
FILE REFERENCE: EITRA.008DV1
CURRENT APPLICATION NUMBER: US/10/287,274
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: US 09/711164
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 469
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 432
LENGTH: 98
TYPE: PRT
ORGANISM: Escherichia coli
US-10-287-274-432
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Query Match
Best Local Similarity 94.4%; Score 34; DB 12; Length 98;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDMSYL 6
DB 67 IDMSYL 72
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RESULT 4
US-09-847-940B-14
Sequence 14, Application US/09847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
```

```
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-14
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Query Match
Best Local Similarity 88.9%; Score 32; DB 10; Length 6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 LDMSYL 6
DB 1 LDMSFL 6
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```
RESULT 5
US-09-847-946A-14
Sequence 14, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hamnig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-14
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```
Query Match
Best Local Similarity 88.9%; Score 32; DB 11; Length 6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 LDMSYL 6
DB 1 LDMSFL 6
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RESULT 6
US-09-974-879-385
Sequence 385, Application US/09974879
Publication No. US20030028003A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P2
CURRENT APPLICATION NUMBER: US/09/974,879
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 09/818,683
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; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,987
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/066,094
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 385
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-974-879-385

Query Match      88.9%; Score 32; DB 11; Length 27;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSY 5
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Db      8 LDMSY 12

RESULT 7
US-09-305-736-385
; Sequence 385, Application US/09305736
; Publication No. US20030088078A1
; GENERAL INFORMATION:
; APPLICANT: Peng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P1
; CURRENT APPLICATION NUMBER: US/09/305,736
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: PCT/US98/23435
; EARLIER FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/064,911
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,912
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,983
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,900
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,988
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,987
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; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,908
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,984
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,985
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/066,094
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,100
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,089
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,095
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,090
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 385
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-305-736-385

Query Match      88.9%; Score 32; DB 11; Length 27;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSY 5
      |||||
Db      8 LDMSY 12

RESULT 8
US-09-818-683-385
; Sequence 385, Application US/09818683
; Publication No. US20030211472A1
; GENERAL INFORMATION:
; APPLICANT: Peng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P1
; CURRENT APPLICATION NUMBER: US/09/818,683
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION DATA REMOVED - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 385
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-818-683-385

Query Match      88.9%; Score 32; DB 12; Length 27;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSY 5
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Db      8 LDMSY 12

RESULT 9
US-10-369-493-12565
; Sequence 12565, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
```

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; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12565
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(376)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12565

Query Match      88.9%; Score 32; DB 12; Length 376;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DMSY 5
        |||||
Db      372 LDMSY 376

RESULT 10
US-10-374-780A-1378
; Sequence 1378, Application US/10374780A
; Publication No. US2004001927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James
; APPLICANT: Brown, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: Patent version 3.2
; SEQ ID NO 1378
; LENGTH: 412
; TYPE: PRT

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; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Orthologous to G1062
US-10-374-780A-1378

Query Match      88.9%; Score 32; DB 12; Length 412;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DMSYL 6
        |||||
Db      57 DMSYL 61

RESULT 11
US-10-156-761-8567
; Sequence 8567, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8567
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8567

Query Match      88.9%; Score 32; DB 15; Length 445;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DMSYL 6
        |||||
Db      394 DMSYL 398

RESULT 12
US-10-369-493-267
; Sequence 267, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 267
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-267

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Query Match 88.9%; Score 32; DB 12; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DMSYL 6
Db 87 DMSYL 91

RESULT 13
US-10-369-493-913
; Sequence 913, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 913
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Archaeoglobus fulgidus
US-10-369-493-913

Query Match 88.9%; Score 32; DB 12; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSYL 6
Db 292 DMSYL 296

RESULT 14
US-10-369-493-13768
; Sequence 13768, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13768
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-13768

Query Match 88.9%; Score 32; DB 12; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DMSYL 6
Db 117 DMSYL 121

Db 117 DMSYL 121

RESULT 15
US-09-815-242-12101
; Sequence 12101, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA, 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12101
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-12101

Query Match 88.9%; Score 32; DB 9; Length 561;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DMSYL 6
Db 117 DMSYL 121

Search completed: February 18, 2004, 15:42:00
Job time : 16.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-15
Perfect score: 36
Sequence: 1 LDMSYL 6

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	6	23	ABR08737	Mutated IKKbeta NE
2	100.0	6	23	AAW48520	NBD mutant peptide
3	100.0	6	24	ABU08430	Human NEMO binding
4	100.0	756	23	ABR77301	Human IKKbeta muta
5	94.4	98	22	AAAG8962	E. coli growth and
6	91.7	193	22	AAU04899	Microsomeopora eve
7	88.9	6	23	ABR08736	Mutated IKKbeta NE
8	88.9	6	23	AAW48519	NBD mutant peptide
9	88.9	6	24	ABU08429	Human NEMO binding

10	32	88.9	320	22	ABG13516
11	32	88.9	320	22	ABG27654
12	32	88.9	393	19	AAV11025
13	32	88.9	393	23	AAU76667
14	32	88.9	455	22	AAAG8777
15	32	88.9	462	23	ABP39455
16	32	88.9	465	22	ABG18718
17	32	88.9	561	22	AAU36508
18	32	88.9	562	23	ABP7802
19	32	88.9	706	18	AAW22231
20	32	88.9	707	18	AAW14137
21	32	88.9	708	22	ABR5681
22	32	88.9	737	23	ABP65156
23	32	88.9	756	23	ABR77300
24	32	88.9	793	22	ABR68973
25	32	88.9	911	17	AAK92508
26	32	88.9	937	22	ABR66195
27	32	88.9	952	22	ABG22297
28	32	88.9	1005	18	AAW11238
29	32	88.9	1317	22	ABG18723
30	32	88.9	1483	21	AAK48640
31	32	88.9	1493	21	AAK48639
32	32	88.9	1495	21	AAK30440
33	32	88.9	1505	21	AAK30439
34	32	88.9	1544	21	AAK48638
35	32	88.9	1556	21	AAK30438
36	32	88.9	1675	22	AAU00418
37	32	88.9	1689	22	AAU00415
38	32	88.9	1894	22	AAK18725
39	32	88.9	5464	22	ABG11810
40	31	86.1	6	23	ABR08725
41	31	86.1	6	23	AAW48530
42	31	86.1	6	23	AAW48555
43	31	86.1	6	24	ABU08418
44	31	86.1	7	23	AAW48534
45	31	86.1	8	23	AAW48527

ALIGNMENTS

RESULT 1
ID ABB08737 standard; peptide; 6 AA.
AC ABB08737;
DE 14-JUN-2002 (first entry)
Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 15.
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; nocotropic; neuroprotective; anti-HIV; human;
KW dermatological; antibacterial; antiparasitic; antineoplastic;
KW antidiabetic; osteopathic; antitumor; mutant; mutagen.
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference S /note="Wildtype Trp substituted by Tyr"
FT WO200183547-A2.
PD 08-NOV-2001.

PR 02-MAY-2001; 2001WO-US40654.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYVA) UNIV YALE.
 PT May MJ, Ghosh S,
 DR WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 binding domain -
 PS
 XX Claim 23; Page 45; 82pp; English.
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (AB08725-AB08742) comprising at least one NEMO binding domain
 CC (AB077313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of Ikbppa. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC sporadic arthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 binding domain of IKKbeta.
 XX
 SO Sequence 6 AA:
 QY Query Match 100.0%; Score 36; DB 23; Length 6;
 DB Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSYL 6
 DB 1 LDMSYL 6
 RESULT 2
 ID AAM48520
 AC AAM48520 standard; Peptide; 6 AA.
 AC AAM48520;
 XX 20-MAR-2002 (first entry)
 DT
 XX NBD mutant peptide SEQ ID NO 15.

XX
 KM Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; neurotropic;
 KM antineumatic; antiaesthetic; osteopathic; antipsoriatic; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NF-kappaB; Ikbppa kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 PD 08-NOV-2001.
 PD
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PT May MJ, Ghosh S, Fandels MA, Phillips K,
 PT WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PS Example 6; Page 48; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antineumatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiallergic, osteopathic,
 CC antiaesthetic, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of Ikbppa kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of Ikbppa. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SO Sequence 6 AA:
 QY Query Match 100.0%; Score 36; DB 23; Length 6;
 DB Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSYL 6
 DB 1 LDMSYL 6
 RESULT 3
 ID ABU08430
 AC ABU08430 standard; peptide; 6 AA.

XX AC ABU08430;
 XX XX
 DT 12-JUN-2003 (first entry)
 DE Human NEMO binding site (NBD) mutant peptide #13.
 XX
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW Ikappab kinase-beta; Ikappab kinase-alpha; IKKalpha; NF-kappab;
 KW nuclear factor-kappab induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; neurotropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antirheumatic; antiarthritic; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX PN US2002156000-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 02-MAY-2001; 2001US-0847940.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2003-209142/20.
 DR N-PSDB; ABX94271, ABX94272.
 XX
 PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappab induction in a cell and for
 PT treating NF-kappab-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 PT
 PS Claim 22; Page 17; 47pp; English.
 XX
 CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on Ikappab kinase-beta (IKKbeta) and Ikappab kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappab (NF-kappab) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappab induction by IKK but do not inhibit
 CC the basal activity of NF-kappab. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 CC
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 36; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSYL 6
 |||||
 1 LDMSYL 6
 DB 1 LDMSYL 6
 RESULT 4
 ABB77301
 ID ABB77301 standard; protein; 756 AA.

XX AC ABB77301;
 XX XX
 DT 14-JUN-2002 (first entry)
 DE Human IKKbeta mutant W741Y.
 XX
 KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappab; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
 KW antiatherosclerotic; virucide; antiaesthetic; antiallergic;
 KW dermatological; antibacterial; antiporiatic; antirheumatic;
 KW antiarthritic; osteopathic; antitumor; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 741
 XX FT /note= "Wildtype Trp substituted by Tyr"
 XX
 XX PN WO200183547-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US40654.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappab induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 PT
 PS Example 11; Page -; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappab (NF-KB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-KB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of Ikappab. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-KB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for

CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKK β gene
 CC mutant, useful in examples of the invention.
 CC Note: The present sequence is not given in the specification but is
 CC derived from GenBank Accession No. 014920 (AB07294).

SO Sequence 756 AA;

Query Match 100.0%; Score 36; DB 23; Length 756;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSYL 6
 DB 737 LDMSYL 742

RESULT 5

AA098962 standard; Protein; 98 AA.

AC AAG98962;

DT 26-SEP-2001 (first entry)

DE E. coli growth and proliferation related protein sequence SEQ ID NO:432.

KM *Escherichia coli*; growth; proliferation; microbial; antimicrobial;
 bacterial infection; microorganism.

OS *Escherichia coli*.

PN WO200134810-A2.

PD 17-MAY-2001.

PF 09-NOV-2000; 2000WO-US30950.

PR 09-NOV-1999; 99US-0164415.

PA (ELIT-) ELITRA PHARM INC.

PI Forsyth RA, Ohlsen K, Zyskind J,

WPI, 2001-335933/35.

DR N-PSDB; AAH84633.

PT Novel nucleic acids that inhibit *Escherichia coli* proliferation, useful
 for screening for homologous genes and for designing expression vectors

PS Claim 19; Page 490-491; 522pp; English.

AAH84373 to AAH84499 represent *Escherichia coli* growth and proliferation
 related DNA sequences (I). AAH84500 to AAH84670 encode the E. coli
 growth and proliferation related proteins given in AAG989078 and AAG98830
 to AAG98999. (I) can be used as potential targets for the generation of
 new antimicrobial agents, and for identification of compounds which
 interact with the gene products of (I). In addition the expression of
 (I) and the purification of the proteins, the purified proteins can be
 used to generate reagents and screen small molecule libraries or other
 candidate compound libraries for compounds that can be further developed
 to yield novel antimicrobial compounds. In addition, nucleic acid probes
 complementary to (I) that are specific for particular species of
 microorganisms can be used to identify particular microorganism species
 in clinical specimens, therefore, providing a rapid and dependable
 method by which to identify the causative agents of a bacterial
 infection. Also, antibodies generated against proteins translated from

CC mRNA transcribed from proliferation-required sequences can also be used
 CC to screen for specific microorganisms that produce such proteins in a
 CC species-specific manner. AAH84371 and AAH84670 represent sequencing
 CC primers used in the isolation of E. coli growth and proliferation
 CC related sequence, which are used in an example from the present
 CC invention.

SO Sequence 98 AA;

Query Match 94.4%; Score 34; DB 22; Length 98;
 Best Local Similarity 83.3%; Pred. No. 67;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSYL 6
 DB 67 LDMSYL 72

RESULT 6

AAU04899 standard; Protein; 193 AA.

AC AAU04899;

DT 26-SEP-2001 (first entry)

DE Micromonospora evernimycin biosynthetic enzyme evrMR2.

KM Evernimycin; antibiotic; bottle-neck gene; orthomycin;
 fermentation; resistance mechanism gene; evrMR2.

OS Micromonospora carbonacea var. africana.

PN WO200151639-A2.

PD 19-JUL-2001.

PF 12-JAN-2001; 2001WO-US01187.

PR 12-JAN-2000; 2000US-0175751.

PA (SCHE) SCHERING CORP.

PI Hosted TJ, Horan AC, Wang TX;

WPI; 2001-442147/47.

DR N-PSDB; AAS08693.

PT New nucleic acid molecules encoding evernimycin pathway gene
 products, useful for improving yields of evernimycin, to produce new
 PT evernimycin and as probes to identify homologous sequences -

PS Claim 19; Fig 11; 109pp; English.

The sequence is a protein, evrMR2, encoded by a resistance mechanism
 CC gene. The protein comprises one of 98 enzymes of the
 CC evernimycin antibiotic biosynthetic pathway. A vector comprising a
 CC M. carbonacea evernimycin biosynthetic pathway resistance gene
 CC product is useful for selecting for a transfected or transformed host
 CC cell. An integrative version of the vector is useful for introducing a
 CC evernimycin pathway gene (a bottle-neck gene) into an actinomycete of
 CC the genus Micromonospora. The DNA encoding the biosynthetic proteins is
 CC useful for synthesizing novel evernimycin-related compounds, arising
 CC from modifications of the DNA sequence designed to change glycosyl and
 CC modified orellanic acid groups contained in evernimycin, for
 CC expressing functional or mutant evernimycin biosynthetic enzyme for
 CC evaluation, diagnosis and preferably biosynthesis of evernimycin or
 CC other secondary metabolic products, improving the yield of evernimycin
 CC and to produce novel evernimycin and also as a hybridization probe to
 CC identify homologous sequences. The encoded polypeptides are useful for
 CC combinatorial biosynthesis to generate libraries of orthomycin, e.g.
 CC evernimycin analogues/homologues and drug discovery. The
 CC DNA encoding the integrase allows for increasing a given gene dosage. The

CC Integrative vector can be used to permanently integrate copies of a
CC heterologous gene of choice into chromosomes of different hosts and to
CC integrate genes which increase the yield of known products or to generate
CC novel products such as hybrid antibiotics or other novel secondary
CC metabolites. The vector can also be used to integrate antibiotic
CC resistance genes in order to carry out bioconversions with compounds to
CC which the strain is normally sensitive and is thus useful in fermentation
CC processes involving e.g. Streptomyces antibiotics.

XX Sequence 193 AA;

CC Query Match 91.7%; Score 33; DB 22; Length 193;

CC Best Local Similarity 83.3%; Pred. No. 2e+02;

CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6

DB 139 LDMSYL 144

RESULT 7

AB08736 ABB08736 standard; peptide; 6 AA.

AC ABB08736;

DT 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 14.

KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
KW osteopathic; cytotoxic; nocotropic; neuroprotective; anti-HIV; human;
KW antileukosclerotic; virucide; antiaesthetic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antineumatic;
KW antidiabetic; osteopathic; antidiabetic; mutant; mutein.

KW Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 5 /note= "Wildtype Trp substituted by Phe"

PN WO200183547-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US40654.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

PA (UYTA) UNIV YALE.

PI May MJ, Ghosh S;

DR MPI; 2002-179350/23.

PT Modulating NF-kappaB induction in a cell, useful for treating e.g.

PT inflammatory disorders, osteoporosis and cancer, comprises contacting a

PT cell with an anti-inflammatory compound comprising at least one NEMO

PT binding domain

PS Claim 23; Page 45; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC comprises contacting a cell with an anti-inflammatory compound
CC (ABB08725-ABB08742) comprising at least one NEMO binding domain

CC (ABB7213). The compound has acts through selective inhibition of
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC interaction results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of I-kappaB. The compound may also
CC act (directly or indirectly) by blocking the recruitment of leukocytes
CC into sites of acute and chronic inflammation, by down-regulating the
CC expression of E-selectin on leukocytes or by blocking osteoclast
CC differentiation. The compound is useful in treating NF-kB mediated
CC conditions, where the condition is an inflammatory disorder, an
CC autoimmune disease, transplant rejection, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC telangiectasia. The inflammatory disorder is asthma, allergies,
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC diseases. The inflammatory disorder may also be dermatitis, eczema,
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC diseases include HIV and influenza. The compound may also be useful for
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC binding domain of IKKbeta.

XX Sequence 6 AA;

CC Query Match 88.9%; Score 32; DB 23; Length 6;

CC Best Local Similarity 83.3%; Pred. No. 9.3e+05;

CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6

DB 1 LDMSYL 6

RESULT 8

AA048519 AAM48519 standard; peptide; 6 AA.

AC AAM48519;

DT 20-MAR-2002 (first entry)

DE NBD mutant peptide SEQ ID NO 14.

KW Anti-inflammatory; antidiabetic; cytotoxic; antipsoriatic; nocotropic;
KW antineumatic; antidiabetic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antileukosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NF-kappaB; I-kappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIT YALE.
 XX
 PI May MJ, Ghosh S, Flinders MA, Phillips K,
 XX WPI, 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Example 6; Page 48; 86pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM4628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antiproliferative, antineoplastic, antiarthritic, osteoprotective,
 CC antidiabetic, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis, transplant rejection, osteoporosis,
 CC Alzheimer's disease, atherosclerosis, viral infections, and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 SQ Sequence 6 AA;
 XX
 XX
 Query Match 88.9%; Score 32; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSYL 6
 |||||
 Db 1 LDMSFL 6
 |||||
 RESULT 9
 ABU08429
 ID ABU08429 standard; peptide; 6 AA.
 XX
 AC ABU08429;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human NEMO binding site (NBD) mutant peptide #12.
 XX
 KM Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KM IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KM nuclear factor-kappaB induction; inflammatory disorder;
 KM autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KM atherosclerosis; viral infection; Ataxia telangiectasia;
 KM transplantation detection; immunosuppressive; osteopathic;
 KM cytostatic; neurotropic; neuroprotective; antiatherosclerotic; virucide;
 KM vasoconstrictive; antineoplastic; antiarthritic; mutant; mutcin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2002156000-A1.
 XX

PD 24-OCT-2002.
 XX
 XX 02-MAY-2001; 2001US-0847940.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 XX
 PA (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI, 2003-209142/20.
 XX
 PT Novel antiinflammatory peptide comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX
 PS Claim 22; Page 17; 47pp; English.
 XX
 CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 CC
 SQ Sequence 6 AA;
 XX
 XX
 Query Match 88.9%; Score 32; DB 24; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSYL 6
 |||||
 Db 1 LDMSFL 6
 |||||
 RESULT 10
 ABG13516
 ID ABG13516 standard; Protein; 320 AA.
 XX
 AC ABG13516;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #13507.
 XX
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 OS
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 XX 31-MAR-2000; 2000US-0540217.
 PR
 XX 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSR-) HYSRO INC.
 PA

XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS77703.
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX
XX Claim 20; SEQ ID No 43875; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 320 AA;
Query Match 88.9%; Score 32; DB 22; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 DMSYL 6
DB 240 DMSYL 244
RESULT 11
ABG27654
ID ABG27654 standard; Protein; 320 AA.
XX
XX ABG27654;
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #27645.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSB-) HYSBQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX

XX
XX WPI; 2001-639362/73.
XX N-PSDB; AAS91841.
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX
XX Claim 20; SEQ ID No 58013; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 320 AA;
Query Match 88.9%; Score 32; DB 22; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 DMSYL 6
DB 240 DMSYL 244
RESULT 12
AAV11025
ID AAV11025 standard; Protein; 393 AA.
XX
XX AAV11025;
XX
XX 08-JUN-1999 (first entry)
XX
XX H. pylori ORF 02ge41622_14875000_c2_65 outer membrane protein.
XX
XX Vaccine; probe; diagnostic; ORF; cell envelope protein;
XX secreted protein; cytoplasmic protein; cellular protein.
XX
XX Helicobacter pylori.
XX
XX WO9824475-A1.
XX
XX 11-JUN-1998.
XX
XX 05-DEC-1997; 97WO-US22104.
XX
XX 14-JUL-1997; 97US-0891928.
XX
XX 05-DEC-1996; 96US-0759625.
XX
XX 25-MAR-1997; 97US-0823745.
XX
XX (ASTR) ASTRA AB.
XX
XX Alm RA, Castriotta LM, Dolg PC, Kabok Z, Smith D;
XX

DR WPI; 1998-333051/29.
 DR N-PSDB; AAX30554.
 XX
 PT New isolated Helicobacter pylori nucleic acids - used to develop
 products for the diagnosis, prevention and treatment of infection by
 PT H. pylori and other Helicobacter species
 XX
 PS Claims 37, 41; Page 187-188; 339pp; English.
 XX
 CC Recombinant or substantially pure preparations of H. pylori polypeptides
 CC are disclosed, together with the nucleic acids encoding them. In all,
 CC 97 ORFs are shown. The proteins are variously cell envelope proteins,
 CC cytoplasmic proteins, secreted proteins or other cellular proteins.
 CC
 CC vaccines containing the nucleic acids or proteins are claimed, as are
 CC probes containing at least 8 nucleotides from the nucleic acid
 CC sequences. The vaccines are useful for treating or reducing the risk of
 CC -H. pylori infections, and the probes can be used diagnostically for
 CC detecting the presence of Helicobacter in a sample. The products are
 CC also of use in screening for compounds having the ability to interfere
 CC with the H. pylori life cycle or to inhibit H. pylori infection.
 CC
 SQ Sequence 393 AA;
 XX
 Query Match 88.9%; Score 32; DB 19; Length 393;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DMSYL 6
 |||||
 Db 284 DMSYL 288
 XX
 RESULT 13
 AAV76667
 ID AAV76667 standard; Protein: 393 AA.
 XX
 AC AAV76667;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Helicobacter pylori LPS biosynthesis enzyme HP1031 from strain J99.
 XX
 KM LPS; lipopolysaccharide; biosynthesis enzyme; HP1031, strain J99;
 KM antibiotic; vaccine; human self epitope.
 XX
 OS Helicobacter pylori.
 OS
 PN WO200207763-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 12-JUL-2001; 2001WO-IB01536.
 XX
 PR 12-JUL-2000; 2000GB-0017149.
 XX
 PA (CHIR-) CHIRON SPA.
 PI Del Giudice G, Rappuoli R;
 PI
 DR WPI; 2002-217026/27.
 XX
 PT Novel Helicobacter pylori useful for prophylaxis and treatment of
 PT Helicobacter pylori infection, comprises mutation that prevents
 PT synthesis of auto-reactive lipopolysaccharide -
 XX
 PS Disclosure; Fig 1; 23pp; English.
 XX
 CC The present invention relates to a new Helicobacter pylori bacterium
 CC having a mutation that affects lipopolysaccharide (LPS) biosynthesis,
 CC where either LPS is not expressed or LPS which is expressed does not
 CC induce antibodies which cross-react with human self epitopes. The
 CC invention is useful for treating or preventing, and in the manufacture
 CC of a vaccine for treatment or prophylaxis of Helicobacter pylori

CC infection. The vaccine does not induce antibodies which cross-react
 CC with human self epitopes. The present amino acid sequence represents
 CC the Helicobacter pylori LPS biosynthesis enzyme HP1031 that was
 CC isolated from strain J99 and was used in the methods of the invention.
 XX
 SQ Sequence 393 AA;
 XX
 Query Match 88.9%; Score 32; DB 23; Length 393;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DMSYL 6
 |||||
 Db 284 DMSYL 288
 XX
 RESULT 14
 AAG82777
 ID AAG82777 standard; Protein: 455 AA.
 XX
 AC AAG82777;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE S. epidermidis open reading frame protein sequence SEQ ID NO:2648.
 XX
 KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
 KW vaccination; endocarditis.
 XX
 OS Staphylococcus epidermidis.
 OS
 PN WO200134809-A2.
 XX
 PD 17-MAY-2001.
 XX
 PF 09-NOV-2000; 2000WO-US30782.
 XX
 PR 09-NOV-1999; 99US-0164258.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 PI
 PI Kimerly WJ;
 PI
 DR WPI; 2001-316495/33.
 XX
 DR N-PSDB; AAH53627.
 XX
 PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 PT useful for vaccinating against infections, e.g. endocarditis -
 XX
 PS Claim 18; Page 694-695; 2188pp; English.
 XX
 CC AAH53304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
 CC (I) and (II) can have antibacterial activity and therefore can be used
 CC in vaccination. The nucleic acids (I) may be used to produce the
 CC S. epidermidis polypeptides (II) via the production of vectors
 CC containing them which are used to produce host cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
 CC polynucleotide sequences from the present invention. AAH55091 to
 CC AAH55098 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequences given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
 CC no sequences are present for SEQ ID NO:4455 to 4464.
 XX
 SQ Sequence 455 AA;

Query Match 88.9%; Score 32; DB 22; Length 455;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5
 |||||
 Db 152 LDMSY 156

RESULT 15

ABP39455
 ID ABP39455 standard; Protein; 462 AA.

XX AC ABP39455;

XX DT 24-JUL-2002 (first entry)

XX DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4300.

XX KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;

XX KM antibacterial; gene therapy.

XX OS Staphylococcus epidermidis.

XX PN US6380370-B1.

XX PD 30-APR-2002.

XX PF 13-AUG-1998; 98US-0134001.

XX PR 14-AUG-1997; 97US-055779P.

XX PR 08-NOV-1997; 97US-064964P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Doucette-Stamm LA, Bush D;

XX DR WPI; 2002-381255/41.

XX DR N-PSDB; ABN92000.

XX PS Novel isolated nucleic acid encoding a Staphylococcus epidermidis

XX PT polypeptide, useful for diagnosing and treating bacterial infections -

XX PS Disclosure; SEQ ID 4300; 267bp; English.

XX CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading

XX CC frame (ORF) nucleic acid sequences which encode the amino acid sequences

XX CC given in ABP35124 to ABP37960. The S. epidermidis sequences have

XX CC antibacterial activity and can be used in gene therapy. The sequences

XX CC can also be used in the diagnosis and treatment of bacterial infections,

XX CC particularly S. epidermidis infections. The sequences can be used to

XX CC screen for compounds able to interfere with the S. epidermidis life

XX CC cycle or inhibit S. epidermidis infection.

XX CC N.B. The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from the

XX SQ Sequence 462 AA;

Query Match 88.9%; Score 32; DB 22; Length 462;

Best Local Similarity 100.0%; Pred. No. 7.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5
 |||||
 Db 159 LDMSY 163

Search completed: February 18, 2004, 14:26:25
 Job time : 22.7763 secs

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OM proteain - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds

(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35
Sequence: 1 LDMSFL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_ricent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	136	P72919	P72919 synechocyst
2	35	100.0	362	O44634	O44634 caenorhabdi
3	35	100.0	573	O8YX81	O8YX81 anabaena sp
4	35	100.0	2621	O9LMZ3	O9LMZ3 arabidopsis
5	35	100.0	2658	O9SGR4	O9SGR4 arabidopsis
6	33	94.3	208	O8E014	O8E014 streptococc
7	33	94.3	216	O8E659	O8E659 streptococc
8	33	94.3	556	O8DC15	O8DC15 vibrio vuln
9	33	94.3	608	O9YX89	O9YX89 drosophila
10	33	94.3	732	O61565	O61565 crassostrea
11	33	94.3	962	O9SVS7	O9SVS7 arabidopsis
12	33	91.4	176	O44486	O44486 caenorhabdi
13	32	91.4	203	O98GA7	O98GA7 rhizobium 1
14	32	91.4	203	O8UDW9	O8UDW9 agrobacteri
15	32	91.4	284	O8E650	O8E650 streptomyce
16	32	91.4	284	O9RKS7	O9RKS7 streptomyce

17	32	91.4	339	16	O9CE52	O9CE52 lactococcus
18	32	91.4	377	16	O9Z4X8	O9Z4X8 streptomyce
19	32	91.4	556	16	O55814	O55814 synechocyst
20	32	91.4	744	4	O8N261	O8N261 homo sapien
21	32	91.4	870	4	O8N639	O8N639 homo sapien
22	32	91.4	927	16	O92882	O92882 listeria in
23	32	91.4	927	16	O8Y482	O8Y482 listeria in
24	32	91.4	939	16	O8Y0R3	O8Y0R3 anabaena sp
25	32	91.4	1466	3	O42930	O42930 schizosacch
26	32	91.4	124	11	O9D247	O9D247 mus musculu
27	31	88.6	131	12	O9Q0P1	O9Q0P1 tomato leaf
28	31	88.6	134	12	O8QYX7	O8QYX7 tomato leaf
29	31	88.6	134	12	O8E558	O8E558 tomato leaf
30	31	88.6	134	12	O8Q110	O8Q110 tobacco cur
31	31	88.6	134	12	O56991	O56991 papaya leaf
32	31	88.6	134	12	O72708	O72708 cotton leaf
33	31	88.6	134	12	O91MP1	O91MP1 pepper leaf
34	31	88.6	134	12	O99DR2	O99DR2 chili leaf
35	31	88.6	134	12	O8V019	O8V019 cotton leaf
36	31	88.6	134	12	O993Y9	O993Y9 tomato leaf
37	31	88.6	134	12	O98742	O98742 tomato leaf
38	31	88.6	134	12	O8JZ16	O8JZ16 tomato leaf
39	31	88.6	134	12	O8JL10	O8JL10 cotton leaf
40	31	88.6	134	12	O72711	O72711 cotton leaf
41	31	88.6	134	12	O91BQ2	O91BQ2 ageratum ye
42	31	88.6	134	12	O8V012	O8V012 hollyhock 1
43	31	88.6	134	12	O91GX4	O91GX4 tobacco gem
44	31	88.6	134	12	O91N49	O91N49 cotton leaf
45	31	88.6	134	12	O9QDE5	O9QDE5 tomato leaf

ALIGNMENTS

RESULT 1
P72919
ID P72919 PRELIMINARY: PRT: 136 AA.
AC P72919:
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein slr1082.
GN slr1082.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita M., Saito S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naro K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.,
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136 (1996).
DR EMBL; D90901; BAA16936.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 136 AA; 15774 MW; E80414D06029605E CRC64;

Query Match 100.0%; Score 35; DB 16; Length 136;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6
Db 42 LDMSFL 47

RESULT 2
O44634

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ID 044634 PRELIMINARY; PRT; 362 AA.
AC 044634
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 42.3 kDa protein.
GN P16B4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RL investigating biology. The C. elegans Sequencing Consortium.";
RT Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Davidson S., Wohlmann P., Bauer C., O'Neal D.;
RT "The sequence of C. elegans cosmid P16B4.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039048; AA894233.1; -.
DR WormPep; P16B4.2; CE17012.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
KW Hypothetical protein.
SQ SEQUENCE 362 AA; 42255 MW; 33D99EF0FD114006 CRC64;

Query Match 100.0%; Score 35; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 26 LDMSFL 31

RESULT 3
O8YXB1 PRELIMINARY; PRT; 573 AA.
ID O8YXB1
AC O8YXB1
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Sulfate permease family protein.
GN ALI1304.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Reel. 8:205-213(2001).
DR EMBL; AP003585; BAB73261.1; -.
DR InterPro; IPR002645; STAS.
DR InterPro; IPR001902; Sulph_transpt.

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DR Pfam; PF01740; STAS; 1.
DR Pfam; PF00916; Sulfate_transp; 1.
DR PROSITE; PS0801; STAS; 1.
KW Complete proteome.
SQ SEQUENCE 573 AA; 60239 MW; F2D1C2P6A8B36CC CRC64;

Query Match 100.0%; Score 35; DB 16; Length 573;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 357 LDMSFL 362

RESULT 4
O9LMZ3 PRELIMINARY; PRT; 2621 AA.
ID O9LMZ3
AC O9LMZ3
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE T6D22.24.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bel Q., Chin C., Chio J., Choi E., Corn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharbeky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thavert A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Becker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC T6D22 from chromosome
RT 1.";
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Becker J.R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Becker J.R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bel B., Chin C., Chio J., Choi E.,
RA Corn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu S., Mukharbeky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thavert A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Becker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC026875; AAF79832.1; -.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
SQ SEQUENCE 2621 AA; 297067 MW; B3534E176F237044 CRC64;

Query Match 100.0%; Score 35; DB 10; Length 2621;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 2184 LDMSFL 2189

RESULT 5

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09SGE4
ID 09SGE4 PRELIMINARY; PRT; 2658 AA.
AC 09SGE4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE T23G18.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsie.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Alcafi H., Bel O., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukherjee N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vayberg M., Yu G., Federpfeil N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC T23G18 from chromosome
RT 1."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC011438; AAP18257.1; -.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_exchanger; 1.
SQ SEQUENCE 2658 AA; 301830 MW; 77ECF9366784293F CRC64;

Query Match 100.0%; Score 35; DB 10; Length 2658;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSFL 6
Db 2221 LDMSFL 2226

RESULT 6
Q8E014 PRELIMINARY; PRT; 208 AA.
ID 08E014;
AC 08E014;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Riboflavin synthase, alpha subunit.
GN RIBS OR SAG0747.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=2603 V/R / Serotype V;
RC MEDLINE=22222988; PubMed=12200547;
RX Terebin H., Masagrand V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wesels M.E., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Cary H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Bretton C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Frazer C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae."
RT Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014225; AAM99634.1; -.
DR TIGR; SAG0747; -.
KW Complete proteome.
SQ SEQUENCE 208 AA; 22666 MW; 4C25AB59FC1BE601 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 208;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSFL 6
Db 198 MDMSFL 203

RESULT 7
Q8E659 PRELIMINARY; PRT; 216 AA.
ID 08E659;
AC 08E659;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN GBS0768.
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaeser P., Rusniok C., Buchliesser C., Chevalier F., Frangeul L.,
RA Msadek T., Zouine M., Couve E., Lallouf L., Poyart C., Trieu-Cuot P.,
RA Kunat F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease."
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL; AL766847; CAD46412.1; -.
DR Sgalliet; gbs0768; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 216 AA; 23587 MW; B5556D5F751CEBF CRC64;

Query Match 94.3%; Score 33; DB 16; Length 216;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSFL 6
Db 206 MDMSFL 211

RESULT 8
Q8DC15 PRELIMINARY; PRT; 556 AA.
ID 08DC15;
AC 08DC15;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sulfate permease and.
GN VVI1638.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CMCP6;
RC Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6."
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016802; AAO10056.1; -.
KW Complete proteome.
SQ SEQUENCE 556 AA; 59064 MW; 1EC2AC082F0602DA CRC64;

Query Match 94.3%; Score 33; DB 16; Length 556;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LDMSFL 6
 DB 356 LDMSFI 361

RESULT 9
 QYXAS9 PRELIMINARY; PRT; 608 AA.

AC QYXAS9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE C99220 protein.
 GN C99220.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCBI_TaxID=7227;
 RX MEDLINE=20196006; PubMed=10731132;
 RC STRAIN=Berkley;
 RP SEQUENCE FROM N.A.

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
 RA Beeson K.Y., Berns P.V., Berman B.P., Bhandari D., Bolintsov S.,
 RA Bortova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burla K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo J., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Foster C., Gabriellian A.B., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenton J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Labo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Klamor I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spadling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN

SEQUENCE FROM N.A.
 RA Celinker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Barton J., An H., Baldwin D., Barton J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galie R.F., Gary N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN

SEQUENCE FROM N.A.
 RA Mista S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.B., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,
 RA Clapp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Seale S.M.J., Smith B., Shu S., Smucniak F., Whitfield B.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN

SEQUENCE FROM N.A.
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN

SEQUENCE FROM N.A.
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003499; AAF46479.2; --
 DR Flybase; FBgn030662; C99220.
 SQ SEQUENCE 608 AA; 70423 MW; 9278ADD4A3745CA CRC64;

Query Match 94.3%; Score 33; DB 5; Length 608;
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
 DB 151 LDMSFI 156

RESULT 10
 ID 061565 PRELIMINARY; PRT; 732 AA.

AC 061565;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE I- κ -appa-B kinase.
 GN IKK.
 OS Crasostrea gigas (Pacific oyster).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
 OC Ostreidae; Ostreidae; Crasostrea.
 NC NCBI_TaxID=29159;
 RN

SEQUENCE FROM N.A.
 RA MEDLINE=99332074; PubMed=10405163;
 RA Becsoubas J.M., Briant L., Montagnani C., Hez S., Devaux C., Roch P.;
 RT "Oyster IKK-like protein shares structural and functional properties
 with its mammalian homologues.";
 RL FEBS Lett. 453:293-298(1999).
 RT -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AF051320; AAC05683.1; --
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_SF; 1.
 KW ATP-binding, kinase, Serine/threonine-protein kinase, Transferase.
 SQ SEQUENCE 732 AA; 84215 MW; 871EB8D1C3E39AF CRC64;

Query Match 94.3%; Score 33; DB 5; Length 732;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
:|||||
Db 719 MDMSFL 724

RESULT 11

Q9SVS7 PRELIMINARY; PRT; 962 AA.
AC Q9SVS7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 108.9 kDa protein.
GN F1722.160 OR AT4G21700.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxId=3702;

SEQUENCE FROM N.A.
RA Bevan M., Van Der Schueren J., Chuang Y.-J., Voet M., Robben J.,
RA Volckaert G., Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Van Der Schueren J., Vandebussche F., Chuang Y.J., Breken M.,
RA Robben J., Volckaert G., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035527; CAB36814.1; -
DR EMBL; AL161555; CAB81277.1; -
DR InterPro; IPR000269; Cunn oxidase.
DR PROSITE; PS01164; COPPER_AMIN_OXID_1; 1.
KW Hypothetical protein.

SO SEQUENCE 962 AA; 108894 MW; 5F48A946474B8927 CRC64;

Query Match 94.3%; Score 33; DB 10; Length 962;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSFL 6
:|||||
Db 889 LDMSFL 894

RESULT 12

O44486 PRELIMINARY; PRT; 176 AA.
AC O44486
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 20.6 kDa protein.
GN F42A6.5

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br15C01 N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for

RT Investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Br15C01 N2;
RA Du Z., Scheet P., Andrews S.;
RT "The sequence of C. elegans cosmid F42A6".
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Br15C01 N2;
RA Waterston R.;
RT "Direct Submission".

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038613; AAB92050.1; -
DR WormPep; F42A6.5; CE17057.
DR InterPro; IPR001357; BRCT.
DR Pfam; PF00533; BRCT; 1.
DR SMART; SM00293; BRCT; 1.
DR PROSITE; PS50172; BRCT; 1.
KW Hypothetical protein.
SO SEQUENCE 176 AA; 20612 MW; 1F9E5E23AF3E25BD CRC64;

Query Match 91.4%; Score 32; DB 5; Length 176;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSFL 6
:|||||
Db 37 LDMSFL 42

RESULT 13

Q98GA7 PRELIMINARY; PRT; 203 AA.
AC Q98GA7
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein ml13416.
GN ML13416.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxId=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idehara K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti".
RL DNA Res. 7:331-338 (2000).
DR EMBL; AP003001; BAB50309.1; -
DR InterPro; IPR000534; Semialdh.
DR Pfam; PF01118; Semialdehyde dh.
KW Hypothetical protein; Complete proteome.

SO SEQUENCE 203 AA; 21716 MW; FC61A883F2E3EEF CRC64;

Query Match 91.4%; Score 32; DB 16; Length 203;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
:|||||
Db 140 LDMSFL 145

RESULT 14

Q8UDW9- PRELIMINARY; PRT; 203 AA.
 AC Q8UDW9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein Atu1999.
 GN Atu1999 OR AGR_C_3633.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Secubal J.C., Kaul R., Monke D.E., Kiteajima J.P.,
 Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D. Sr.,
 Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 Kutayavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
 Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 Neeter E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58."
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 Quirillo B., Goldman B.S., Cao Y., Askenazi M., Halling L.,
 Houmel K., Gordon J., Vaubin M., Iartchouk O., Epp A., Liu F.,
 Mollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58."
 RL Science 294:2323-2328(2001).
 DR EMBL/ AEO09151; AAL42992.1; -;
 DR EMBL/ AEO08117; AAK87755.1; -;
 KW Hypothetical protein, Complete proteome
 SQ SEQUENCE 203 AA; 21846 MW; D5BF6AC4E3C6B7CB CRC64;
 Query Match 91.4%; Score 32; DB 16; Length 203;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSFL 6
 DB 140 LDWTFPL 145
 RESULT 15
 O86850 PRELIMINARY; PRT; 284 AA.
 AC O86850;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 31.0 kDa protein.
 GN ORPA.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M145;
 RA Takano E., Chakraborty R., Mihira T., Yamada Y., Bibb M.;
 RT "Characterisation of acbR, and acbA genes involved in gamma-
 butyrolactone binding and synthesis in Streptomyces coelicolor.";

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL/ AJ007731; CA07626.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 284 AA; 30969 MW; 38DE00712A09BE7D CRC64;
 Query Match 91.4%; Score 32; DB 2; Length 284;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSFL 6
 DB 125 LDWTFPL 130
 Search completed: February 18, 2004, 14:35:55
 Job time : 18.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds

(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-14

Sequence: 1 LDMSFL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

PIR 76:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	136	S74785	hypothetical prote
2	35	100.0	362	T32669	hypothetical prote
3	35	100.0	573	AE1969	sulfate permease f
4	35	100.0	2658	A86216	protein T23G18.2 (
5	33	94.3	962	T05845	hypothetical prote
6	32	91.4	176	T32618	hypothetical prote
7	32	91.4	203	AB2822	conserved hypothet
8	32	91.4	203	B97600	hypothetical prote
9	32	91.4	339	C86874	ABC transporter pe
10	32	91.4	377	T36246	hypothetical glycolate
11	32	91.4	404	A64151	hypothetical prote
12	32	91.4	556	S76624	integral membrane
13	32	91.4	927	AG1739	transmembrane prot
14	32	91.4	927	AH1369	transmembrane prot
15	32	91.4	939	AE2275	hypothetical prote
16	32	91.4	1466	T39557	vacuolar protein s
17	31	88.6	21	A60420	lens intrininc mem
18	31	88.6	134	S59886	C2 protein - tomat
19	31	88.6	135	QCCY4	AL2 protein - tomat
20	31	88.6	135	S07593	hypothetical prote
21	31	88.6	204	AB0188	phosphoribosyl-ATP
22	31	88.6	225	T17795	hypothetical prote
23	31	88.6	242	B96571	hypothetical prote
24	31	88.6	264	S51829	alpha-amylase inh
25	31	88.6	266	B84848	hypothetical prote
26	31	88.6	350	AG2980	dibenzanthropene d
27	31	88.6	350	G98302	thermophilic desul
28	31	88.6	355	A12867	endo-1,4-Delta-xyla
29	31	88.6	356	A42053	gap junction prote

30	31	88.6	357	2	A49024	connexin40 - dog
31	31	88.6	358	2	S23111	connexin 40 - mouse
32	31	88.6	358	2	I36429	connexin40 - human
33	31	88.6	365	2	E97644	endo-1,4-beta-xyla
34	31	88.6	369	2	B37819	connexin-42 - chic
35	31	88.6	383	2	T38772	protein phosphates
36	31	88.6	400	2	T11921	NADH2 dehydrogenase
37	31	88.6	400	2	I50219	connexin 45.6 - ch
38	31	88.6	402	2	I46053	connexin44 - bovin
39	31	88.6	416	2	S25764	connexin 46 - rat
40	31	88.6	432	2	I39176	intrinsic membrane
41	31	88.6	440	2	I49624	gap junction prote
42	31	88.6	510	2	A45338	connexin-56 - chic
43	31	88.6	569	2	T43531	probable potassium
44	31	88.6	570	2	H87368	copper-binding pro
45	31	88.6	575	2	D84668	hypothetical prote

ALIGNMENTS

RESULT 1

S74785 hypothetical protein elr1082 - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000

C:Accession: S74785

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.

O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yanada, M.; Yasui

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

8.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74785

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-136 <KAN>

A:Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BA16936.1; PID:g16520

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: *Synechocystis* hypothetical protein slr0489

Query Match

Best Local Similarity 100.0%; Score 35; DB 2; Length 136;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6

DB 42 LDMSFL 47

RESULT 2

T32669 hypothetical protein F16B4.2 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

R:Davidson, S.; Wohlmann, P.; Bauer, C.; O'Neal, D.

A:Description: The sequence of C. elegans cosmid F16B4.

A:Reference number: Z21208

A:Accession: T32669

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-362 <DAV>

A:Cross-references: EMBL:AF039048; PIDN:AA94233.1; GSPDB:GN00023; CESP:F16B4.2

A:Experimental source: strain Bristol N2; clone F16B4

C:Genetics:

A:Gene: CESP:F16B4.2

A:Map position: 5

A:introns: 48/2; 112/2; 160/3; 255/3; 291/2; 333/3

Query Match 100.0%; Score 35; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
|||||
Db 26 LDMSFL 31

RESULT 3

AB1969
sulfate permease family protein [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C/Accession: AB1969

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Ref. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A/Reference number: AB1907; PMID:21595285; PMID:11759840

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-573 <XLR>

A/Cross-references: GB:BA000019; PIDN:BA073261.1; PID:G1130651; GSPDB:GN00179

A/Experimental source: strain PCC 7120

C/Genetics:

A/Supplementary: integral membrane protein HP0228

Query Match 100.0%; Score 35; DB 2; Length 573;
Best Local Similarity 100.0%; Pred. No. 74;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
|||||
Db 357 LDMSFL 362

RESULT 4

AB6216
protein T23G18.2 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C/Accession: AB6216

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Holt, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Malt, R.; Marziani, R.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: AB6141; PMID:21016719; PMID:11130712

A/Accession: AB6216

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-2658 <STO>

A/Cross-references: GB:AB051172; NID:56579214; PIDN:AA018257.1; GSPDB:GN00141

C/Genetics:

A/Map position: 1

Query Match 100.0%; Score 35; DB 2; Length 2658;
Best Local Similarity 100.0%; Pred. No. 35e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
|||||
Db 2221 LDMSFL 2226

RESULT 5

T05845
hypothetical protein F17L22.160 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 24-Nov-1999

C/Accession: T05845

R/Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; I

submitted to the Protein Sequence Database, February 1999

A/Reference number: Z15454

A/Accession: T05845

A/Molecule type: DNA

A/Residues: 1-962 <BNV>

A/Cross-references: EMBL:AL035527

A/Experimental source: cultivar Columbia; BAC clone F17L22

C/Genetics:

A/Map position: 4

A/Note: F17L22.160

C/Supplementary: Arabidopsis thaliana hypothetical protein F17L22.160

Query Match 94.3%; Score 33; DB 2; Length 962;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
|||||
Db 889 LDMSFL 894

RESULT 6

T32618
hypothetical protein F42A6.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C/Accession: T32618

R/Du, Z.; Scheet, P.; Andrews, S.

submitted to the EMBL Data Library, December 1997

A/Description: The sequence of C. elegans cosmid F42A6.

A/Reference number: Z21201

A/Accession: T32618

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-176 <DUZ>

A/Cross-references: EMBL:AF038613; PIDN:AB92050.1; GSPDB:GN00022; CESP:F42A6.5

A/Experimental source: strain Bristol N2; clone F42A6

C/Genetics:

A/Map position: 4

A/Introns: 51/3; 109/3

Query Match 91.4%; Score 32; DB 2; Length 176;
Best Local Similarity 83.3%; Pred. No. 77;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
|||||
Db 37 LDMSFL 42

RESULT 7

AB2822
conserved hypothetical protein Atu1999 [imported] - Agrobacterium tumefaciens (strain C)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

C/Accession: AB2822

R/Wood, D.W.; Serubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McCle,

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; PMID:21608550; PMID:11743193

A:Accession: AB2822
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-203 <KUR>
A:Cross-references: GB:AE008688; PIDN:AA14292.1; PID:g17740453; GSPDB:GN00186
C:Genetics:
A:Gene: Atul999
A:Map position: circular chromosome

Query Match 91.4%; Score 32; DB 2; Length 203;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 140 LDMSFL 145

RESULT 8
B97600
hypothetical protein AGR_C_3633 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: B97600
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollem, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:21608551; PMID:11743194
A:Accession: B97600
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-203 <KUR>
A:Cross-references: GB:AE007669; PIDN:AAK8755.1; PID:g15157123; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_3633
A:Map position: circular chromosome

Query Match 91.4%; Score 32; DB 2; Length 203;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 140 LDMSFL 145

RESULT 9
C86874
ABC transporter permease protein ecab [imported] - Lactococcus lactis subsp. lactis (str
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: C86874
R:Boletorin, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: AB6625; PMID:21235186; PMID:11337471
A:Accession: C86874
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-339 <STO>
A:Cross-references: GB:AE005176; PID:g12725040; PIDN:AAK06093.1; GSPDB:GN00146
C:Experimental source: strain IL1403
C:Genetics:
A:Gene: ecab

Query Match 91.4%; Score 32; DB 2; Length 339;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 140 LDMSFL 145

DB 158 LDMAFL 163

RESULT 10
T36246
probable glycolate oxidase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C:Accession: T36246
R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21602
A:Accession: T36246
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-377 <SAU>
A:Cross-references: EMBL:AL035640; PIDN:CB38520.1; GSPDB:GN00070; SCODEB:SCE63.05
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCODEB:SCE63.05
A:Superfamily: (S)-2-hydroxy-acid oxidase (S)-2-hydroxy-acid oxidase homology
P:2-296/Domain: (S)-2-hydroxy-acid oxidase homology <2HY>

Query Match 91.4%; Score 32; DB 2; Length 377;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 207 LDMSFL 212

RESULT 11
A64151
hypothetical protein H10396 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: A64151
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,
J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; PMID:95350630; PMID:7542800
A:Accession: A64151
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-404 <TIGR>
A:Cross-references: GB:U52723; GB:L42023; MID:g1573363; PIDN:AAK22055.1; PID:g1573367;
A>Note: best homolog was a hypothetical protein from Escherichia coli

Query Match 91.4%; Score 32; DB 2; Length 404;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 366 LDMAFL 371

RESULT 12
S76624
integral membrane protein HP0228 homolog 2 - Synecchocystis sp. (strain PCC 6803)
N:Alternate names: low affinity sulfate transporter; protein slr0096
C:Species: Synecchocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S76624
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis

8.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S76624
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-556 <KAN>
 A:Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PIDN:BA10568.1; PID:g100173
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Superfamily: Integral membrane protein HP0228

Query Match 91.4%; Score 32; DB 2; Length 556;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
 |||||
 Db 364 VDMWFL 369

RESULT 13

AG1739
 transmembrane protein [imported] - *Listeria innocua* (strain C14p11262)

C:Species: *Listeria innocua*
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: AG1739

R:Gasser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entlian, K.D.; Feihl, H.; Science 294, 849-852, 2001
 A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurupkat, G.; Madeno, E.; Maltournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AG1739

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-927 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC97687.1; PID:G16414982; GSPDB:GN00178
 A:Experimental source: strain C14p11262

C:Genetics:
 A:Gene: 11n2460

Query Match 91.4%; Score 32; DB 2; Length 927;
 Best Local Similarity 83.3%; Pred. No. 4.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
 |||||
 Db 83 LDMSFL 88

RESULT 14

AH1369

transmembrane protein [imported] - *Listeria monocytogenes* (strain EGD-e)

C:Species: *Listeria monocytogenes*
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: AH1369

R:Gasser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entlian, K.D.; Feihl, H.; Science 294, 849-852, 2001
 A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurupkat, G.; Madeno, E.; Maltournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AH1369

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-927 <GLA>

A:Cross-references: GB:NC_003210; PIDN:CAD00438.1; PID:G16411848; GSPDB:GN00177
 A:Experimental source: strain EGD-e

C:Genetics:
 A:Gene: 1m02360

Query Match 91.4%; Score 32; DB 2; Length 927;
 Best Local Similarity 83.3%; Pred. No. 4.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
 |||||
 Db 83 LDMSFL 88

RESULT 15

AE2275
 hypothetical protein alr3756 [imported] - *Nostoc* sp. (strain PCC 7120)

C:Species: *Nostoc* sp. PCC 7120
 A>Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C:Accession: AE2275

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iritani, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *N*
 A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE2275

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-939 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA075455.1; PID:G17132890; GSPDB:GN00179
 A:Experimental source: strain PCC 7120

C:Genetics:
 A:Gene: alr3756

Query Match 91.4%; Score 32; DB 2; Length 939;
 Best Local Similarity 83.3%; Pred. No. 4.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
 |||||
 Db 648 LDMSFL 653

Search completed: February 18, 2004, 14:38:50
 Job time : 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds

(Without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35

Sequence: 1 LDMSFL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 45 summaries

Database :
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
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8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
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19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	23	ABB08736
2	35	100.0	6	23	AA48519
3	35	100.0	6	24	ABU08429
4	35	100.0	23	ABB77300	Human NEMO binding
5	33	94.3	23	AAU58740	Human IKKbeta muta
6	33	94.3	23	ABF30274	Proionibacterium
7	33	94.3	23	ABP25952	Streptococcus poly
8	33	94.3	22	ABB64315	Drosophila melanog
9	32	91.4	6	23	ABB08737

10	32	91.4	6	23	AA48520
11	32	91.4	6	24	ABU08430
12	32	91.4	37	21	AA659894
13	32	91.4	37	21	AA660632
14	32	91.4	56	22	ABB03835
15	32	91.4	56	24	ABU13129
16	32	91.4	339	23	ABB55349
17	32	91.4	756	23	ABB77301
18	32	91.4	927	23	ABB49720
19	31	88.6	71	22	AAU63276
20	31	88.6	83	21	AA600107
21	31	88.6	97	22	AAU55876
22	31	88.6	124	21	AA658122
23	31	88.6	137	22	AA67051
24	31	88.6	149	21	AA623584
25	31	88.6	150	21	AA635712
26	31	88.6	157	22	AA691029
27	31	88.6	178	21	AA623583
28	31	88.6	234	21	AA648093
29	31	88.6	234	21	AA648116
30	31	88.6	242	23	ABB91342
31	31	88.6	259	21	AA626244
32	31	88.6	264	21	AA616701
33	31	88.6	266	21	AA611935
34	31	88.6	277	15	AA648747
35	31	88.6	277	17	AA602719
36	31	88.6	280	21	AA611934
37	31	88.6	315	21	AA649092
38	31	88.6	315	21	AA649115
39	31	88.6	317	22	AB659701
40	31	88.6	317	23	AB659607
41	31	88.6	343	21	AA649114
42	31	88.6	358	23	ABP23968
43	31	88.6	373	19	ABP55723
44	31	88.6	382	17	AA600496
45	31	88.6	417	19	AA649009

ALIGNMENTS

RESULT 1
ABB08736
ID ABB08736 standard, peptide; 6 AA.

14-JUN-2002 (first entry)

Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 14.

IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
kinase activation; leukocyte; inflammation; B-selectin; osteoclast;
autoimmune disease; transplant rejection; osteoporosis; cancer;
Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
coronary artery disease; immunosuppression; anti-inflammatory;
osteoporosis; cytotoxic; neurotrophic; neuroprotective; anti-HIV; human;
antiartherosclerotic; virucide; antipneumonia; antiallergic;
dermatological; antibacterial; antiparasitic; antineoplastic;
antiarthritic; osteoprotective; antitumor; mutant; mucin.

OS Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
Misc-difference 5
/note="Wildtype Trp substituted by Phe"

WO200183547-A2.

08-NOV-2001.
XX

NBD mutant peptide
Human NEMO binding
Arabidopsis thaliana
Arabidopsis thaliana
Human musculoskeletal
Novel human musc
Lactococcus lactis
Human IKKbeta muta
Listeria monocytog
Propionibacterium
Human secreted pro
Propionibacterium
lung cancer associ
Human dilydrocota
Arabidopsis thaliana
C. glutamicum prote
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Herbicide daily activ
Zea mays zmc2b me
Bacteriophage Dp-1
Arabidopsis thaliana
G-protein coupled
G-protein coupled
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Connexin protein C
Bifidobacterium 10
Candida albicans s
Mouse alpha 3 con

PF 02-MAY-2001; 2001WO-US40654.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (UYVA) UNITV YALE.
 PA
 PI May MJ, Ghosh S;
 XX
 XX WPI; 2002-179350/23.
 DR
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorder, osteoporosis and cancer, comprising contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 XX Claim 23; Page 45; 82pp; English.
 PS
 XX The invention relates to modulating NF-kappaB (NF-KB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-KB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of Ikbppab. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-KB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC polyarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections,
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 CC
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSFL 6
 DB 1 LDMSFL 6
 XX
 XX
 XX
 AC AAM48519;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD mutant peptide SEQ ID NO 14.

XX
 XX Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; nocotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; Ikbppab kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECTIS PHARM INC.
 PA (UYVA) UNITV YALE.
 PI
 PI May MJ, Ghosh S, Fandels MA, Phillips K;
 XX
 XX WPI; 2002-121889/16.
 DR
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Example 6; Page 48; 86pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compound have antiaesthetic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC nocotropic, immunosuppressive, dermatological, neuroprotective,
 CC antineoplastic, antithrombotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of Ikbppab kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of Ikbppab. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSFL 6
 DB 1 LDMSFL 6
 XX
 XX
 XX
 AC AAM48519;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD mutant peptide SEQ ID NO 14.

XX AC ABU08429;
 XX DT 12-JUN-2003 (first entry)
 XX DE Human NEMO binding site (NBD) mutant peptide #12.
 XX KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IKKbeta kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplacental detection; immunosuppressive; osteopathic;
 KW cytotoxic; neurotropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antineumatic; antitarrhctic; mutant; mutein.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN US2002156000-A1.
 XX PD 24-OCT-2002.
 XX PF 02-MAY-2001; 2001US-0847940.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (MAYM/) MAY M J.
 XX PA (GHOS/) GHOSH S.
 XX PI May MJ, Ghosh S;
 XX DR WPI; 2003-209142/20.
 XX PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX PS Claim 22; Page 17; 47pp; English.
 XX CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplacental detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 XX SQ Sequence 6 AA;
 QY Best Local Similarity 100.0%; Score 35; DB 24; Length 6;
 Db Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 LDMSFL 6
 1 LDMSFL 6
 RESULT 4
 ABB77300 standard; protein; 756 AA.
 ID ABB77300
 XX

AC ABB77300;
 XX DT 14-JUN-2002 (first entry)
 XX DE Human IKKbeta mutant W741F.
 XX KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytotoxic; neurotropic; neuroprotective; anti-HIV; human;
 KW antiatherosclerotic; virucide; antiaesthetic; antiallergic;
 KW dermatological; antibacterial; antiparasitic; antineumatic;
 KW antitarrhctic; osteopathic; antitumor; mutant; mutein.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200183547-A2.
 XX PD 08-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-US40654.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (UYVA) UNIV YALE.
 XX PI May MJ, Ghosh S;
 XX DR WPI; 2002-179350/23.
 XX PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX PS Example 11; Page -; 82pp; English.
 XX CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of NEMO
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,

CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of an IKK β gene
CC mutant, useful in examples of the invention.
CC Note: The present sequence is not given in the specification but is
CC derived from GenBank Accession No. U14920 (AB077294).
XX
SO Sequence 756 AA;
Query Match 100.0%; Score 35; DB 23; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSFL 6
DB 737 LDMSFL 742
RESULT 5
ID AAU58740 standard; Protein: 59 AA.
XX
AC AAU58740;
XX
DT 13-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #19636.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopetrotic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PE 20-APR-2001; 2001WO-US12865.
XX
PR 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
PA (CORI-) CORIAX CORP.
XX
PI Skelky YAM, Persing DH, Mitcham JT, Wang SG, Bhatia A;
PI L'etoisneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI: 2001-616774/71.
DR N-PSDB: AAS59594.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
PS Example 1, SEQ ID NO 19935; 1069pp; English.
XX
CC Sequences AAU93105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and endophthalmitis.
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SO Sequence 59 AA;
Query Match 94.3%; Score 33; DB 22; Length 59;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSFL 6
DB 18 LDMSFL 23
RESULT 6
ID ABP30274 standard; Protein: 208 AA.
XX
AC ABP30274;
XX
DT 02-JUL-2002 (first entry)
XX
DE Streptococcus polypeptide SEQ ID NO 9724.
XX
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
OS Streptococcus agalactiae.
XX
PN WO200234771-A2.
XX
PD 02-MAY-2002.
XX
PE 29-OCT-2001; 2001WO-GB04789.
XX
PR 27-OCT-2000; 2000GB-0026333.
PR 24-NOV-2000; 2000GB-0028727.
PR 07-MAR-2001; 2001GB-0005640.
XX
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
PI Telford J, Maignan V, Margatit Ros YI, Grandi G, Fraser C;
PI Tettelin H;
XX
DR WPI: 2002-352536/38.
DR N-PSDB: ABN70905.
XX
PT New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX
PS Claim 1; Page 4099; 4525pp; English.
XX
CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be

CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

XX Sequence 208 AA;

SO Query Match 94.3%; Score 33; DB 23; Length 208;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
 :|||||
 Db 198 MDMSFL 203

RESULT 7
 ABB25952
 ID ABB25952 standard; Protein; 216 AA.
 XX ABB25952;
 AC ABB25952;
 XX 02-JUL-2002 (first entry)
 DT Streptococcus polypeptide SEQ ID NO 1080.
 DE Streptococcus polypeptide SEQ ID NO 1080.
 XX Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
 XX group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX Streptococcus agalactiae.
 OS WO200234771-A2.
 XX WO200234771-A2.
 PN 02-MAY-2002.
 XX 29-OCT-2001; 2001WO-GB04789.
 PF 27-OCT-2000; 2000GB-0026333.
 XX 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX Telford J, Maignant V, Margart Ros YI, Grandi G, Fraser C;
 PI Tettein H;
 XX WPI; 2002-352536/38.
 DR N-PSDB; ABB6583.
 XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 XX Claim 1; Page 3263; 4525pp; English.

XX The invention relates to a protein (ABB25413-ABB30895) from group B
 CC streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acid encoding (I), ABB604-ABB71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

XX Sequence 216 AA;

SO Query Match 94.3%; Score 33; DB 23; Length 216;
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
 :|||||
 Db 206 MDMSFL 211

RESULT 8
 ABB64315
 ID ABB64315 standard; Protein; 788 AA.
 XX ABB64315;
 AC ABB64315;
 XX 26-MAR-2002 (first entry)
 DT Drosophila melanogaster polypeptide SEQ ID NO 19737.
 DE Drosophila melanogaster polypeptide SEQ ID NO 19737.
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX Drosophila melanogaster.
 OS WO200171042-A2.
 XX WO200171042-A2.
 PN 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US09231.
 PF 23-MAR-2000; 2000US-191637P.
 XX 11-JUL-2000; 2000US-0614150.
 PR (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR N-PSDB; ABL08418.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX Disclosure; SEQ ID NO 19737; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57373-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 788 AA;

SO Query Match 94.3%; Score 33; DB 22; Length 788;
 Best Local Similarity 83.3%; Pred. No. 9.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
 :|||||
 Db 331 LDMSFL 336

RESULT 9
 ABB08737
 ID ABB08737 standard; peptide; 6 AA.
 XX
 XX ABB08737;
 AC
 DT 14-JUN-2002 (first entry)
 XX
 DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 15.
 XX
 KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBP; NF-kappaB; NF-kB;
 KW Kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
 KW osteopathic; cytotoxic; neutropenic; neutropenic; anti-HIV; human;
 KW antileukemic; antileukemic; antileukemic; antileukemic;
 KW dermatological; antibacterial; antipsoriatic; antineoplastic;
 KW antithrombotic; osteopathic; antileukemic; mutant; mutagen.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH MISC-difference 5 /note= "Wildtype Trp substituted by Tyr"
 FT
 PT
 XX
 XX MO200183547-A2.
 PN
 XX
 PD 08-NOV-2001.
 PD
 PF 02-MAY-2001; 2001WO-US40654.
 PF
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 PR
 XX (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S;
 PI
 DR WPI; 2002-179350/23.
 DR
 XX
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 PT
 XX
 XX Claim 23; Page 45; 82pp; English.
 PS
 XX
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of Ikbppa. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and

CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 XX
 Query Match 91.4%; Score 32; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSFL 6
 DB 1 LDMSYL 6
 XX
 RESULT 10
 AAM48520
 ID AAM48520 standard; Peptide; 6 AA.
 XX
 XX AAM48520;
 AC
 XX
 DT 20-MAR-2002 (first entry)
 DT
 DE NBD mutant peptide SEQ ID NO 15.
 DE
 XX
 XX Anti-inflammatory; antithrombotic; cytotoxic; antipsoriatic; neutropenic;
 KW antineoplastic; antithrombotic; osteopathic; antibacterial; vitruide;
 KW immunosuppressive; dermatological; neutropenic; antileukemic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; Ikbppa kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 KW
 OS Synthetic.
 OS
 XX
 XX MO200183554-A2.
 PN
 XX
 PD 08-NOV-2001.
 PD
 PF 02-MAY-2001; 2001WO-US14346.
 PF
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Flindels MA, Phillips K;
 PI
 DR WPI; 2002-121889/16.
 DR
 XX
 XX Novel anti-inflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PT
 XX
 XX Example 6; Page 48; 88pp; English.
 PS
 XX The invention relates to an anti-inflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM8525-AAM4619). The antiinflammatory compounds have antiaesthetic,
 CC cytotoxic, antipneumatic, antirheumatic, antiallergic, osteoprotective,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of I-kappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of I-kappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g., asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

CC
 XX
 SQ Sequence 6 AA;

Query Match 91.4%; Score 32; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6
 |||||
 Db 1 LDMSYL 6

RESULT 11

ABU08430
 ID ABU08430 standard; peptide; 6 AA.

XX AC ABU08430;

XX DT 12-UTN-2003 (first entry)

XX DE Human NEMO binding site (NBD) mutant peptide #13.

XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW I-kappaB kinase-beta; I-kappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytotoxic; nootropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antirheumatic; antiallergic; mutant; mutein.

OS Homo sapiens.
 OS Synthetic.

XX PN US2002156000-A1.

XX PD 24-OCT-2002.

XX PF 02-MAY-2001; 2001US-0847940.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (MATM/) MAY M J.

XX PA (GHOS/) GHOSH S.

XX PI May MJ, Ghosh S;

XX DR MPI: 2003-209142/20.

XX DR N-PSDB; ABX94271, ABX94272.

XX PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,

PT psoriasis, vasculitis -
 XX Claim 22; Page 17; 47pp; English.

XX The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on I-kappaB kinase-beta (IKKbeta) and I-kappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.

XX
 XX SQ Sequence 6 AA;

Query Match 91.4%; Score 32; DB 24; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6
 |||||
 Db 1 LDMSYL 6

RESULT 12

AAG59894
 ID AAG59894 standard; Protein; 37 AA.

XX AC AAG59894;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 77522.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

XX PR 16-APR-1999; 99US-0128845.

XX PR 19-APR-1999; 99US-0130077.

XX PR 21-APR-1999; 99US-0130449.

XX PR 23-APR-1999; 99US-0130510.

XX PR 23-APR-1999; 99US-0130891.

XX PR 28-APR-1999; 99US-0131448.

XX PR 30-APR-1999; 99US-0132408.

XX PR 30-APR-1999; 99US-0132407.

XX PR 04-MAY-1999; 99US-0132484.

XX PR 05-MAY-1999; 99US-0132485.

XX PR 06-MAY-1999; 99US-0132486.

PR	06-MAY-1999;	99US-0132487.
PR	07-MAY-1999;	99US-0132863.
PR	11-MAY-1999;	99US-0134256.
PR	14-MAY-1999;	99US-0134218.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
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Query Match 91.4%; Score 32; DB 21; Length 37;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSPL 6
DB 3 LDMAFL 8

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XX EP1033405-A2.
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Query Match 91.4%; Score 32; DB 21; Length 37;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSFL 6
Db 3 LDMAFL 8

RESULT 14
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XX ABB03835;
AC ABB03835;
XX 08-JAN-2002 (first entry)
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XX
DE Human musculoskeletal system related polypeptide SEQ ID NO 1782.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antifalergic; hepatotropic; antidiabetic; antiinflammatory; antilucer;
XX vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cariant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein;
XX musculoskeletal system.
XX
XX Homo sapiens.
XX
XX WO200155367-A1.
PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01338.
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XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
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 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 DR WPI; 2001-451937/48.
 DR N-PSDB; AALJ5417.
 XX
 PT Isolated polypeptide for treating, preventing and/or prognosing
 PT disorders related to the musculoskeletal system including
 PT musculoskeletal cancers and also for testing and detection e.g.
 PT diagnosis -
 PT
 XX
 PS Claim 11; SEQ ID NO 1782; 781bp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (AALJ34669-AALJ7666) and proteins
 CC (ABR03087-ABR04109) associated with the musculoskeletal system useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. The genes are isolated from a range of human
 CC tissues disclosed in the specification. The nucleic acids, proteins,
 CC antibodies and (ant)agonists are useful in the diagnosis, treatment
 CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
 CC other cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 56 AA;
 Query Match 91.4%; Score 32; DB 22; Length 56;
 Best Local Similarity 83.3%; Pred. No. 87;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
 Db 27 LDMSFL 32

RESULT 15
 ABU13129 standard; Protein; 56 AA.

XX
 AC ABU13129;
 DT 26-FEB-2003 (first entry)
 XX
 DE Novel human musculoskeletal system antigen #749.
 XX
 KM Musculoskeletal system antigen; cancer; metastasis;
 KM re-vascularisation; thrombosis; arteriosclerosis; mineral content;
 KM cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
 KM post-operative tissue repair; limb regeneration; neuronal growth;
 KM neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KM AIDS-related complex; chondrocyte growth; bone regeneration;
 KM periodontal regeneration; tissue transport; bone graft; skin aging;
 KM keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
 KM cell growth; organ transplant; cell differentiation; body height;
 KM weight; hair colour; eye colour; skin; percentage of adipose tissue;
 KM pigmentation; cosmetic surgery; metabolism; biorhythm; cardiac rhythm;
 KM depression; tendency for violence; pain; reproductive capability;
 KM hormone level; endocrine level; appetite; libido; memory; stress;
 KM storage capability; fat content; lipid content; protein content;
 KM carbohydrate content; vitamin content; cofactor content;
 KM nutritional component.
 XX
 OS Homo sapiens.
 XX
 PN US2002147140-A1.
 PD 10-OCT-2002.
 XX
 PF 17-JAN-2001; 2001US-0764877.
 XX
 PR 31-JAN-2000; 2000US-179065P.
 PR 04-FEB-2000; 2000US-180628P.
 PR 28-JUN-2000; 2000US-214886P.
 PR 07-JUL-2000; 2000US-216647P.
 PR 07-JUL-2000; 2000US-216880P.
 PR 11-JUL-2000; 2000US-217487P.
 PR 11-JUL-2000; 2000US-217496P.
 PR 14-JUL-2000; 2000US-218290P.
 PR 26-JUL-2000; 2000US-220963P.
 PR 26-JUL-2000; 2000US-220964P.
 PR 14-AUG-2000; 2000US-224518P.
 PR 14-AUG-2000; 2000US-224519P.
 PR 14-AUG-2000; 2000US-225267P.
 PR 14-AUG-2000; 2000US-225268P.
 PR 14-AUG-2000; 2000US-225270P.
 PR 14-AUG-2000; 2000US-225447P.
 PR 14-AUG-2000; 2000US-225757P.
 PR 14-AUG-2000; 2000US-225758P.
 PR 22-AUG-2000; 2000US-226868P.
 PR 30-AUG-2000; 2000US-228924P.
 PR 01-SEP-2000; 2000US-228287P.
 PR 01-SEP-2000; 2000US-229343P.
 PR 01-SEP-2000; 2000US-229344P.
 PR 01-SEP-2000; 2000US-229345P.
 PR 05-SEP-2000; 2000US-229509P.
 PR 05-SEP-2000; 2000US-229511P.
 PR 08-SEP-2000; 2000US-231413P.
 PR 21-SEP-2000; 2000US-234223P.
 PR 21-SEP-2000; 2000US-234274P.
 PR 25-SEP-2000; 2000US-234974P.
 PR 27-SEP-2000; 2000US-235814P.
 PR 29-SEP-2000; 2000US-236327P.
 PR 29-SEP-2000; 2000US-236367P.

PR 29-SEP-2000; 2000US-236368P.
 PR 29-SEP-2000; 2000US-236369P.
 PR 29-SEP-2000; 2000US-236370P.
 PR 02-OCT-2000; 2000US-236802P.
 PR 02-OCT-2000; 2000US-237037P.
 PR 02-OCT-2000; 2000US-237038P.
 PR 02-OCT-2000; 2000US-237039P.
 PR 02-OCT-2000; 2000US-237040P.
 PR 13-OCT-2000; 2000US-239335P.
 PR 20-OCT-2000; 2000US-240960P.
 PR 20-OCT-2000; 2000US-241785P.
 PR 20-OCT-2000; 2000US-241809P.
 PR 01-NOV-2000; 2000US-244617P.
 PR 17-NOV-2000; 2000US-249299P.
 PR 08-DEC-2000; 2000US-251856P.
 PR 08-DEC-2000; 2000US-251868P.
 PR 08-DEC-2000; 2000US-251869P.

XX
 PA (ROSE/) ROSEN C A.
 PA (RUBEN/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI; 2003-128199/12.
 DR N-PSDB; ABX58405.
 XX
 PT Isolated nucleic acid molecules encoding musculoskeletal system
 associated polypeptides, useful for detecting disorders, e.g. cancer -
 XX
 PS Claim 11; SEQ ID NO 1782; 321pp; English.

CC The invention describes an isolated nucleic acid molecule comprising a
 CC sequence encoding musculoskeletal system associated polypeptides useful
 CC for detecting disorders, e.g., cancer or cancer metastases, in animals
 CC or humans. The nucleic acid; stimulates re-vascularisation of ischemic
 CC tissues associated with conditions such as thrombosis, arteriosclerosis,
 CC and other cardiovascular conditions; treats wounds due to injuries,
 CC burn, post-operative tissue repair, and ulcers; stimulates angiogenesis
 CC and limb regeneration; stimulates neuronal growth; can treat and prevent
 CC neuronal damage occurring in certain disorders or neurodegenerative
 CC conditions, such as, Alzheimer's disease, Parkinson's disease, and
 CC AIDS-related complex; stimulates chondrocyte growth, thus they can be
 CC used to enhance bone and periodontal regeneration and aid in tissue
 CC transplants or bone grafts; prevents skin aging due to sunburn by
 CC stimulating keratinocyte growth; prevents hair loss, since FGF family
 CC members activate hair-forming cells and promotes melanocyte growth;
 CC stimulates growth and differentiation of hematopoietic cells and bone
 CC marrow cells when used in combination with other cytokines; maintains
 CC organs before transplantation or for supporting cell culture of primary
 CC tissues; induces tissue of mesodermal origin to differentiate in early
 CC embryos; increases or decreases the differentiation or proliferation of
 CC embryonic stem cells, besides, haematopoietic lineage; modulates
 CC mammalian characteristics, such as, body height, weight, hair colour, eye
 CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape
 CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes
 CC mammal's mental state or physical state by influencing biorhythms;
 CC cardiac rhythms, depression, tendency for violence, tolerance for pain,
 CC reproductive capabilities, hormonal or endocrine levels, appetite,
 CC libido, memory, or stress; increases or decreases storage capabilities,
 CC fat content, lipid, protein, carbohydrate, vitamin, minerals, cofactors
 CC or other nutritional components. This is the amino acid sequence of a
 CC novel human musculoskeletal system antigen.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from the US patent office at
 CC ftp:seqdata.uspto.gov/sequence.html?DocID=20020147140.

XX
 SQ Sequence 56 AA;
 XX
 Query Match 91.4%; Score 32; DB 24; Length 56;
 Best Local Similarity 83.3%; Pred. No. 87;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LDMSFL	6
Db	27	LDMSFL	32

Search completed: February 18, 2004, 14:26:25
Job time : 23.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDM5AL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_23:*
2: sp_Archaea:*
3: sp_Bacteria:*
4: sp_Fungi:*
5: sp_Human:*
6: sp_Invertebrate:*
7: sp_Mammal:*
8: sp_Mhc:*
9: sp_Organelle:*
10: sp_Phage:*
11: sp_Plant:*
12: sp_Rodent:*
13: sp_Virus:*
14: sp_Vertebrate:*
15: sp_Unclassified:*
16: sp_Xvirus:*
17: sp_Bacteriophage:*
18: sp_Archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	295	16	Q9RL11
2	31	93.9	192	16	Q9PCP5
3	31	93.9	266	2	Q9EUB5
4	31	93.9	345	5	Q9YXR2
5	31	93.9	359	5	Q9NE98
6	31	93.9	455	16	Q8PM34
7	31	93.9	652	5	Q9V553
8	31	93.9	666	2	Q8L311
9	31	93.9	666	5	Q8SX14
10	31	93.9	1006	3	Q07324
11	31	93.9	1040	3	Q94147
12	31	93.9	1394	3	Q08409
13	31	93.9	2297	16	Q54155
14	31	93.9	10917	2	Q93NM6
15	30	90.9	90	2	Q50164
16	30	90.9	124	5	Q9VP65

17	30	90.9	154	5	Q9NSH2	Q9NSH2 caenorhabdit
18	30	90.9	163	17	Q9PSE2	Q9PSE2 halobacteri
19	30	90.9	208	16	Q9RY28	Q9RY28 deinococcus
20	30	90.9	231	2	Q9RHB7	Q9RHB7 bradyrhizob
21	30	90.9	256	11	Q9CUA9	Q9CUA9 mus musculu
22	30	90.9	256	11	Q9CXU7	Q9CXU7 mus musculu
23	30	90.9	280	16	Q97GH1	Q97GH1 clostridium
24	30	90.9	360	5	Q16933	Q16933 ancylostoma
25	30	90.9	365	16	Q9K123	Q9K123 vibrio chol
26	30	90.9	380	16	Q9KPM8	Q9KPM8 vibrio chol
27	30	90.9	384	16	Q8ZGR2	Q8ZGR2 yersinia pe
28	30	90.9	391	16	Q98PD4	Q98PD4 rhizobium l
29	30	90.9	401	16	Q916R0	Q916R0 pseudomonas
30	30	90.9	403	16	Q9L111	Q9L111 streptomyce
31	30	90.9	407	16	Q8DKX4	Q8DKX4 synchococc
32	30	90.9	442	5	Q19242	Q19242 caenorhabdi
33	30	90.9	476	16	Q9PFA6	Q9PFA6 xylella fas
34	30	90.9	487	10	Q8LR21	Q8LR21 oryza sativ
35	30	90.9	542	11	Q8BXR2	Q8BXR2 mus musculu
36	30	90.9	564	11	Q9CTV2	Q9CTV2 mus musculu
37	30	90.9	572	16	Q9S1S8	Q9S1S8 streptomyce
38	30	90.9	574	12	Q8B400	Q8B400 porcine lym
39	30	90.9	578	12	Q8B417	Q8B417 porcine lym
40	30	90.9	578	12	Q8B3X0	Q8B3X0 porcine lym
41	30	90.9	580	12	Q8UTD0	Q8UTD0 porcine lym
42	30	90.9	600	4	Q9UFI3	Q9UFI3 homo sapien
43	30	90.9	638	16	Q9RXV9	Q9RXV9 deinococcus
44	30	90.9	660	2	Q8GR31	Q8GR31 streptomyce
45	30	90.9	1026	3	Q42948	Q42948 schizosacch

ALIGNMENTS

RESULT 1
Q9RL11 PRELIMINARY; PRT; 295 AA.
ID Q9RL11
AC Q9RL11
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SCO0307.
GN SCO0307 OR SC059.16.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA MEDLINE=97000351; PubMed=8643436;
RX Redenbach M., Kleser H.M., Denepate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

No art

RA Cronin A., Frazer A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleiser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabbinowitz E., Rajendram M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wierzok A., Woodward J., Barrett B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL939105; CAB55664.1; -
 DR InterPro: IPR002086; Aldelyde_dehydr.
 DR InterPro: IPR001387; HTH_3.
 DR Pfam: PF01381; HTH_3; 1.
 DR SMART: SM00530; HTH_XRE; 1.
 DR PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 295 AA; 32188 MW; 91AF744D7736075 CRC64;

Query Match 100.0%; Score 33; DB 16; Length 295;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 DB 234 LDMSAL 239

RESULT 2
 ID Q9PCP5 PRELIMINARY; PRT; 192 AA.
 AC Q9PCP5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Tyrocyphophan repressor binding protein.
 GN Xf1733.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 NCBI_TaxID=2371;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=985C;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinhard P.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvares R., Alves L.M.C., Araya J.B., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Bionese M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carrero D.M., Carer H.,
 RA Coutinho N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
 RA Faciniani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Gartner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohnes J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsumura A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.B. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silva J.F., Silvestri M.L.Z., Siqueira M.J., de Souza A.A.,
 RA de Souza A.P., Terenzi W.F., Truffi D., Teal S.M., Tsunako M.H.,
 RA Valada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zaitz M., Meidanis J., Secubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa";
 RL Nature 406:151-159(2000).
 DR EMBL: AB003996; AAP84542.1; -

DR InterPro: IPR001226; Flavodoxin.
 DR Pfam: PF00258; Flavodoxin; 1.
 DR PROSITE: PS00201; FLAVODOXIN; 1.
 KM Complete proteome.
 SQ SEQUENCE 192 AA; 20309 MW; 38474F2CAC40A7D4 CRC64;

Query Match 93.9%; Score 31; DB 16; Length 192;
 Best Local Similarity 83.3%; Pred. No. 3.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 DB 43 LDMSAL 48

RESULT 3
 ID Q9EUB5 PRELIMINARY; PRT; 266 AA.
 AC Q9EUB5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Hypothetical 29.4 kDa protein.
 GN ORF55.
 OS Corynebacterium equi (Rhodococcus equi).
 OG Plasmid PREAT701 (p33701), and Plasmid virulence.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Corynebacteriaceae; Nocardia; Rhodococcus.
 NCBI_TaxID=43767;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC33701, and 103; PLASMID=PREAT701 (p33701), and virulence;
 RX PubMed=11083803;
 RA Takai S., Sekizaki T., Kakuda T., Nakamura M., Suzuki K., Ogino N.,
 RL Submitted (Feb-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC33701, and 103; PLASMID=PREAT701 (p33701), and virulence;
 RX PubMed=11083803;
 RA Takai S., Hines S.A., Sekizaki T., Nicholson V.M., Alberin D.A.,
 RA Osaki M., Takamatsu D., Nakamura M., Suzuki K., Ogino N., Kakuda T.,
 RA Dan H., Prescott J.F.;
 RT "DNA sequence and comparison of virulence plasmids from Rhodococcus
 RT equi ATCC 33701 and 103.";
 RL Infect. Immun. 68:6840-6847(2000).
 DR EMBL: AP001204; BAB16664.1; -
 DR EMBL: AP016907; AAG21758.1; -
 KM Hypothetical protein; Plasmid.
 SQ SEQUENCE 266 AA; 29450 MW; 26B9B0B9717FF8B6 CRC64;

Query Match 93.9%; Score 31; DB 2; Length 266;
 Best Local Similarity 83.3%; Pred. No. 4.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 DB 30 LDMSAL 35

RESULT 4
 ID Q9YXR2 PRELIMINARY; PRT; 345 AA.
 AC Q9YXR2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE CG8191 protein (REL1665p).
 GN CG8191.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachytera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RX [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zheng Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chape M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abiri J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
 RA Butris K.C., Busen D.A., Butler H., Cadieu L.B., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davernport L.B., Davies P.,
 RA de Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Katush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laevo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murthy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relarte K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spiraling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tecor C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan W., Zhang Q., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."; Science 287:2185-2195 (2000).
 RL
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Change M., Chavez C., Dorsett V., Drensek D., Farfan D., Friese B.,
 RA Harris R., Gonzalez M., Guatin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Munguel C.J., Nunco J., Pacleb J., Pargass V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celinker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003500; AAF48496.1; -
 DR EMBL; AY071134; AAL48756.1; -
 DR Playbase; Pfgn0030675; CG8191.
 SQ SEQUENCE 345 AA; 39831 MW; 0613409F8F007B9C CRC64;

Query Match 93.9%; Score 31; DB 5; Length 345;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 DB 136 LDMSAI 141

RESULT 5
 Q9NE98 PRELIMINARY; PRT; 399 AA.
 AC Q9NE98;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE Hypothetical 43.5 kDa protein.

GN L4603.06.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 RX NCBI_TaxID=5664;
 CN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Friedlin;
 RA Maany D., Fumelle B., Goffeau A., Ivens A.C., Quail M.,
 RA Rajandream M.A., Barrell B.G.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Friedlin;
 RX MEDLINE=98146435; PubMed=9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the *Leishmania major* Friedlin genome."; Genome Res. 8:135-145(1998).
 RL Genome Res. 8:135-145(1998).
 DR EMBL; AL161416; CAB77684.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 399 AA; 43458 MW; BB86021C2BB3E18 CRC64;

Query Match 93.9%; Score 31; DB 5; Length 399;
 Best Local Similarity 83.3%; Pred. No. 6.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 DB 388 LDMSAI 393

RESULT 6
 Q8PM34 PRELIMINARY; PRT; 455 AA.
 ID Q8PM34;
 AC Q8PM34;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Kynurenine 3-monoxygenase.
 GN XAC1600.
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Queiroz R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
 RA Camarotte G., Cammarvan F., Cardoso J., Chambergro F., Clapina L.P.,
 RA Ciccarelli R.M.B., Coutinho L.L., Curcio-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamara R.B., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two *Xanthomonas* pathogens with differing host specificities."; Nature 417:459-463(2002).
 RL Nature 417:459-463(2002).
 DR EMBL; AE011792; AAM36468.1; -
 DR InterPro; IPR000733; Flav_monoxygenase.
 DR InterPro; IPR003042; Rng_mnoxygenase.
 DR Pfam; PF01360; Monoxygenase; 1.
 DR PRINTS; PR00420; RINGMONOXGNASE.
 KW Monoxygenase; Complete proteome.
 SQ SEQUENCE 455 AA; 50857 MW; DAD9F44B9761A618 CRC64;

Query Match 93.9%; Score 31; DB 16; Length 455;
 Best Local Similarity 83.3%; Pred. No. 7.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 DB 435 LDMSAL 440

RESULT 7
 ID Q9V553 PRELIMINARY; PRT; 652 AA.
 AC Q9V553;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG8027 protein.
 GN CG8027.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_Taxid=7227;
 OK [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Suton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 RA de Pabloe B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glaeser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spter B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskae R., Tector C., Turner R., Ventner E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Ventner J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003834; AAF58967.1; -;
 DR FLYBase; FBgn0033392; CG8027.
 DR InterPro; IPR000800; Notch.
 DR Pfam; PF00066; notch; 1.
 SO SEQUENCE 652 AA; 75752 MW; 2728764810039458 CRC64;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 DB 447 LDMSAL 452

RESULT 8
 ID Q8L311 PRELIMINARY; PRT; 666 AA.
 AC Q8L311;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cytochrome b subunit B.
 GN CYOB.
 OS Vitreoscilla sp. (strain C1).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nisseriales;
 OC Neisseriaceae; Vitreoscilla.
 NC NCB1_Taxid=96942;
 OK [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C1;
 RA Webster D.A., Hwang K.-W., Kim S.-K., Kim K.-J., Chung Y.-T.,
 RA Stark B.C.;
 RT "Sequence and characterization of the cytochrome b operon of
 RT Vitreoscilla.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTERAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AF439739; AAM20915.1; -;
 DR InterPro; IPR000883; COX1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1. 1.
 KW Copper; Electron transport; Heme; Oxidoreductase; Respiratory chain;
 KW Transmembrane; Transport.
 SQ SEQUENCE 666 AA; 74470 MW; B5F3EAB67282E7C CRC64;

Query Match 93.9%; Score 31; DB 2; Length 666;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 DB 5 LDMSAL 10

RESULT 9
 ID Q8SX14 PRELIMINARY; PRT; 666 AA.
 AC Q8SX14;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE RE350339.
 GN CG8027.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_Taxid=7227;
 OK [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Doranek V., Dreanek D., Farfan D., Fries E.,
 RA George R., Gonzalez W., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Pargae V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celnikner S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY089618; AAL90356.1; -;

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DR  P1yBase: F6gn033392; CCG8027.
DR  InterPro: IPR000800; Notch.
DR  Pfam: PF00066; notch.1.
SQ  SEQUENCE 666 AA; 77745 MW; F6FDB6D1C39248 CRC64;

Query Match
Best Local Similarity 93.9%; Score 31; DB 5; Length 666;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6
Db 461 LDMSAM 466

RESULT 10
ID 007324 PRELIMINARY; PRT; 1006 AA.
AC 007324;
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TRENBLrel. 23, Last annotation update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE ATP dependent permease (yeast homolog).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RA De haan M.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=94019318; PubMed=8413243;
RA Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
RA Sherman F.;
RT "CYC2 encodes a factor involved in mitochondrial import of yeast
RT cytochrome c.";
RL Mol. Cell. Biol. 13:6442-6451(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=94169519; PubMed=7764548;
RA Lee Y.S., Shintzu J., Yoda K., Yamasaki M.;
RT "Molecular cloning of a gene, DHS1, which complements a drug-
RT hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
RL Bioesci. Biotechnol. Biochem. 58:391-395(1994).
DR EMBL: X87331; CAA60760.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR001202; WW_Reps_WWP.
DR Pfam: PF00005; ABC_tran.1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA_1.
DR PROSITE: PS01159; WW_DOMAIN_1; 1.
KM ATP-binding.
SQ SEQUENCE 1006 AA; 113961 MW; 0EA9408A1AD1CA7F CRC64;

Query Match
Best Local Similarity 93.9%; Score 31; DB 3; Length 1006;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6
Db 629 IDMSAL 634

RESULT 11
ID 094147 PRELIMINARY; PRT; 1040 AA.
AC 094147;
DT 01-MAY-1999 (TRENBLrel. 10, Created)

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DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE ORF YOR011W (fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 1-488 FROM N.A.
RA Petersson B., Sterky F., Uhlen M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA De haan M., Grivell L.A., Maarse A.C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z74920; CAA99202.1; -.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR001202; WW_Reps_WWP.
DR Pfam: PF00005; ABC_tran.1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA_1.
DR PROSITE: PS01159; WW_DOMAIN_1; 1.
KM ATP-binding.
FT NON TER
SQ SEQUENCE 1040 AA; 117840 MW; B32B0F1D33906B5C CRC64;

Query Match
Best Local Similarity 93.9%; Score 31; DB 3; Length 1040;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6
Db 663 IDMSAL 668

RESULT 12
ID 008409 PRELIMINARY; PRT; 1394 AA.
AC 008409;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Chromosome XV reading frame ORF YOR011W.
GN AUS1 OR YOR011W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 1-842 FROM N.A.
RA Petersson B., Sterky F., Uhlen M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 355-1394 FROM N.A.
RA De haan M., Grivell L.A., Maarse A.C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z74919; CAA99199.1; -.
DR SGD: S0005537; AUS1.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR001202; WW_Reps_WWP.
DR Pfam: PF00005; ABC_tran.2.
DR ProDom: PD000006; ABC_transporter; 2.
DR SMART: SM00382; AAA_1.

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DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 DR PROSITE; PS01159; MW_DOMAIN_1; 1.
 DR ATP-binding.
 SQ SEQUENCE 1394 AA; 157749 MW; 357A35A0FCFC93B CRC64;

Query Match 93.9%; Score 31; DB 3; Length 1394;
 Best Local Similarity 83.3%; Pred. No. 2.4e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 :|||||
 Db 1017 IDMSAL 1022

RESULT 13
 OS4155 PRELIMINARY; PRT; 2297 AA.
 AC OS4155;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Polyketide synthase.
 GN SC05692 OR SC37.12.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Oliver K., Harris D.,
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA MEDLINE=97000351; PubMed=884336;
 RA Redenbach M., Kleiser H.M., Denapate D., Eichner A., Callum J.,
 RA Knaebel H., Hopwood D.A.;
 RL "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=2196410; PubMed=1200953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,
 RA Huang C.H., Kleiser I., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabbittowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wieruszka A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RL "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 RL EMBL; AL339125; CAA16183.1; -.
 DR HSSP; P25715; IMLA.
 DR InterPro; IPR001227; Ac transferase.
 DR InterPro; IPR003408; Ala synthase.
 DR InterPro; IPR004839; Aminotransf.2.
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR InterPro; IPR001917; Nitransf.2.
 DR InterPro; IPR006163; Pp bind.
 DR Pfam; PF00698; Acyl transf. 1.
 DR Pfam; PF02490; Ala_synthase; 1.

DR Pfam; PF00155; aminotran_1.2; 1.
 DR Pfam; PF00501; AMP-binding; 1.
 DR Pfam; PF00109; ketoacyl-synt; 1.
 DR Pfam; PF02801; ketoacyl-synt C; 1.
 DR Pfam; PF00550; pp-binding; 1.
 DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; 1.
 DR PROSITE; PS00751; ACP_DOMAIN; 2.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
 DR Phosphopantetheine; Transferase; Complete proteome.
 SQ SEQUENCE 2297 AA; 241989 MW; C67B5846153EB46 CRC64;

Query Match 93.9%; Score 31; DB 16; Length 2297;
 Best Local Similarity 83.3%; Pred. No. 4e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 :|||||
 Db 1641 IDMSAL 1646

RESULT 14
 OS3NM6 PRELIMINARY; PRT; 10917 AA.
 ID OS3NM6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE AmpHC.
 GN AMPHC.
 OS Streptomyces nodosus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=40318;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Caffrey P., Lynch S.V., Flood E.M., Finnan S.M., O'Leary M.;
 RL "The amphoterin biosynthetic gene cluster from Streptomyces
 nodosus.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- COFACTOR: ZINC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY.
 DR EMBL; AF357202; AAK7514.1; -.
 DR InterPro; IPR001227; Ac transferase.
 DR InterPro; IPR002328; ADR_zinc.
 DR InterPro; IPR002085; Adh_zn_family.
 DR InterPro; IPR004410; FAD.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR InterPro; IPR006162; Ppantne_attach.
 DR InterPro; IPR006163; Pp_bind.
 DR Pfam; PF00698; Acyl_transf. 6.
 DR Pfam; PF00109; ketoacyl-synt; 1.
 DR Pfam; PF00107; adh_zinc; 1.
 DR Pfam; PF02801; ketoacyl-synt C; 6.
 DR Pfam; PF00550; pp-binding; 6.
 DR TIGRfams; TIGR00128; fad; 6.
 DR PROSITE; PS00751; ACP_DOMAIN; 6.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 6.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 5.
 DR Metal-binding; Oxidoreductase; Phosphopantetheine; Transferase; Zinc.
 SQ SEQUENCE 10917 AA; 1132905 MW; 15AC5956B5810A1 CRC64;

Query Match 93.9%; Score 31; DB 2; Length 10917;
 Best Local Similarity 83.3%; Pred. No. 1.9e+04;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 :|||||
 Db 8165 IDMSAL 8170

RESULT 15

OS0164
ID OS0164 PRELIMINARY; PRT; 90 AA.
AC OS0164;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TRENBLrel. 01, Last annotation update)
DE U2968.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Robison K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U15187; AAA63116.1; -. F0187130F41A846 CRC64;
SQ SEQUENCE 90 AA; 9642 MW; F0187130F41A846 CRC64;
Query Match 90.9%; Score 30; DB 2; Length 90;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 LDMSAL 6
DB 65 LDMSAV 70

Search completed: February 18, 2004, 14:35:54
Job time : 19.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDMSAL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	330	YD31_ARCFU	028938 archaeoglob
2	31	93.9	226	CXB2_SHEEP	P46691 ovls arles
3	31	93.9	333	Y237_SYNY3	055480 synochocyt
4	31	93.9	666	COL4_BRUJA	P98057 bradyrhizob
5	31	93.9	984	PKL2_HUMAN	Q16513 homo sapien
6	30	90.9	208	TRP2_DEIRA	Q9128 delnococcus
7	30	90.9	261	YFUR_BACSU	034662 rhizobium s
8	30	90.9	377	Y4WD_RHISN	P55682 homo sapien
9	30	90.9	516	PROD_HUMAN	043272 homo sapien
10	29	87.9	223	SWAP_HUMAN	P02743 homo sapien
11	29	87.9	224	SAMP_PIG	O19063 sus scrofa
12	29	87.9	234	SAMP_MESAU	P07629 mesocricetu
13	29	87.9	286	CXAB_RAT	P28333 rattus norv
14	29	87.9	286	SGBU_ECOLI	P37679 escherichia
15	29	87.9	296	CYCG_RHOSH	053143 rhodobacter
16	29	87.9	313	Y763_TREPA	083744 treponema p
17	29	87.9	378	CXAI_XENLA	P16663 xenopus lae
18	29	87.9	380	CXAI_BRARE	057474 brachydanio
19	29	87.9	381	CXAI_CHICK	P14154 gallus galli
20	29	87.9	381	CXAI_HUMAN	P17302 homo sapien
21	29	87.9	381	CXAI_MOUSE	P23742 mus musculu
22	29	87.9	381	CXAI_RAT	P08050 rattus norv
23	29	87.9	382	CXAI_BOVIN	P18246 bos taurus
24	29	87.9	394	PGK_BACST	P18912 bacillus st
25	29	87.9	446	SHR_BOMMO	Q17239 bombyx mori
26	29	87.9	451	GNDF_PSEPU	P42206 pseudomonas
27	29	87.9	455	UHPT_CHLPU	Q92709 chlamydia p
28	29	87.9	456	UHPT_CHLPU	Q92709 chlamydia p
29	29	87.9	456	UHPT_CHLPU	Q92709 chlamydia m
30	29	87.9	482	TRPE_CHLPU	Q92709 chlamydia t
31	29	87.9	517	LAOI_HUMAN	000515 homo sapien
32	29	87.9	517	LAOI_HUMAN	P57016 mus musculu
33	29	87.9	548	NODO_BRUJA	Q45269 bradyrhizob

34	29	87.9	600	1	GLMS_HALNI	Q9h00 h glucosami
35	29	87.9	630	1	GLMS_SYNY3	P72720 s glucosami
36	29	87.9	644	1	VP4_BTV11	P33428 bluetongue
37	29	87.9	644	1	VP4_BTV13	P33429 bluetongue
38	29	87.9	644	1	VP4_BTV2A	P33427 bluetongue
39	29	87.9	654	1	VP4_BTV10	P07132 bluetongue
40	29	87.9	754	1	RIR1_BP14	P32282 bacterioph
41	29	87.9	842	1	PKL2_RAT	P08874 rattus norv
42	29	87.9	926	1	MAY3_SCHCO	P37934 schizophyll
43	29	87.9	941	1	GCSP_MYCTU	Q50601 mycobacteri
44	29	87.9	946	1	PKL1_RAT	Q63433 rattus norv
45	29	87.9	958	1	YATB_SCHRO	Q09764 schizosacch

ALIGNMENTS

RESULT 1
ID YD31_ARCFU STANDARD, PRT, 330 AA.
AC 028938;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein AF1331.
GN AF1331.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxId=2234;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Richardson D.L., Kierlavage A.R., Graham D.B., Kyrtsov N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370 (1997).
CC -----
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CC -----
CC EMBL, AE001012; AAB89926.1; -
CC PIR, B69416; B69416.
DR TIGR, AF1331, -
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 330 AA; 38741 MW; 1B32F8BF5E9C7621 CRC64;
SQ
Query Match 100.0%; Score 33; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
LDMSAL 6
177 LDMSAL 182
RESULT 2

CX82_SHEEP STANDARD; PRT; 226 AA.
 ID _CXB2_SHEEP
 AC P46651;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gap junction beta-2 protein (Connexin 26) (Cx26).
 GN GJB2
 OS Ovis aries (Sheep).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cornea;
 RA Dong Y., Green C., Donaldson P.J., Kistler J.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: One gap junction consists of a cluster of closely packed
 CC pairs of transmembrane channels, the connexons, through which
 CC materials of low mw diffuse from one cell to a neighboring cell.
 CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. BETA-TYPE (GROUP 1)
 CC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; U17592; AAA67446.1; -;
 CC InterPro; IPR000500; Connexin.
 CC DR Pfam; PF00029; connexin; 1.
 CC DR PRINTS; PR00206; CONNEXIN.
 CC DR SMART; SM00037; CNX; 1.
 CC DR PROSITE; PS00407; CONNEXINS_1; 1.
 CC DR PROSITE; PS00408; CONNEXINS_2; 1.
 CC KW Gap junction; Transmembrane.
 CC FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 21 40 POTENTIAL.
 CC FT DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 76 98 POTENTIAL.
 CC FT DOMAIN 99 131 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 132 154 POTENTIAL.
 CC FT DOMAIN 155 192 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 193 215 POTENTIAL.
 CC FT DOMAIN 216 226 CYTOPLASMIC (POTENTIAL).
 CC SQ SEQUENCE 226 AA; 26215 MW; DCE2FC1B4FCEFD CRC64;
 Query Match 93.9%; Score 31; DB 1; Length 226;
 Best Local Similarity 83.3%; Pred. No. 61;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LDMSAL 6
 Db 1 MDMSAL 6
 RESULT 3
 YZ37_SYNV3 STANDARD; PRT; 333 AA.
 AC Q55480;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical sugar kinase slr0537.
 GN slr0537.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kocant H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 64% to 92% of the genome.";
 RL DNA Res. 2:153-166(1995).
 CC -1- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
 CC -----
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 CC -----
 CC EMBL; D64006; BAA10827.1; -;
 CC PIR; S75980; S75980.
 CC DR HSP; Q9TW2; 1DG.
 CC DR InterPro; IPR002173; PFKB.
 CC DR InterPro; IPR002139; Ribokinase.
 CC DR Pfam; PF00294; PFKB; 1.
 CC DR PRINTS; PR00990; RIBOKINASE.
 CC DR PROSITE; PS00583; PFKB_KINASES_1; FALSE NEG.
 CC DR PROSITE; PS00584; PFKB_KINASES_2; 1.
 CC KW Hypothetical protein; Transferase; Kinase; Complete proteome.
 CC SQ SEQUENCE 333 AA; 35184 MW; CBCE13D0FEE90D CRC64;

Query Match 93.9%; Score 31; DB 1; Length 333;
 Best Local Similarity 83.3%; Pred. No. 89;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LDMSAL 6
 Db 146 MDMSAL 151
 RESULT 4
 CO14_BRAJA STANDARD; PRT; 666 AA.
 ID CO14_BRAJA
 AC P98057;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Probable cytochrome c oxidase polypeptide I (EC 1.9.3.1) (Fourth
 DE terminal oxidase).
 GN blr2715.
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OC NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=94259305; PubMed=8200541;
 RA Surpin M.A., Moshiri F., Murphy A.M., Maier R.J.;
 RT "Genetic evidence for a fourth terminal oxidase in Bradyrhizobium
 RT japonicum.";
 RL Gene 143:73-77(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA 110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamiyama K., Uchiyama T.,
 RA Sasano S., Watanabe A., Idegawa K., Iritani M., Kawashima K.,
 RA Kohara S., Matsumoto M., Shimo S., Teurtoke H., Wada T., Yamada M.,
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).

```
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- PATHWAY: Respiratory chain; terminal step.
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
CC -----
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CC -----
DR EMBL; L25841; AAA26210.1; -.
DR EMBL; AF005944; BAC47980.1; -.
DR HSSP; P18401; 1FT.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain;
KW Complete proteome.
FT METAL 105 105
FT FT METAL 283 283
FT FT METAL 287 287
FT FT METAL 332 332
FT FT METAL 333 333
FT FT METAL 418 418
FT FT METAL 420 420
FT FT METAL 420 420
FT FT CROSSLINK 283 287
FT FT CONFLICT 204 204
SQ SEQUENCE 666 AA; 74469 MW; F04F4870CD039661 CRC64;
Query Match 93.9%; Score 31; DB 1; Length 666;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSAL 6
DB 5 LDMSAL 10
RESULT 5
PKL2 HUMAN STANDARD; PRT; 984 AA.
AC 016513; O9H1W4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C-like 2 (EC 2.7.1.-) (Protein-kinase C-related kinase
DE 2).
GN PRKCL2 OR PRK2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxId=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=95080426; PubMed=798719;
RA Palmer R.H., Ridden J., Parker P.J.;
RT "Identification of multiple, novel, protein kinase C-related gene
RT products."
RL FEBS Lett. 356:5-8(1994).
RP 12
RP SEQUENCE FROM N.A.
RX TISSUE=B-cell;
RX MEDLINE=95154310; PubMed=7851406;
RA Palmer R.H., Ridden J., Parker P.J.;
RT "Cloning and expression patterns of two members of a novel protein-
RT kinase-C-related kinase family."
```

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RL Eur. J. Biochem. 227:344-351(1995).
RN [3]
RP SEQUENCE OF 17-984 FROM N.A.
RA Brown A.;
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: EXHIBITS A PREFERENCE FOR HIGHLY BASIC PROTEIN
CC SUBSTRATES (BY SIMILARITY).
CC -1- ENZYME REGULATION: ACTIVATED BY LIPIDS, PARTICULARLY CARDIOLIPIN
CC AND TO A LESSER EXTENT BY OTHER ACIDIC PHOSPHOLIPIDS AND
CC UNSATURATED FATTY ACIDS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PTM: AUTOPHOSPHORYLATED.
CC -1- PTM: ACTIVATED BY LIMITED PROTEOLYSIS WITH TRYPSIN (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL; U33052; AAC50208.1; -.
DR EMBL; S75548; AAB33346.1; -.
DR EMBL; AL136381; CAC17575.1; -.
DR PIR; S67527; S67527.
DR HSSP; O63450; 1A06.
DR Genew; HGNC:9406; PRKCL2.
DR MIM; 602549; -.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000961; Kinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000861; RM_repeat.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF02185; HRI; 3.
DR Pfam; PF00069; kinase; 1.
DR Pfam; PF00433; kinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00074; HRI; 3.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; ATP-binding; Serine/threonine-protein kinase;
KW Phosphorylation.
FT DOMAIN 657 916
FT NP BIND 653 671
FT BINDING 686 686
FT ACT_SITE 782 782
FT CONFLICT 207 207
SQ SEQUENCE 984 AA; 112034 MW; 687EC417A0F51CID CRC64;
Query Match 93.9%; Score 31; DB 1; Length 984;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSAL 6
DB 919 LDMSAL 924
RESULT 6
TRPF DEIRA
ID TRPF DEIRA STANDARD; PRT; 208 AA.
AC O9RYZ8;
DT 15-SEP-2003 (Rel. 42, Created)
```

DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE N-(5'-phosphoribosyl)anthranilate isomerase (EC 5.3.1.24) (PRAI).
 GN TRPF OR DR0123.
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 Dodson R.J., Helt D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 Motie K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
 Makarewicz K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 Ratzman K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 Fraser C.M.;
 RA "Genome sequence of the radioreistant bacterium Deinococcus
 RT radiodurans R1.";
 RL Science 286:1571-1577(1999).
 CC -1- CATALYTIC ACTIVITY: N-(5'-phospho-beta-D-riboseyl)-anthranilate = 1-
 CC (2-carboxyphenylamino)-1-deoxy-D-ribose 5-phosphate.
 CC -1- PATHWAY: Tryptophan biosynthesis; third step.
 CC -1- SIMILARITY: BELONGS TO THE TRPF FAMILY.
 CC -----
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 CC -----
 DR EMBL; AEO01875; AAF09715.1; -.
 DR PIR; D75556; D75556.
 DR HSSP; Q56320; IDL3.
 DR TIGR; DR0123; -.
 DR HAMAP; MF_00135; -; 1.
 DR InterPro; IPR001240; PRAI.
 DR Pfam; PF00697; PRAI; 1.
 KM Isomerase; Tryptophan biosynthesis; Complete proteome.
 SQ SEQUENCE 208 AA; 21156 MW; CF98D22823AC2833 CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 208;
 Best Local Similarity 83.3%; Pred. No. 85;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSAL 6
 Db 144 LDMAAL 149
 RESULT 7
 YFJR_BACSU STANDARD; PRT; 261 AA.
 ID YFJR_BACSU
 AC O34969;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical oxidoreductase yfjr (EC 1.1.-.-).
 GN YFJR.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AC327;
 RX MEDLINE=97124190; PubMed=8969503;
 RA Yamamoto H., Uchiyama S., Sekiguchi J.,
 RT "Cloning and sequencing of a 40.6 kb segment in the 73 degrees-76
 degrees region of the Bacillus subtilis chromosome containing genes

RT for trehalose metabolism and acetoin utilization.";
 RL Microbiology 142:3057-3065(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunec F., Ogatawara N., Moser I., Albertini A.M., Allont G.,
 Azevedo V., Besterio M.G., Bessieres P., Bolotin A., Borchert S.,
 Brouillet R., Boursier L., Brans A., Braun M., Briganti S.C., Bron S.,
 Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter R.M.,
 Choi S.K., Codani J.J., Conerton I.F., Cumming N.J., Daniel R.A.,
 Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 Entian K.D., Errington J., Fabre C., Ferrari E., Foulger D.,
 Fritze C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grand G.,
 Guisephi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 Joris B., Karmata D., Kasahara Y., Kjaer-Blanchard M., Klein C.,
 Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 Kurita K., Lapides A., Lardinois S., Lauber J., Lazarevic V.,
 Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
 Paro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 Prescan E., Puig P., Purnelle B., Rapoport G., Ray M., Reynolds S.,
 Rieger M., Rivolta E., Rochna E., Roche B., Rose M., Sadale Y.,
 Sato T., Scanlan B., Schleich S., Schroeder R., Scifone F.,
 Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
 Sorokin A., Taccoti B., Takegi T., Takahashi H., Takemura K.,
 Takeuchi M., Tamakoshi A., Tanaka T., Tappara P., Tognoni A.,
 Tosoer V., Uchiyama S., Vandenbol M., Vannier F., Vassarelli A.,
 Viari A., Wandt R., Wedler E., Wedler H., Weitzenecker T.,
 Winters P., Wipat A., Yamamoto H., Yamane K., Yasuno K., Yata K.,
 Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Darchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis".
 RL Nature 390:249-256(1997).
 CC -1- SIMILARITY: BELONGS TO THE 3-HYDROXYISOBUTYRATE DEHYDROGENASE
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; D83967; BAA23388.1; -.
 DR EMBL; D78509; BAA24303.1; -.
 DR EMBL; 259108; CAB12628.1; -.
 DR PIR; A69807; A69807.
 DR Subtilist; BG12914; YfJR.
 DR InterPro; IPR002204; 3-hydroxyisobut dh.
 DR PROSITE; PS00895; 3-HYDROXYISOBUT DH; FALSE NEG.
 KM Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
 FT ACT_SITE 146 146
 SQ SEQUENCE 261 AA; 27866 MW; 6C9A8CAC8C71CA66 CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 261;
 Best Local Similarity 83.3%; Pred. No. 11e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSAL 6
 Db 251 LDMAAL 256
 RESULT 8
 Y4WD_RHSN STANDARD; PRT; 377 AA.
 ID Y4WD_RHSN
 AC P55682;
 DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 01-NOV-1997 (Rel. 35, last annotation update)
 DE Hypothetical transport protein Y4WD.
 GN Y4WD.
 OS Rhizobium sp. (strain NGR234).
 OC Bacteroides; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 NCBI_TaxID=394;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97305956; PubMed=9163424;
 RA Feilberg C.A., Fellay R., Batroch A., Broughton W.J., Rosenthal A.,
 Perret X.;
 RT "Molecular basis of symbiosis between Rhizobium and legumes";
 RL Nature 387:394-401(1997).
 CC -1- FUNCTION: COULD BE INVOLVED IN A TRANSPORT SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: TO R.MELILOTI M0SC.
 CC
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 CC
 CC EMBL; AB000103; AAB91911.1; -
 DR InterPro; IPR007114; MFS.
 KM Hypothetical protein; Transmembrane; Transport; Plasmid.
 FT TRANSMEM 4 24 POTENTIAL.
 FT TRANSMEM 41 61 POTENTIAL.
 FT TRANSMEM 85 105 POTENTIAL.
 FT TRANSMEM 134 154 POTENTIAL.
 FT TRANSMEM 159 179 POTENTIAL.
 FT TRANSMEM 192 212 POTENTIAL.
 FT TRANSMEM 278 298 POTENTIAL.
 FT TRANSMEM 301 321 POTENTIAL.
 FT TRANSMEM 327 347 POTENTIAL.
 FT TRANSMEM 356 376 POTENTIAL.
 SQ SEQUENCE 377 AA; 39051 MW; 49CF6B4A0D74BD CRC64;
 QY
 Db 1 LDMSAL 6
 221 LDMSAV 226
 Query Match 90.9%; Score 30; DB 1; Length 377;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RT hyperproliferation.";
 RL Hum. Genet. 101:69-74(1997).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum, and Kidney;
 RX MEDLINE=99206616; PubMed=10192398;
 RA Gogoe J.A., Sanchez M., Takacs Z., Beck K.D., Luine V., Lucas L.R.,
 Nadler J.V., Karayorgou M.;
 RT "The gene encoding proline dehydrogenase modulates sensorimotor gating
 RT in mice.";
 RL Nat. Genet. 21:434-439(1999).
 CC -1- FUNCTION: CONVERTS PROLINE TO DELTA-1-PYRROLINE-5-CARBOXYLATE.
 CC -1- PATHWAY: Conversion from proline to glutamate; first step.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SKELETAL MUSCLE AND BRAIN,
 CC TO A LESSER EXTENT IN HEART AND KIDNEY, AND WEAKLY IN LIVER,
 CC PLACENTA AND PANCREAS.
 CC -1- DISEASE: Defects in PRODH are the cause of type I hyperproliferation
 CC [MIM:239500], a disorder characterized by elevated serum proline
 CC levels. May be involved in the psychiatric and behavioral
 CC phenotypes associated in the 22q11 velocardiofacial syndrome.
 CC -1- SIMILARITY: BELONGS TO THE PROLINE OXIDASE FAMILY.
 CC
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 CC
 CC EMBL; U82811; AAB88789.1; -
 DR EMBL; AF120278; AAD24775.1; -
 DR Genew; HGNC:9453; PRODH.
 DR GK; O43272; -
 DR MIM; 606810; -
 DR MIM; 239500; -
 DR GO; GO:0004657; P:proline dehydrogenase activity; TAS.
 DR InterPro; IPR002872; Pro_dh.
 DR Pfam; PF01619; Pro_dh; 1.
 KM Oxidoreductase; Proline metabolism; Mitochondrion; Transic peptide.
 FT TRANSIT 1 ? ? MITOCHONDRION (POTENTIAL).
 FT CHAIN 1 516 PROLINE OXIDASE.
 FT CONFLICT 80 80 S -> T (IN REF. 2).
 SQ SEQUENCE 516 AA; 59216 MW; 2FA5B1B4461C450A CRC64;
 QY
 Db 1 LDMSAL 6
 231 LDMSAL 236
 Query Match 90.9%; Score 30; DB 1; Length 516;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RT "Human serum amyloid P component. cDNA isolation, complete sequence
 RT of pre-serum amyloid P component, and localization of the gene to
 RT chromosome 1.";
 RL J. Biol. Chem. 260:7752-7756(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8713751; PubMed=3029048;
 RA Ohnishi S., Maeda S., Shimada K., Arai T.;
 RT "Isolation and characterization of the complete complementary and
 RT genomic DNA sequences of human serum amyloid P component.";
 RL J. Biochem. 100:849-858(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Skeletal muscle;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stetson M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loguillano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Small D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 20-223.
 RX MEDLINE=6033713; PubMed=4055725;
 RA Prell P., Pras M., Frangione B.;
 RT "The primary structure of human tissue amyloid P component from a
 RT patient with primary idiopathic amyloidosis.";
 RL J. Biol. Chem. 260:12895-12898(1985).
 RN [5]
 RP SEQUENCE OF 20-49.
 RX MEDLINE=79042150; PubMed=81686;
 RA Thompson A.R., Enfield D.L.;
 RT "Human plasma P component: isolation and characterization.";
 RL Biochemistry 17:4304-4311(1978).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=94159098; PubMed=8114934;
 RA Emeley J., White H.E., O'Hara B., Oliva G., Srinivasan N.,
 RA Tinkle J.J., Blundell T.L., Pepys M.B., Wood S.P.;
 RT "Structure of pentameric human serum amyloid P component.";
 RL Nature 367:338-345(1994).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=97360233; PubMed=9217261;
 RA Hohenester E., Hutchinson W.L., Pepys M.B., Wood S.P.;
 RT "Crystal structure of a decameric complex of human serum amyloid P
 RT component with bound dAMP.";
 RL J. Mol. Biol. 269:570-578(1997).
 CC -1- FUNCTION: CAN INTERACT WITH DNA AND HISTONES AND MAY SCAVENGE
 CC NUCLEAR MATERIAL RELEASED FROM DAMAGED CIRCULATING CELLS. MAY ALSO
 CC FUNCTION AS A CALCIUM-DEPENDENT LECTIN.
 CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISC
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; D00097; BA00060.1; -;
 DR EMBL; M10944; AAA60302.1; -;
 DR EMBL; X04608; CAA28275.1; -;
 DR EMBL; BC007039; AAH07039.1; -;
 DR EMBL; BC007058; AAH07058.1; -;
 DR PIR; A25503; YELAP.
 DR PDB; 1SAC; 31-UTL-94.
 DR PDB; 1LGN; 24-DEC-97.
 DR GLYCOSULEDB; P02743; -;
 DR SWISS-2DPAGE; P02743; HUMAN.
 DR Genew; HGNC:584; APCs.
 DR MIM; 104770; -;
 DR GO; GO:0005615; Cytoplasmic space; TAS.
 DR GO; GO:0003794; F-acute-phase response protein activity; TAS.
 DR GO; GO:0005208; F-amyloid protein; TAS.
 DR GO; GO:0003754; F-chaperone activity; TAS.
 DR GO; GO:0005211; F-plasma glycoprotein; TAS.
 DR GO; GO:0005209; F-plasma protein; TAS.
 DR GO; GO:0006462; F-protein complex assembly, multichaperone pa. . .; TAS.
 DR GO; GO:0006457; F-protein folding; TAS.
 DR InterPro; IPR01759; Pentaxin.
 DR Pfam; PF00354; Pentaxin; 1.
 DR PRINTS; PR00895; PENTAXIN.
 DR Prodom; PD002153; Pentaxin; 1.
 DR SMART; SM00159; PTX; 1.
 DR PROSITE; PS00289; PENTAXIN; 1.
 DR Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin; Signal; Polymorphism;
 KW 3D-structure.
 FT SIGNAL. 1 19
 FT CHAIN 20 223
 FT DOMAIN 20 223
 FT DISULFID 55 114
 FT CARBOHYD 51 51
 FT
 FT VARIANT 152 152
 FT
 FT VARIANT 155 155
 FT
 FT VARIANT 158 158
 FT
 FT CONFLICT 101 101
 FT STRAND 21 21
 FT TURN 24 25
 FT STRAND 26 30
 FT STRAND 38 42
 FT STRAND 49 49
 FT STRAND 51 59
 FT STRAND 66 73
 FT STRAND 74 75
 FT TURN 76 76
 FT STRAND 77 86
 FT TURN 87 88
 FT STRAND 89 94
 FT TURN 95 96
 FT STRAND 97 102
 FT STRAND 111 118
 FT TURN 119 121
 FT STRAND 123 128
 FT TURN 129 130
 FT STRAND 131 132
 FT STRAND 136 137
 FT TURN 140 141
 FT STRAND 144 144
 FT STRAND 149 152
 FT HELIX 165 167
 FT STRAND 171 179
 FT HELIX 185 193

FT TURN 194 194
 FT STRAND 202 203
 FT TURN 204 205
 FT STRAND 207 212
 FT STRAND 216 219
 SQ SEQUENCE 223 AA; 25387 MW; 6C88A515F88B933 CRC64;
 Query Match 87.9%; Score 29; DB 1; Length 223;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMOAL 6
 Db 202 LDMOAL 207

RESULT 11
 SAMP_PIG STANDARD; PRT; 224 AA.
 AC 019063;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DR Serum amyloid P-component precursor (SAP).
 GN APCS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Landrace; TISSUE=Liver;
 RA Ozawa A., Matsumoto M., Kajikawa M., Hanazono M., Yasue H.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -1 SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
 CC -1 SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: AB005546; BAA21474.1; -.
 DR HSP; P02743; ISAC.
 DR InterPro: IPR001759; Pentaxin.
 DR Pfam: PF00354; pentaxin; 1.
 DR PRINTS: PR00895; PENTAXIN.
 DR ProDom: PD002153; PENTAXIN; 1.
 DR SMART: SM00159; PTX; 1.
 DR PROSITE: PS00289; PENTAXIN; 1.
 DR Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin; signal.
 KW SIGNAL
 FT CHAIN 1 19
 FT DOMAIN 20 224 SERUM AMYLOID P-COMPONENT.
 FT DISULFID 55 114 PENTAXIN.
 FT CARBOHYD 51 51 BY SIMILARITY.
 SQ SEQUENCE 224 AA; 25641 MW; 9D18676915BBD66 CRC64; (POTENTIAL).

Query Match 87.9%; Score 29; DB 1; Length 224;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMOAL 6
 Db 203 LDMOAL 208

RESULT 12
 SAMP_MESAU STANDARD; PRT; 234 AA.
 AC P07629;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DR Serum amyloid P-component precursor (Female protein) (FP) (SAP(FP)).
 GN PTX2 OR SAP.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OC NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94012761; PubMed=7691816;
 RA Rudnick C.M., Dowton S.B.;
 RT "Serum amyloid P (female protein) of the Syrian hamster. Gene
 RT structure and expression."
 RL J. Biol. Chem. 268:21760-21769 (1993).
 RN [2]
 RP SEQUENCE OF 24-234 FROM N.A.
 RX MEDLINE=85218787; PubMed=2408337;
 RA Dowton S.B., Woods D.E., Mantzouranis E.C., Colten H.R.;
 RT "Syrian hamster female protein: analysis of female protein primary
 RT structure and gene expression."
 RL Science 228:1206-1208 (1985).
 RN [3]
 RP SEQUENCE OF 25-48.
 RX MEDLINE=81241327; PubMed=6166709;
 RA Coe J.E., Margosian S.S., Slayter H.S., Sogn J.A.;
 RT "Hamster female protein. A new Pentaxin structurally and
 RT functionally similar to C-reactive protein and amyloid P component."
 RL J. Exp. Med. 153:977-991 (1981).
 RN [4]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=95187705; PubMed=7881902;
 RA Srinivasan N., White H.E., Emaley J., Wood S.P., Peyys M.B.,
 RA Blundell T.L.;
 RT "Comparative analyses of pentaxins: implications for proteome
 RT assembly and ligand binding."
 RL Structure 2:1017-1027 (1994).
 CC -1 SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 MISCELLANEOUS: PLASMA CONCENTRATION OF PP ARE ALTERED BY SEX
 CC STEROIDS AND BY STIMULI THAT ELICIT AN ACUTE PHASE RESPONSE.
 CC -1 SIMILARITY: BELONGS TO THE PENTAXIN FAMILY. ORTHOLOG OF HUMAN SAP.
 CC -----
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 CC -----
 CC EMBL: L22024; AAA03577.1; -.
 DR EMBL: M11342; AAA36980.1; -.
 DR PIR: A44177; A44177.
 DR PIR: A48593; A48593.
 DR PDB: 1HAS; 15-OCT-95.
 DR InterPro: IPR001759; Pentaxin.
 DR Pfam: PF00354; pentaxin; 1.
 DR PRINTS: PR00895; PENTAXIN.
 DR ProDom: PD002153; Pentaxin; 1.
 DR SMART: SM00159; PTX; 1.
 DR PROSITE: PS00289; PENTAXIN; 1.
 DR Lectin; Pentaxin; Plasma; Acute phase; signal; Amyloid; Glycoprotein;
 KW 3D-structure.
 FT SIGNAL 1 22 POTENTIAL.

```

FT CHAIN 23 234 SERUM AMYLOID P-COMPONENT.
FT DOMAIN 23 234 PENTAXIN.
FT DISULFID 58 117 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 27 27 T -> S (IN REF. 3).
FT CONFLICT 43 43 K -> N (IN REF. 3).
FT CONFLICT 76 76 A -> T (IN REF. 2).
FT STRAND 24 24
FT TURN 27 28
FT STRAND 29 33
FT STRAND 41 44
FT STRAND 52 52
FT STRAND 54 62
FT STRAND 69 76
FT TURN 77 78
FT STRAND 79 89
FT TURN 90 91
FT STRAND 92 97
FT TURN 98 99
FT STRAND 100 105
FT STRAND 113 121
FT TURN 122 125
FT STRAND 126 131
FT TURN 132 133
FT STRAND 134 135
FT STRAND 139 140
FT TURN 143 144
FT STRAND 147 147
FT STRAND 152 155
FT HELIX 168 170
FT STRAND 174 182
FT HELIX 188 196
FT TURN 197 197
FT STRAND 205 205
FT TURN 207 208
FT STRAND 210 210
FT STRAND 212 215
FT STRAND 219 222
FT HELIX 226 234
SQ SEQUENCE 234 AA; 26463 MW; 6161F0383062D2DB CRC64;

Query Match 87.9%; Score 29; DB 1; Length 234;
Best Local Similarity 83.3%; Pred. NO. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DMSAL 6
DB 205 LDMSAL 210

RESULT 13
CXAG RAT STANDARD; PRT; 286 AA.
ID CXAG RAT
AC P2823;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gap junction alpha-6 protein (Connexin 33) (Cx33).
GN GA6 OR CXN-33.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112940; PubMed=1370487;
RA Hefflinger J.-A., Bruzzone R., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Paul D.L.;
RT "Four novel members of the connexin family of gap junction proteins.
RT Molecular cloning, expression, and chromosome mapping.";
RT J. Biol. Chem. 267:2057-2064(1992).
CC -1- FUNCTION: One gap junction consists of a cluster of closely packed
CC pairs of transmembrane channels, the connexons, through which

```

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CC materials of low mw diffuse from one cell to a neighboring cell.
CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in testis.
CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
CC SUBFAMILY.
CC -----
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CC -----
CC DR EMBL, M76534; AAA0998.1; -.
CC DR PIR, C42053; C42053.
CC DR InterPro, IPR000500; Connexin.
CC DR Pfam, PF00029; connexin.1.
CC DR PRINTS, PR00206; CONNEXIN.
CC DR SMART, SM00037; CNX, 1.
CC DR PROSITE, PS00407; CONNEXINS_1; 1.
CC DR PROSITE, PS00408; CONNEXINS_2; 1.
CC KW Gap junction; Transmembrane.
FT DOMAIN 1 23 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 24 23
FT DOMAIN 42 41 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 77 99 POTENTIAL.
FT DOMAIN 100 151 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 152 174 POTENTIAL.
FT DOMAIN 175 209 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 210 232 POTENTIAL.
FT DOMAIN 233 286 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 286 AA; 32860 MW; A585266ACA2ACCF2 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. NO. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSAL 6
DB 3 DMSAL 7

RESULT 14
SGBU ECOLI STANDARD; PRT; 286 AA.
ID SGBU ECOLI
AC P37679;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative hexulose-6-phosphate isomerase (EC 5.-.-.-) (HUMPI).
GN SGBU OR B3582.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=KL2 / MG1655;
RX MEDLINE=9416500; PubMed=8041620;
RX Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RA "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT region from 76.0 to 81.5 minutes.";
RT Nucleic Acids Res. 22:2576-2586(1994).
RN [2]
RP DISCUSSION OF SEQUENCE.
RA Reizer U., Charbit A., Reizer A., Sela M.H. Jr.;
RT "Novel phosphotransferases system genes revealed by bacterial genome
RT analysis: operons encoding homologues of sugar-specific permease
RT domains of the phosphotransferase system and pentose catabolic
RT enzymes.";
RL Genome Sci. Technol. 1:53-75(1996).

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CC -1- FUNCTION: ISOMERIZATION OF D-ARABINO-6-HEXULOSE 3-PHOSPHATE TO
CC D-FRUCTOSE 6-PHOSPHATE.
CC -1- PATHWAY: PROBABLY PART OF A SUGAR METABOLIC PATHWAY ALONG WITH
CC SGBH.
CC -1- SIMILARITY: BELONGS TO THE HUMPI FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U00039; AAB18559.1; ALT INIT.
DR EMBL; AE000435; AAC76606.1; ALT_INIT.
DR EcGene; EG12286; ggbu
DR InterPro; IPR004560; Hx16Piso_put.
DR Pfam; PF03809; Hx16Piso_put; 1.
DR TIGRFAMs; TIGR00542; Hx16Piso_put; 1.
DR Isomerase; Complete proteome.
SQ SEQUENCE 286 AA; 32455 MW; 4C849F575E937BF9 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSA 5
Db 48 LDMSA 52

RESULT 15
CYCG_RHOSH STANDARD; PRT; 296 AA.
AC Q53143;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Diheme cytochrome C-type.
GN CYCG
OS Rhodobacter sphaeroides (Rhodospirillum rubrum)
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A..
RC STRAIN:ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=95362655; PubMed=7543472;
RA Flory J.E., Donohue T.J.;
RT "Organization and expression of the Rhodobacter sphaeroides cycFG
RT operon."
RL J. Bacteriol. 177:4311-4320 (1995).
CC -1- FUNCTION: DIHEME C-TYPE CYTOCHROME, THAT IS PARTICULARLY EXPRESSED
CC WHEN CELLS GENERATE ENERGY VIA AEROBIC RESPIRATION.
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- PTM: BINDS TWO HEME GROUPS PER MOLECULE (POTENTIAL).
CC -1- SIMILARITY: TO ACETOBACTER ALCOHOL DEHYDROGENASE CYTOCHROME C
CC SUBUNIT.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L36880; AAD09146.1; -
DR InterPro; IPR003088; Cyt_C1.
DR InterPro; IPR003219; CytC adh.
DR InterPro; IPR000345; CytC_heme_bind.
DR Pfam; PF00034; Cytochrome_c; 1.

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DR ProDom; PD011584; CytC adh; 1.
DR PROSITE; PS00190; CYTOCHROME C; 2.
DR Electron transport; Heme; Membrane.
FT BINDING 52 52 HEME 1 (COVALENT) (BY SIMILARITY).
FT BINDING 55 55 HEME 1 (COVALENT) (BY SIMILARITY).
FT METAL 56 56 IRON (HEM 1 AXIAL LIGAND)
FT BINDING 202 202 HEME 2 (COVALENT) (BY SIMILARITY).
FT BINDING 205 205 HEME 2 (COVALENT) (BY SIMILARITY).
FT METAL 206 206 IRON (HEM 2 AXIAL LIGAND)
FT (BY SIMILARITY).
SQ SEQUENCE 296 AA; 31727 MW; 4C4A9D8F695B5BFD CRC64;

Query Match 87.9%; Score 29; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSA 5
Db 241 LDMSA 245

Search completed: February 18, 2004, 14:28:11
Job time : 4.55263 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 / Search time 6.5921 Seconds

(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDMSAL 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	330	2	B69416
2	31	93.9	192	2	P82645
3	31	93.9	333	2	S75980
4	31	93.9	984	2	S67527
5	31	93.9	1394	2	S66876
6	31	93.9	2297	2	T34918
7	30	90.9	163	2	D84320
8	30	90.9	208	2	D75556
9	30	90.9	261	2	A69807
10	30	90.9	280	2	D97195
11	30	90.9	365	2	P82398
12	30	90.9	380	2	D83088
13	30	90.9	384	2	AC0149
14	30	90.9	401	2	D83618
15	30	90.9	442	2	T20638
16	30	90.9	476	2	E82758
17	30	90.9	572	2	T37128
18	30	90.9	638	2	F75547
19	30	90.9	1026	2	T39612
20	30	90.9	1293	2	T30871
21	30	90.9	1471	2	F86218
22	30	90.9	1616	2	T00713
23	29	87.9	32	2	A24047
24	29	87.9	94	2	S77047
25	29	87.9	119	2	S74925
26	29	87.9	119	2	S75488
27	29	87.9	119	2	S74836
28	29	87.9	119	2	S75590
29	29	87.9	150	2	A83754

30	29	87.9	171	2	S75475	transposase glr152
31	29	87.9	177	2	AG2498	hypothetical prote
32	29	87.9	211	2	A44177	female protein - g
33	29	87.9	214	2	G83488	probable permease
34	29	87.9	215	2	H82830	conserved hypothet
35	29	87.9	223	1	YLHUP	serum amyloid P-co
36	29	87.9	232	2	P82729	conserved hypothet
37	29	87.9	234	2	A48593	serum amyloid P-co
38	29	87.9	242	2	G87696	hypothetical prote
39	29	87.9	279	2	F70612	hypothetical prote
40	29	87.9	282	2	S76906	transposase glr023
41	29	87.9	282	2	S76382	transposase glr035
42	29	87.9	282	2	S76312	transposase glr135
43	29	87.9	282	2	S77237	transposase glr135
44	29	87.9	282	2	S75484	transposase glr135
45	29	87.9	286	1	C42053	gap junction prote

ALIGNMENTS

RESULT 1

B69416 hypothetical protein AF1331 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C>Date: 05-Dec-1997 #sequence_rev100 05-Dec-1997 #text_change 22-Oct-1999

C:Accession: B69416

R:Klenk, H.B.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Usterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.

A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A:Reference number: A69250; PMID:98049343; PMID:9389475

A:Accession: B69416

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-330 <KLE>

A:Cross-references: GB:AE001012; GB:AE000782; NID:G2689335; PIDN:AA89926.1; PID:G26492

A:Query Match

Best Local Similarity 100.0%; Score 33; DB 2; Length 330;

Query Match 100.0%; Pred. No. 69;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6

Db 177 LDMSAL 182

RESULT 2

P82645

tryptophan repressor binding protein XF1733 [imported] - Xylella fastidiosa (strain 9a)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_rev100 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: P82645

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ

Nature 406, 151-157, 2000

A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; PMID:20365717; PMID:10910347

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: P82645

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-192 <SIM>

A:Cross-references: GB:AE003996; GB:AE003849; NID:G9106790; PIDN:AA894542.1; GSPDB:GNOC

A:Experimental source: strain 9a5c

R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carrero, D.M.; Carrer,

de-Neco, E.; Docena, C.; El-Dorri, H.; Facinican, A.P.; Ferreira, A.J.S.

Submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, M.C.; Froh

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chdo, M.A.; Madalira, A.M.B.N.; Madalira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
 A.; Nethers, M.L.; Nethers, E.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
 Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawaak
 A.; Nethers, M.L.; Nethers, E.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
 Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawaak
 M.; Tanaka, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A.; Reference number: A59328
 A;Contents: annotation
 C;Genetics:
 A;Gene: XP1733

Query Match 93.9%; Score 31; DB 2; Length 192;
 Best Local Similarity 83.3%; Pred. No. 93;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 :|||||
 Db 43 MDMSAL 48

RESULT 3
 S75980
 hypothetical protein slr0537 - *Synechocystis* sp. (strain PCC 6803)

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Date: 25-Apr-1997

R;Kaneho, T.; Sato, S.; Kocani, H.; Tanaka, A.; Asami, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Rep. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
 8.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S75980

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Cross-references: EMBL:D44006; GB:AB001339; NID:g1001291; PIDN:BA10827.1; PID:g100134
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Superfamily: probable ribokinase

Query Match 93.9%; Score 31; DB 2; Length 333;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 :|||||
 Db 146 MDMSAL 151

RESULT 4
 S67527
 protein kinase (EC 2.7.1.-) PRK2 - human

C;Species: *Homo sapiens* (man)

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jul-2000

C;Accession: S67527; I67464

R;Palmer, R.H.; Ridden, J.; Parker, P.J.
 Eur. J. Biochem. 227, 344-351, 1995

A;Title: Cloning and expression patterns of two members of a novel protein-kinase-C-rela
 A;Reference number: I53327; MUID:95154310; PMID:7851406

A;Accession: S67527

A;Molecule type: mRNA

A;Residues: 1-984 <PML>

A;Cross-references: EMBL:S75548; NID:g914099; PIDN:AAB3346.1; PID:g914100

A;Experimental source: fetal brain

A;Accession: I67464

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: mRNA

A;Residues: 1-984 <RKS>

A;Cross-references: GB:S75548; NID:g914099; PIDN:AAB3346.1; PID:g914100
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 F;555-916/Domain: protein kinase homology <KIN>

F:663-671/Region: protein kinase ATP-binding motif
 F:686/Active site: Lys #status predicted

Query Match 93.9%; Score 31; DB 2; Length 984;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 :|||||
 Db 919 IDMSAL 924

RESULT 5
 S66876
 ATP-dependent transport protein homolog YOR011w - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: ATP-dependent permease homolog; protein O2601; protein UNA841

C;Species: *Saccharomyces cerevisiae*

C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002

C;Accession: S66876; S66877; S54617; S61995; S72144

R;Peterson, B.; Sterky, F.; Uhlen, M.
 submitted to the Protein Sequence Database, July 1996

A;Reference number: S66882

A;Accession: S66876

A;Molecule type: DNA

A;Residues: 1-841 <PBT>

A;Cross-references: EMBL:S74919; MIPS:YOR011w

A;Experimental source: strain S288C

R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
 submitted to the Protein Sequence Database, July 1996

A;Reference number: S66877

A;Accession: S66877

A;Molecule type: DNA

A;Residues: 355-1394 <DEM>

A;Cross-references: EMBL:X87331

R;Sterky, F.; Uhlen, M.
 submitted to the EMBL Data Library, December 1995

A;Reference number: S61981

A;Accession: S61995

A;Molecule type: DNA

A;Residues: 389-841 <STB>

A;Cross-references: EMBL:U43491; NID:g1150992; PIDN:AAC49491.1; PID:g1151007

R;Sterky, F.; Holmberg, A.; Pettersson, B.; Uhlen, M.
 Yeast 12, 1091-1095, 1996

A;Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from *Saccha*
 A;Reference number: S72130; MUID:97051599; PMID:8896276

A;Accession: S72144

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 389-841 <ST2>

A;Cross-references: EMBL:U43491; NID:g1150992; PIDN:AAC49491.1; PID:g1151007

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995

C;Genetics:
 A;Gene: SGD:YUS1

A;Cross-references: SGD:S0005537

A;Map position: 15R

A;Note: YOR011w

C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

C;Keywords: ATP; nucleotide binding; P-loop; transmembrane protein

F:49-249/Domain: ATP-binding cassette homology <ABC1>

F:391-407/Domain: transmembrane #status predicted <TM1>

F:421-437/Domain: transmembrane #status predicted <TM2>

F:476-492/Domain: transmembrane #status predicted <TM3>

F:501-517/Domain: transmembrane #status predicted <TM4>

F:527-543/Domain: transmembrane #status predicted <TM5>

F:540-656/Domain: transmembrane #status predicted <TM6>

F/766-954/Domain: ATP-binding cassette homology <ABC2>
 F/762-789/Region: nucleotide-binding motif A (p-loop)
 F/1107-1123/Domain: transmembrane #status predicted <TM7>
 F/1166-1182/Domain: transmembrane #status predicted <TM8>
 F/1226-1242/Domain: transmembrane #status predicted <TM9>

Query Match 93.9%; Score 31; DB 2; Length 1394;
 Best Local Similarity 83.3%; Pred. No. 7.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 DB 1017 LDMSAL 1022

RESULT 6
 T34918
 polyketide synthase - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Nov-2000

C/Accession: T34918
 R/Oliver, K.; Harrell, D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, January 1998
 A/Reference number: 221558
 A/Accession: T34918

A/Status: preliminary; translated from GB/EMBL/DBD8
 A/Molecule type: DNA
 A/Residues: 1-2297 <OLI>
 A/Cross-references: EMBL:AL021409; PIDN:CAAL1613.1; GSPDB:GNO0070; SCODEB:SC3F7.12
 A/Experimental source: strain A3(2)
 C/Genetics:

A/Genes: SCODEB:SC3F7.12
 C/Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acetate-CoA ligase
 C/Keywords: carrier protein
 F/80-583/Domain: acetate-CoA ligase homology <ACL>
 F/701-771/Domain: acyl carrier protein homology <ACP>
 F/818-1205/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
 F/1315-1600/Domain: [acyl-carrier-protein] 5-malonyltransferase homology <AMT>

Query Match 93.9%; Score 31; DB 2; Length 2297;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 DB 1641 LDMSAL 1646

RESULT 7
 DB4320
 hypothetical protein Vng1679h (imported) - Halobacterium sp. NRC-1
 C/Species: Halobacterium sp. NRC-1
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C/Accession: DB4320
 R/Ng, W.V.; Kennedy, S.P.; Mahatras, G.G.; Benjicic, B.; Pan, M.; Shukla, H.D.; Laaky, S.
 ; Leitauer, B.; Keller, K.; Cruz, R.; Danon, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
 pong, K.H.; Alam, M.; Prells, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A/Title: Genome sequence of Halobacterium species NRC-1.
 A/Reference number: A84160; MID:20504483; PMID:11016550
 A/Accession: DB4320

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-163 <STO>
 A/Cross-references: GB:AE004437; NID:G10581148; PIDN:AA31928.1; GSPDB:GNO0138
 C/Genetics:
 A/Genes: VNG1679H

Query Match 90.9%; Score 30; DB 2; Length 163;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 DB 142 LDMSAL 147

RESULT 8
 D75556
 phosphoribosylanthranilate isomerase - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C/Accession: D75556
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 ; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S
 .; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MID:20036896; PMID:10567266
 A/Accession: D75556

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-208 <WHI>
 A/Cross-references: GB:AE001875; GB:AE000513; NID:G6457790; PIDN:ANF09715.1; PID:G6457
 A/Experimental source: strain R1
 C/Genetics:

A/Genes: DR0123
 C/Superfamily: 1
 A/Map position: 1
 C/Superfamily: phosphoribosylanthranilate isomerase; trpF homology

Query Match 90.9%; Score 30; DB 2; Length 208;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
 DB 144 LDMSAL 149

RESULT 9
 A69807
 3-hydroxyisobutyrate dehydrogenase homolog yfjR - Bacillus subtilis
 C/Species: Bacillus subtilis
 C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 18-Aug-2000
 C/Accession: A69807

R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berti
 C.; Bron, S.; Brouillet, S.; Bruscia, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cl
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
 Nature 390, 249-256, 1997

A/Authors: Poulger, D.; Fritz, C.; Fujita, M.; Fuma, S.; Galizzi, A.; Gall
 iech, J.; Harwood, C.R.; Hentut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A.; Luthers, L.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maguda, S.; Mauel
 y, M.; Ogasawara, N.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
 ; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
 A.; Authors: Schlach, S.; Schoerer, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser
 akuchi, M.; Tanakoshi, A.; Tanaka, T.; Tempere, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida
 A.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A/Reference number: A69580; MID:98044033; PMID:9384377
 A/Accession: A69807

A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-261 <KUN>
 A/Cross-references: GB:Z99108; GB:AL009126; NID:G2631055; PIDN:CA12628.1; PID:G263112
 A/Experimental source: strain 168
 C/Genetics:

A/Genes: yfjR
 C/Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
 F/2-240/Domain: 3-hydroxyisobutyrate dehydrogenase homology #status atypical <HIB>

Query Match 90.9%; Score 30; DB 2; Length 261;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
|||:
Db 251 LDMSAL 256

RESULT 10

D97195
Probable xylosyltransferase [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C/Accession: D97195
R/No: 1
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: D97195
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-280 <KUR>
A/Cross-references: GB:AE001437; PIDN:AK60351.1; PID:G15025409; GSPDB:GN00168
C/Experimental source: Clostridium acetobutylicum ATCC824
A/Genetic: CAC2396

Query Match 90.9%; Score 30; DB 2; Length 280;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
|||:
Db 212 LDMSAL 217

RESULT 11

F82398
Transcription regulator Arac/Xy1S family VCA0926 [imported] - Vibrio cholerae (strain NL
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C/Accession: F82398
R/No: 1
J. Bacteriol. 183, 4823-4838, 2001
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: F82398
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-365 <HEI>
A/Cross-references: GB:AE004420; GB:AE003853; NID:G9656361; PIDN:AAF96823.1; GSPDB:GN001
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetic: A/Map position: 2

Query Match 90.9%; Score 30; DB 2; Length 365;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
|||:
Db 70 LDMSAL 75

RESULT 12

D82088
Chromate resistance protein VC2339 [imported] - Vibrio cholerae (strain
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C/Accession: D82088
R/No: 1
J. Bacteriol. 183, 4823-4838, 2001
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: D82088
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-401 <STO>
A/Cross-references: GB:AE004460; GB:AE004091; NID:G9946055; PIDN:AA03617.1; GSPDB:GNO
C/Experimental source: strain PA01

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Baes, S.; Qin, H.; Dragol, I.; Sellers,
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: D82088
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-380 <HEI>
A/Cross-references: GB:AE004304; GB:AE003852; NID:G9656905; PIDN:AAF95482.1; GSPDB:GNO
C/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetic: A/Map position: 1
C/Superfamily: chromate resistance protein A

Query Match 90.9%; Score 30; DB 2; Length 380;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
|||:
Db 344 LDMSAL 349

RESULT 13

AG0149
Probable membrane protein YPO1221 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C/Accession: AG0149
R/No: 1
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AG0149
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-384 <KUR>
A/Cross-references: GB:AL590842; PIDN:CA090058.1; PID:G15979278; GSPDB:GN00175
C/Genetic: A/Map position: 2

Query Match 90.9%; Score 30; DB 2; Length 384;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
|||:
Db 228 LDMSAL 233

RESULT 14

D83618
beta-ketoadipyl CoA thiolase Pcaf PA0228 [imported] - Pseudomonas aeruginosa (strain P.
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Accession: D83618
R/No: 1
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat.
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: D83618
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-401 <STO>
A/Cross-references: GB:AE004460; GB:AE004091; NID:G9946055; PIDN:AA03617.1; GSPDB:GNO
C/Experimental source: strain PA01

A:Gene: pcacF; PA0228
C:Superfamily: acetyl-CoA acetyltransferase

Query Match 90.9%; Score 30; DB 2; Length 401;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
:|||||
Db 45 VDWSAL 50

RESULT 15

T20638

hypothetical protein T06H11.4 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C/Accession: T20638; T24630

R/Kershaw, J.

submitted to the EMBL Data Library, June 1995

A/Reference number: Z19303

A/Accession: T20638

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-442 <NT>

A/Cross-references: EMBL:Z49887; PIDN:CAA90060.1; GSPDB:GN00028; CESP:T06H11.4

A/Experimental source: clone F0989

R/Kershaw, J.

submitted to the EMBL Data Library, June 1995

A/Reference number: Z19914

A/Accession: T24630

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-442 <NT>

A/Cross-references: EMBL:Z49889; PIDN:CAA90069.1; GSPDB:GN00028; CESP:T06H11.4

A/Experimental source: clone T06H11

C/Genetics:

A:Gene: CESP:T06H11.4

A/Map position: X

A/Intons: 45/1; 95/3; 150/2; 208/3; 250/2; 292/3

C:Superfamily: molybdenum cofactor biosynthesis protein moea-2

Query Match 90.9%; Score 30; DB 2; Length 442;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
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Db 39 VDWSAL 44

Search completed: February 18, 2004, 14:38:49
Job time : 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds

75.239 million cell updates/sec

Title:	US-09-643-260-13
Parfact score:	22

Sequence:

Scoring table: BLOSUM62

Gapor 10.0 , Gapext 0.5

Searched: 801455 beqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database

- 1: /cgn2_6/ptodata1/1/pubppaa/PSO7_PUBCOMB.dep:*
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- 9: /cgn2_6/ptodata1/1/pubppaa/USO9A_PUBCOMB.dep:*
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- 11: /cgn2_6/ptodata1/1/pubppaa/USO9C_PUBCOMB.dep:*
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- 15: /cgn2_6/ptodata1/1/pubppaa/USO10C_PUBCOMB.dep:*
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- 17: /cgn2_6/ptodata1/1/pubppaa/USO6_NEW_PUB.dep:*
- 18: /cgn2_6/ptodata1/1/pubppaa/USO6_PUBCOMB.dep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	100.0	6	10	US-09-847-940B-13	Sequence 13, App1
2	33	100.0	7	11	US-09-847-946A-13	Sequence 13, App1
3	33	100.0	5	12	US-10-148-786A-25	Sequence 25, App1
4	31	93.9	77	12	US-10-148-786A-8	Sequence 8, App1
5	31	93.9	333	12	US-10-369-483-2852	Sequence 2852, App1
6	31	93.9	334	12	US-10-217-574-18	Sequence 18, App1
7	31	93.9	374	12	US-10-217-555-18	Sequence 18, App1
8	31	93.9	502	9	US-09-695-072-13	Sequence 13, App1
9	31	93.9	502	10	US-09-986-552-13	Sequence 13, App1
10	31	93.9	502	12	US-10-023-8894-16	Sequence 16, App1
11	31	93.9	502	12	US-10-024-197-16	Sequence 16, App1
12	31	93.9	502	12	US-10-306-686-13	Sequence 13, App1
13	31	93.9	502	15	US-10-023-888-16	Sequence 16, App1
14	31	93.9	502	15	US-10-023-889-16	Sequence 16, App1
15	31	93.9	502	15	US-10-023-890-16	Sequence 16, App1

16	31	93.9	652	12	US-10-320-801-91	Sequence 91, Appl
17	31	93.9	984	12	US-10-354-385-106	Sequence 106, Appl
18	31	93.9	984	12	US-10-029-905-10	Sequence 10, Appl
19	31	93.9	1394	12	US-10-369-493-22253	Sequence 22353, A
20	30	90.9	1384	12	US-10-029-386-34138	Sequence 34138, A
21	30	90.9	208	12	US-10-369-499-23401	Sequence 23401, A
22	30	90.9	403	15	US-10-156-761-14428	Sequence 14428, A
23	30	90.9	476	12	US-10-310-154-397	Sequence 397, Appl
24	30	90.9	516	14	US-10-119-633-2	Sequence 2, Appl11
25	30	90.9	1293	12	US-10-1084-846A-50	Sequence 50, Appl1
26	30	90.9	2747	12	US-10-402-842-2	Sequence 2, Appl11
27	30	90.9	19725	12	US-10-084-846A-4	Sequence 4, Appl11
28	29	87.9	175	12	US-10-320-797-3024	Sequence 3024, Ap
29	29	87.9	203	12	US-10-262-473-4	Sequence 4, Appl11
30	29	87.9	223	12	US-10-062-473-2	Sequence 2, Appl11
31	29	87.9	268	12	US-10-084-846A-16	Sequence 16, Appl
32	29	87.9	227	15	US-10-156-761-14290	Sequence 14290, A
33	29	87.9	292	12	US-10-238-075-301	Sequence 301, App
34	29	87.9	297	11	US-09-557-796-30	Sequence 30, Appl
35	29	87.9	300	12	US-10-314-657-11	Sequence 11, Appl
36	29	87.9	324	15	US-10-156-761-7691	Sequence 7691, Ap
37	29	87.9	345	11	US-09-735-055-34	Sequence 34, Appl
38	29	87.9	352	12	US-10-289-762-702	Sequence 702, App
39	29	87.9	382	12	US-10-024-296A-113	Sequence 113, Appl
40	29	87.9	382	12	US-10-024-296A-115	Sequence 115, Appl
41	29	87.9	382	12	US-10-042-211A-113	Sequence 113, Appl
42	29	87.9	382	12	US-10-042-211A-115	Sequence 115, Appl
43	29	87.9	382	12	US-10-438-537-6	Sequence 6, Appl1
44	29	87.9	382	12	US-10-372-683-28	Sequence 28, Appl
45	29	87.9	426	12	US-10-369-493-3236	Sequence 3236, Ap

ALIGNMENTS

```

RESULT 1
US-09-847-940B-13
; Sequence 13 Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description: NBD mutan
; US-09-847-940B-13

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Query Match	100.0%;	Score 33;	DB 10;	length 6;
Best Local Similarity	100.0%;	Pred. No. 78+05;		
Matches	6;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
Qy	1	LDWSAL	6	
db	1	LDWSAL	6	

RESULT 2
US-09-847-946A-13
; Sequence 13, Application US/098479466
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathy
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NBD peptide
US-09-847-946A-13

Query Match 100.0%; Score 33; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 1 LDMSAL 6

RESULT 3
US-10-148-786A-25
Sequence 25, Application US/10148786A
Publication No. US20030143656A1
GENERAL INFORMATION:
APPLICANT: Aleassi, Dario
APPLICANT: Biondi, Riccardo
TITLE OF INVENTION: Protein Kinase Regulation
FILE REFERENCE: 002.00210
CURRENT APPLICATION NUMBER: US/10/148,786A
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 53
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-10-148-786A-25

Query Match 93.9%; Score 31; DB 12; Length 53;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 12 LDMSAL 17

RESULT 4
US-10-148-786A-8
Sequence 8, Application US/10148786A
Publication No. US20030143656A1
GENERAL INFORMATION:
APPLICANT: Aleassi, Dario
APPLICANT: Biondi, Riccardo
TITLE OF INVENTION: Protein Kinase Regulation
FILE REFERENCE: 002.00210
CURRENT APPLICATION NUMBER: US/10/148,786A
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 68

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 77
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-10-148-786A-8

Query Match 93.9%; Score 31; DB 12; Length 77;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 12 LDMSAL 17

RESULT 5
US-10-369-493-2852
Sequence 2852, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2852
LENGTH: 333
TYPE: PRT
ORGANISM: Synechocystis sp.
US-10-369-493-2852

Query Match 93.9%; Score 31; DB 12; Length 333;
Best Local Similarity 83.3%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 146 MDMSAL 151

RESULT 6
US-10-217-574-18
Sequence 18, Application US/10217574
Publication No. US20040005687A1
GENERAL INFORMATION:
APPLICANT: Barford, David
APPLICANT: Yang, Jing
APPLICANT: Hemmings, Brian A
APPLICANT: Cron, Peter D
TITLE OF INVENTION: Kinase Crystal Structures
FILE REFERENCE: 44237
CURRENT APPLICATION NUMBER: US/10/217,574
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: GB 0119860.5
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: GB 020985.1
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: GB 0216215.4
PRIOR FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18

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; LENGTH: 334
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Sequence source
; OTHER INFORMATION: uncertain
US-10-217-574-18

Query Match      93.9%; Score 31; DB 12; Length 334;
Best Local Similarity 83.3%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
DB      269 LDMSAL 274

RESULT 7
US-10-217-555-18
; Sequence 18, Application US/10217555
; Publication No. US2004009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemminge, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Sequence source
; OTHER INFORMATION: uncertain
US-10-217-555-18

Query Match      93.9%; Score 31; DB 12; Length 334;
Best Local Similarity 83.3%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
DB      269 LDMSAL 274

RESULT 8
US-09-895-072-13
; Sequence 13, Application US/09895072
; Patent No. US2002002550A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM M
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 210119US00NT
; CURRENT APPLICATION NUMBER: US/09/895,072
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: US 09/635,872
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 502
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```

; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-895-072-13

Query Match      93.9%; Score 31; DB 9; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
DB      372 LDMSAM 377

RESULT 9
US-09-986-552-13
; Sequence 13, Application US/09986552
; Patent No. US20020150981A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASE:
; FILE REFERENCE: 215089US77DIV
; CURRENT APPLICATION NUMBER: US/09/986,552
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/635,872
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-986-552-13

Query Match      93.9%; Score 31; DB 10; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
DB      372 LDMSAM 377

RESULT 10
US-10-023-894-16
; Sequence 16, Application US/10023894
; Publication No. US2003014369A1
; GENERAL INFORMATION:
; APPLICANT: KORNFIELD, WILLIAM
; APPLICANT: KORNFIELD, Stuart
; TITLE OF INVENTION: EXPRESSION OF LYSOSOMAL HYDROLASE IN CELLS EXPRESSING PRO-N-
; FILE REFERENCE: ACETYLGLUCOSAMINE-1-PHOSPHODIESTER ALPHA-N-ACETYL GLUCOSIMANID;
; FILE REFERENCE: 217139US77
; CURRENT APPLICATION NUMBER: US/10/023,894
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-023-894-16

Query Match      93.9%; Score 31; DB 12; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
DB      372 LDMSAM 377
```

```

RESULT 11
US-10-024-197-16
; Sequence 16, Application US/10024197
; Publication No. US2003013924A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: HIGHLY PHOSPHORYLATED ACID BETA-GLUCOSIDASE AND METHODS
; TITLE OF INVENTION: TREATING GAUCHER'S DISEASE
; FILE REFERENCE: 209794US0
; CURRENT APPLICATION NUMBER: US/10/024,197
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-024-197-16

Query Match          93.9%; Score 31; DB 12; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
        |||||:
Db      372 LDMSAM 377

RESULT 12
US-10-306-686-13
; Sequence 13, Application US/10306686
; Publication No. US20030148460A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: PHOSPHODIESTER ALPHA-GLUCANASE OF THE LYSOSOMAL TARGETING PATHWAY
; FILE REFERENCE: 230397US77D1V
; CURRENT APPLICATION NUMBER: US/10/306,686
; CURRENT FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: 09/636,596
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-08-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-306-686-13

Query Match          93.9%; Score 31; DB 12; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
        |||||:
Db      372 LDMSAM 377

RESULT 13
US-10-023-888-16
; Sequence 16, Application US/10023888
; Publication No. US20030119086A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: SOLUBLE GLCNAC PHOSPHOTRANSFERASE
; FILE REFERENCE: 203515US77
; CURRENT APPLICATION NUMBER: US/10/023,888
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502

```

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; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-023-888-16

Query Match          93.9%; Score 31; DB 15; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
        |||||:
Db      372 LDMSAM 377

RESULT 14
US-10-023-889-16
; Sequence 16, Application US/10023889
; Publication No. US20030124652A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS OF PRODUCING HIGH MANNOSE GLYCOPROTEINS IN COMPLEX CARB
; FILE REFERENCE: 203512US77
; CURRENT APPLICATION NUMBER: US/10/023,889
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-023-889-16

Query Match          93.9%; Score 31; DB 15; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
        |||||:
Db      372 LDMSAM 377

RESULT 15
US-10-023-890-16
; Sequence 16, Application US/10023890
; Publication No. US20030124653A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHOD OF PRODUCING GLYCOPROTEINS HAVING REDUCED COMPLEX CARBOH
; FILE REFERENCE: 203510US77
; CURRENT APPLICATION NUMBER: US/10/023,890
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-023-890-16

Query Match          93.9%; Score 31; DB 15; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
        |||||:
Db      372 LDMSAM 377

Search completed: February 18, 2004, 15:41:59
Job time : 16.7529 secs

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XX	02-MAY-2001; 2001IWO-US40654.
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(UYUA) UNIV YALE.
XX	
P1	May MJ, Ghosh S;
XX	
DR	WPI; 2002-179350/23.
PT	Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT	inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT	cell with an anti-inflammatory compound comprising at least one NEMO
XX	binding domain -
PS	Claim 23, Page 45; 82pp; English.
XX	
CC	The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC	comprises contacting a cell with an anti-inflammatory compound
CC	(ABB087225-ABB08742) comprising at least one NEMO binding domain
CC	(ABB77313). The compound has acts through selective inhibition of
CC	cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC	with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC	interaction results in inhibition of IKKbeta kinase activation and
CC	subsequent decreased phosphorylation of Ikapab. The compound may also
CC	act (directly or indirectly) by blocking the recruitment of leukocytes
CC	into sites of acute and chronic inflammation, by down-regulating the
CC	expression of E-selectin on leukocytes or by blocking osteoclast
CC	differentiation. The compound is useful in treating NF-kB mediated
CC	conditions, where the condition is an inflammatory disorder, an
CC	autoimmune disease, transplant rejection, osteoporosis, cancer,
CC	Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC	relating to cancer. The inflammatory disorder is asthma, allergies,
CC	urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC	bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC	burns. The inflammatory disorder may also be dermatitis, eczema,
CC	psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC	spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC	polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC	cryoglobulinemia or multiple sclerosis. For chronic viral infections
CC	caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC	diseases include HIV and influenza. The compound may also be useful for
CC	treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC	sunburn or aging. The compound may be used to replace corticosteroids in
CC	any application in which corticosteroids are used, including
CC	immunosuppression in transplants and cancer therapy. Also for identifying
CC	anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
CC	The compound may be administered alone or in combination with other known
CC	anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC	binding domain of IKKbeta.
XX	
XX	Sequence 6 AA;
QY	1 LDWSAL 6
DB	1 LDWSAL 6
QY	100.0%; Score 33; DB 23; Length 6;
DB	100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0.
XX	
XX	AA048518 standard; Peptide; 6 AA.
XX	AA048518;
XX	20-MAR-2002 (first entry)
XX	
XX	NBD mutant peptide SEQ ID NO 13.
DE	

XX	Anti-inflammatory; antiaesthetic; cytostatic; antiproliferative; neurotropic;
KW	antirheumatic; antiarthritic; osteopathic; antibacterial; vitamin;
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW	cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS	Synthetic.
PN	WO200183554-A2.
PD	08-NOV-2001.
PF	02-MAY-2001; 2001WO-0514346.
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	(PRAE-) PRAECIS PHARM INC.
PA	(TYTA) UNITV YALE.
PI	May MJ, Ghosh S, Findeis MA, Phillips K;
XX	WPI; 2002-121889/16.
DR	XX
XX	Novel anti-inflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	Example 6; Page 48; 88pp; English.
PS	XX
XX	The invention relates to an anti-inflammatory compound (especially
CC	AMM48628-AMM48645), comprising a membrane translocation domain
CC	(AMM48620-AMM48627 or AMM48646-AMM48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AMM48525-AMM48619). The anti-inflammatory compounds have antiaesthetic,
CC	cytostatic, antiproliferative, antineumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	neurotropic, antiatherosclerotic, vitamin and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NF-kappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursts; autoimmune diseases such as lupus, polyarthritis, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	XX
XX	Sequence 6 AA;
QY	Query Match 100.0%; Score 33; DB 23; Length 6;
DB	Best Local Similarity 100.0%; Pred. No. 9 3e+05;
DB	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 LDMSAL 6
DB	1 LDMSAL 6
DB	ABU08428
ID	ABU08428 standard; peptide; 6 AA.

XX AC ABU08428;
 XX DT 12-JUN-2003 (first entry)
 XX DE Human NEMO binding site (NBD) mutant peptide #11.
 XX KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; neutropenic; neuroprotective; antithrombotic; vincristine;
 KW vasotropic; antineumatic; antitartaric; mutant; mutein.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN US2002156000-A1.
 XX PD 24-OCT-2002.
 XX PF 02-MAY-2001; 2001US-0847940.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (MAYM/) MAY M J.
 XX PA (GHOS/) GHOSH S.
 XX PI May MJ, Ghosh S;
 XX DR WPI; 2003-209142/20.
 XX PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for mediating NF-kappaB induction in a cell and for
 PT creating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX PS Claim 22; Page 17; 47pp; English.
 XX CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 XX SQ Sequence 6 AA;
 XX
 XX Query Match 100.0%; Score 33; DB 24; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMASL 6
 |||||
 Db 1 LDMASL 6
 RESULT 4
 ABB77299 standard; protein; 756 AA.
 ID ABB77299 standard; protein; 756 AA.
 XX

AC ABB77299;
 XX DT 14-JUN-2002 (first entry)
 XX DE Human IKKbeta mutant W741A.
 XX KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; neutropenic; neuroprotective; anti-HIV; human;
 KW dermatological; antiviral; antitumor; antiallergic;
 KW antineoplastic; antibacterial; antiparasitic; antitubercular;
 KW antitartaric; osteopathic; antitumor; mutant; mutein.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200183547-A2.
 XX PD 08-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-US40654.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (UYVA) UNIV YALE.
 XX PI May MJ, Ghosh S;
 XX DR WPI; 2002-179350/23.
 XX PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX PS Example 11; Page -; 82pp; English.
 XX CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77213). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyomyelitis, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,

CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of an IKK β gene
CC mutant, useful in examples of the invention.
CC Note: The present sequence is not given in the specification but is
CC derived from GenBank Accession No. 014920 (AB077294).
XX
SQ Sequence 756 AA;
Query Match 100.0%; Score 33; DB 23; Length 756;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 737 LDMSAL 742
QY 1 LDMSAL 6
ID AAY94732 standard; peptide; 53 AA.
XX
AC AAY94732;
XX
DT 29-JAN-2001 (first entry)
XX
DE Region A of protein kinase C related protein kinase 2.
XX
KM Substrate specificity; phosphoinositide-dependent protein kinase 1;
KM PK1; protein kinase C related protein kinase 2; PK2; cancer; apoptosis;
KM mechanical tissue damage; ischemic disease; stroke;
KM myocardial infarction; antigenic peptide.
XX
OS Unidentified.
XX
PN WO200056864-A2.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-GB01004.
XX
PR 19-MAR-1999; 99GB-0006245.
XX
PA (UYDU-) UNIV DUNDEE.
XX
PI Aleesi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
XX WPI; 2000-647155/62.
XX
PT Altering substrate specificity of phosphoinositide-dependent protein
XX kinase 1 to phosphorylate Ser473 in addition to Thr308 by exposing to
XX interacting polypeptide -
XX
PS Disclosure; Page 12; 103pp; English.
XX
CC This invention relates to a method for altering the substrate
CC specificity of phosphoinositide-dependent protein kinase 1 (PK1) by
CC exposing it to an interacting polypeptide. Included in the invention are
CC a preparation comprising PK1 and an interacting polypeptide, PK1 with
CC altered specificity is useful for phosphorylating a residue corresponding
CC to the Ser/Thr residue of a substrate with the following peptide
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PK1 is also used for
CC phosphorylating protein kinase C related protein kinase 2 (PK2). The
CC compound identified by methods of the invention that are capable of
CC altering the substrate specificity of PK1 are useful for manufacturing a
CC medicament for treating a patient who is in need of modulation of the
CC insulin signalling pathway and/or PK1, PK2 or PK2 signalling. A
CC compound that is capable of reducing the activity (i.e. the PK1 and/or
CC the PK2 activity) of PK1 may be useful in treating cancer. PK1,
CC e.g. via protein kinase B and/or SGK, may be capable of providing a

CC survival signal that protects cells from apoptosis induced in a variety
CC of ways. Reduction of the activity of PK1 may promote apoptosis and may
CC be useful in treating cancer. Conditions in which aiding apoptosis may be
CC of benefit may also include resolution of inflammation. A compound
CC capable of increasing the activity of PK1 may be useful in treating
CC diabetes or obesity, or may be useful in inhibiting apoptosis. Increased
CC activity of PK1 may lead to increased levels of leptin, which may lead
CC to weight loss. The compounds may suppress apoptosis, which may aid cell
CC survival during or following cell damaging processes and in treating
CC disease in which apoptosis is involved. Examples of the diseases include,
CC mechanical (including heart) tissue injury or ischemic disease, for
CC example stroke and myocardial infarction, or neural injury. The present
CC sequence represents a region of protein kinase C related protein kinase
CC 2 (PK2) which interacts with PK1.
XX
SQ Sequence 53 AA;
Query Match 93.9%; Score 31; DB 21; Length 53;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 12 LDMSAL 17
QY 1 LDMSAL 6
ID AAB99802 standard; peptide; 53 AA.
XX
AC AAB99802;
XX
DT 20-SEP-2001 (first entry)
XX
DE Protein kinase derived interacting peptide #4.
XX
KM Protein kinase; identification; hydrophobic pocket; interacting;
KM cancer; diabetes; inhibition; apoptosis; tissue injury;
KM ischaemic injury; stroke.
XX
OS Homo sapiens.
XX
PN WO200144497-A2.
XX
PD 21-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-GB04598.
XX
PR 02-DEC-1999; 99US-0168559.
XX
PA (UYDU-) UNIV DUNDEE.
XX
PI Aleesi D, Biondi R;
XX WPI; 2001-390252/41.
XX
PT Identifying modulators of protein kinase (PK) activity, useful in
XX developing drugs for treating cancer or diabetes, by measuring the
XX ability of the compound to modulate or mimic the interaction of PK with
XX interacting polypeptides -
XX
PS Disclosure; Page 25; 180pp; English.
XX
CC The present invention describes a method for identifying a compound that
CC modulates protein kinase activity. The method comprises measuring the
CC ability of the compound to inhibit, promote or mimic the interaction of
CC a hydrophobic pocket-containing protein kinase with an interacting
CC polypeptide. The interacting polypeptide interacts with the hydrophobic
CC pocket of the protein kinase and/or comprises the amino acid sequence
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays
CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
CC or polynucleotides from the present invention are useful in medicine.

CC particularly in the manufacture of a medicament for treating a patient
CC in need of modulation of signaling by a hydrophobic pocket-containing
CC protein kinase. Specifically, the patient has cancer or diabetes or is
CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue
CC injury or ischemic injury, including stroke. The compound or
CC composition is also useful for inhibiting the degree or rate of
CC phosphorylation by the protein kinase. The interacting polypeptide or
CC compound is useful in methods of establishing a hydrophobic pocket-
CC containing protein kinase, where the protein kinase is exposed to the
CC compound or polypeptide. AAB9786 to AAB9847 represent amino acid
CC sequences, and AAB44210 and AAB44211 represent oligonucleotide sequences,
CC used in the exemplification of the present invention.

[illegible]

RESULT 7
 AAB99793
 ID AAB99793 standard; Peptide; 77 AA.
 XX
 AC AAB99793;
 XX
 DT 20-SEP-2001 (first entry)
 XX
 DE 3-phosphonositide-dependent protein kinase 1 binding peptide P1F.
 XX
 KW Protein kinase; identification; hydrophobic pocket; interacting;
 KW cancer; diabetes; inhibition; apoptosis; tissue injury;
 KW ischaemic injury; stroke.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN MO20014497-A2.
 XX
 PD 21-JUN-2001.
 XX
 PF 04-DEC-2000; 2000MO-GB04598.
 XX
 PR 02-DEC-1999; 99US-0168559.
 XX
 XX (UYDU-) UNIV DUNDEE.
 PA
 XX Alesse1 D, Biondi R;
 PI
 DR WPI; 2001-390252/41.
 XX
 PT Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PT ability of the compound to modulate or mimic the interaction of PK with
 PT interacting polypeptides -
 PT
 PS Disclosure; Page 22; 180pp; English.
 XX
 CC The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of
 CC a hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays
 CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
 CC or polynucleotides from the present invention are useful in medicine,
 CC particularly in the manufacture of a medicament for treating a patient
 CC in need of modulation of signalling by a hydrophobic pocket-containing

protein kinase. Specifically, the patient has cancer or diabetes or is in need of inhibition of apoptosis, e.g. a patient suffering from tissue injury or ischemic injury, including stroke. The compound or composition is also useful for inhibiting the degree or rate of phosphorylation by the protein kinase. The interacting polypeptide or compound is useful in methods of stabilising a hydrophobic pocket-containing protein kinase, where the protein kinase is exposed to the compound or polypeptide. AAB9786 to AAB9847 represent amino acid sequences, and ABA44210 and AHA44211 represent oligonucleotide sequences, used in the exemplification of the present invention.

```
SQ Sequence      77 AA;
Query Match     93.9%; Score 31; DB 22; Length 77;
Best Local Similarity    83.3%; Pred No. 1.4e+02;
Matches        5; Conservative   1; Mismatches    0; Indels    0; Gaps    0
```

```
OY          1 LDMSAL 6
           :|||||
db         12 IDMSAL 17
```

CC	RESULT 8
XX	AAB99835
ID	AAB99835 standard; Protein; 315 AA.
XX	
AC	AAB99835;
XX	
DT	20-SEP-2001 (first entry)
XX	
DE	AGC protein kinase family member PRK2 protein sequence.
XX	
XX	Protein kinase; identification; hydrophobic pocket; interacting;
KW	cancer; diabetes; inhibition; apoptosis; tissue injury;
KW	ischaemic injury; stroke.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200144497-A2.
XX	
PD	21-JUN-2001.
XX	
PP	04-DEC-2000; 2000WO-GB04598.
XX	
PR	02-DEC-1999; 99US-0168559.
XX	
PA	(UYDU-) UNIV DUNDEE.
PI	Aleesi D, Biondi R;
DR	WPI; 2001-390252/41.
XX	
PT	Identifying modulators of protein kinase (PK) activity, useful in
PT	developing drugs for treating cancer or diabetes, by measuring the
PT	ability of the compound to modulate or mimic the interaction of PK with
PT	interacting polypeptides -
XX	
PS	Disclosure; Fig 16; 180pp; English.
XX	
CC	The present invention describes a method for identifying a compound that
CC	modulates protein kinase activity. The method comprises measuring the
CC	ability of the compound to inhibit, promote or mimic the interaction of
CC	a hydrophobic pocket-containing protein kinase with an interacting
CC	polypeptide. The interacting polypeptide interacts with the hydrophobic
CC	pocket of the protein kinase and/or comprises the amino acid sequence
CC	Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays
CC	for developing pharmaceutical compounds or drugs. Compounds, polypeptides
CC	or polynucleotides from the present invention are useful in medicine,
CC	particularly in the manufacture of a medicament for treating a patient
CC	in need of modulation of signalling by a hydrophobic pocket-containing
CC	protein kinase. Specifically, the patient has cancer or diabetes or is
CC	in need of inhibition of apoptosis, e.g. a patient suffering from tissue

CC Injury or ischemic injury, including stroke. The compound or
 CC composition is also useful for inhibiting the degree or rate of
 CC phosphorylation is also useful for inhibiting the degree or rate of
 CC compound is useful in methods of stabilizing a hydrophobic pocket-
 CC containing protein kinase, where the protein kinase is exposed to the
 CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid
 CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,
 CC used in the exemplification of the present invention.

XX Sequence 315 AA;

Query Match 93.9%; Score 31; DB 22; Length 315;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMSAL 6
 Db 250 IDMSAL 255

RESULT 9

ID ABB63738 standard; Protein; 345 AA.

XX ABB63738;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 18006.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.

XX Drosophila melanogaster.

XX NO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001MO-US09221.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PMD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL07841.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX Disclosure; SEQ ID NO 18006; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB10511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (AAB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 345 AA;

Query Match 93.9%; Score 31; DB 22; Length 345;
 Best Local Similarity 83.3%; Pred. No. 6.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LDMSAL 6
 Db 136 IDMSAL 141

RESULT 10

ID AAB99822 standard; Protein; 385 AA.

XX AAB99822;

XX 20-SEP-2001 (first entry)

XX AGC protein kinase family member PRK2 protein sequence.

XX Protein kinase; identification; hydrophobic pocket; interacting;
 KM cancer; diabetes; inhibition; apoptosis; tissue injury;
 KM ischemic injury; stroke.

XX Homo sapiens.

XX Synthetic.

XX WO200144497-A2.

XX 21-JUN-2001.

XX 04-DEC-2000; 2000MO-GB04598.

XX 02-DEC-1999; 99US-0168559.

XX (UYDU-) UNIV DUNDEE.

XX Alesai D, Biondi R;

XX WPI; 2001-390252/41.

XX Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PT ability of the compound to modulate or mimic the interaction of PK with
 PT interacting polypeptides -

XX Disclosure; Fig 15; 180pp; English.

XX The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of
 CC a hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays
 CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
 CC or polynucleotides from the present invention are useful in medicine,
 CC particularly in the manufacture of a medicament for treating a patient
 CC in need of modulation of signalling by a hydrophobic pocket-containing
 CC protein kinase. Specifically, the patient has cancer or diabetes or is
 CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue
 CC injury or ischemic injury, including stroke. The compound or
 CC composition is also useful for inhibiting the degree or rate of
 CC phosphorylation by the protein kinase. The interacting polypeptide or
 CC compound is useful in methods of stabilizing a hydrophobic pocket-
 CC containing protein kinase, where the protein kinase is exposed to the
 CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid
 CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,
 CC used in the exemplification of the present invention.

XX Sequence 385 AA;

Query Match 93.9%; Score 31; DB 22; Length 385;
 Best Local Similarity 83.3%; Pred. No. 7.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6
 Db 320 IDMSAL 325

RESULT 11
 ID ABB59094 standard; Protein: 652 AA.
 XX ABB59094
 AC ABB59094;
 XX 26-MAR-2002 (first entry)
 DT
 XX Drosophila melanogaster polypeptide SEQ ID NO 4074.
 DE
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL03197.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PT
 PS Disclosure; SEQ ID NO 4074; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AAB57737-AB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SO Sequence 652 AA;

Query Match 93.9%; Score 31; DB 22; Length 652;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6
 Db 447 LDMSAM 452

RESULT 12
 ID AAY94736 standard; Protein: 984 AA.
 XX AAY94736;
 AC AAY94736;
 XX 29-JAN-2001 (first entry)
 DT
 XX

DE Protein kinase C related protein kinase 2.
 XX
 KM Substrate specificity; phosphoinositide-dependent protein kinase 1;
 KM PDK1; protein kinase C related protein kinase 2; PKR2; cancer; apoptosis;
 KM mechanical tissue damage; ischemic disease; stroke;
 KM myocardial infarction; antigenic peptide.
 XX
 OS
 XX Unidentified.
 XX
 PN WO200056864-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 17-MAR-2000; 2000WO-GB01004.
 XX
 PR 19-MAR-1999; 99GB-0006245.
 XX
 PA (YUDU-) UNIV DUNDEE.
 XX
 PI Alesset D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
 DR WPI; 2000-647155/62.
 XX
 PT Altering substrate specificity of phosphoinositide-dependent protein
 PT kinase 1 to phosphorylate Ser473 in addition to Thr308 by exposing to
 PT interacting polypeptide -
 PT
 PS Disclosure; Fig 11; 103pp; English.
 XX
 CC This invention relates to a method for altering the substrate
 CC specificity of phosphoinositide-dependent protein kinase 1 (PKI), by
 CC exposing it to an interacting polypeptide. Included in the invention are
 CC a preparation comprising PDK1 and an interacting polypeptide, PDK1 with
 CC altered specificity is useful for phosphorylating a residue corresponding
 CC to the Ser/Thr residue of a substrate with the following peptide
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PDK1 is also used for
 CC phosphorylating protein kinase C related protein kinase 2 (PRK2). The
 CC compound identified by methods of the invention that are capable of
 CC altering the substrate specificity of PDK1 are useful for manufacturing a
 CC medicament for treating a patient who is in need of modulation of the
 CC insulin signalling pathway and/or PDK1, PDK2 or PRK2 signalling. A
 CC compound that is capable of reducing the activity (i.e. the PDK1 and/or
 CC the PDK2 activity) of PDK1 may be useful in treating cancer. PDK1, e.g.
 CC via protein kinase B and/or SGK, may be capable of providing a survival
 CC signal that protects cells from apoptosis induced in a variety of ways.
 CC Reduction of the activity of PDK1 may promote apoptosis and may be useful
 CC in treating cancer. Conditions in which aiding apoptosis may be benefit
 CC may also include resolution of inflammation. A compound capable of
 CC increasing the activity of PDK1 may be useful in treating diabetes or
 CC obesity, or may be useful in inhibiting apoptosis. Increased activity of
 CC PDK1 may lead to increased levels of leptin, which may lead to weight
 CC loss. The compounds may suppress apoptosis, which may aid cell survival
 CC during or following cell damaging processes and in treating disease in
 CC which apoptosis is involved. Examples of the diseases include, mechanical
 CC (including heat) tissue injury or ischemic disease, for example stroke
 CC and myocardial infarction, or neural injury. The present sequence
 CC represents a protein kinase C related protein kinase 2 amino acid
 CC sequence, used in the course of the invention.
 CC
 XX
 SO Sequence 984 AA;

Query Match 93.9%; Score 31; DB 21; Length 984;
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6
 Db 919 IDMSAL 924

RESULT 13
 ID AAO15489 standard; Protein: 984 AA.
 XX AAO15489
 ID AAO15489 standard; Protein: 984 AA.

XX AA015489;
AC 03-OCT-2002 (first entry)
DT
XX
DE Human serin-threonin-kinase PRK2.
KW Human; DHAM-kinase inhibitor; guanylate kinase 1; PRK2;
KW deregulated in hyperactive macrophage kinase inhibitor; GUK1;
KW serin-threonin-kinase; PAK2; inflammatory condition;
KW chronic inflammatory airway disease; chronic bronchitis;
KW chronic obstructive pulmonary disease; COPD.
XX
OS Homo sapiens.
XX WO200252036-A2.
PN
XX
PD 04-JUL-2002.
PP
XX 15-DEC-2001; 2001WO-EPI1844.
PR 22-DEC-2000; 2000US-257854P.
PA (BOEH) BOEHRINGER INGELHEIM PHARMA KG.
XX
XX Jung B, Mueller S, Kraut N;
PI
XX WPI; 2002-583570/62.
DR N-Psdb; AAL44147.
XX
XX
PT Determining activators or inhibitors of 'deregulated in hyperactive
PT macrophage (DHAM)-kinase for treating chronic inflammatory airway
PT diseases, by measuring DHAM-kinase function after it is contacted with
PT a test substance -
XX
XX Claim 8; Page 41-47; 48pp; English.
XX
XX The invention comprises a method for determining whether a substance is
CC an activator or an inhibitor of a DHAM-kinase (deregulated in hyperactive
CC macrophage kinase). DHAM-kinases used in the invention include guanylate
CC kinase 1 (GUK1), serin-threonin-kinase PAK2 and serin-threonin-kinase
CC PRK2. The method of the invention is useful for identifying substances
CC that influence inflammatory conditions of chronic inflammatory airway
CC diseases (e.g. chronic bronchitis or chronic obstructive pulmonary
CC disease - COPD). The present amino acid sequence represents the human
CC serin-threonin-kinase PRK2.
XX
SQ Sequence 984 AA;
Query Match 93.9%; Score 31; DB 23; Length 984;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 LDMSAL 6
DB 919 IDMSAL 924
RESULT 14
AAG56197
ID AAG56197 standard; Protein; 53 AA.
XX
AC AAG56197;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 72196.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.

XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132663.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137232.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139839.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.

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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145224.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145293.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 25-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.

PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0158294.
PR 13-OCT-1999; 99US-0158295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 90.9%; Score 30; DB 21; Length 57;
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GenCore version 5.1.6
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Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSWL 6

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Listing first 45 summaries

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5	36	100.0	8	11 US-09-847-946A-92	Sequence 92, Appl
6	36	100.0	8	11 US-09-847-946A-100	Sequence 100, Appl
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ALIGNMENTS

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; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 27
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

No art

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; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
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; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
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; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
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; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
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; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
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; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-91

Query Match          100.0%; Score 36; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDYSWL 6
       |||||
DB      1 LDYSWL 6
```

```
RESULT 8
US-09-847-946A-94
; Sequence 94, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-94

Query Match          100.0%; Score 36; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDYSWL 6
       |||||
DB      1 LDYSWL 6

RESULT 9
US-09-847-946A-97
; Sequence 97, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-97

Query Match          100.0%; Score 36; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDYSWL 6
| | | | |
DB 3 LDYSWL 8

RESULT 10

US-09-847-946A-98
; Sequence 98, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-98

Query Match 100.0%; Score 36; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
| | | | |
DB 2 LDYSWL 7

RESULT 11
US-09-847-946A-93
; Sequence 93, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-93

Query Match 100.0%; Score 36; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDYSWL 6
| | | | |
DB 2 LDYSWL 7

RESULT 12

US-09-847-946A-96
; Sequence 96, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-96

Query Match 100.0%; Score 36; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
| | | | |
DB 3 LDYSWL 8

RESULT 13
US-09-847-946A-90
; Sequence 90, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-90

Query Match 100.0%; Score 36; DB 11; Length 11;

US-09-847-946A-90

Query Match 100.0%; Score 36; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
|||||
DB 3 LDYSWL 8

RESULT 14

US-10-074-978A-310
Sequence 310, Application US/10074978A
Publication No. US20040010119A1
GENERAL INFORMATION:
APPLICANT: Leite, Mario
APPLICANT: Spytek, Kimberly A
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Fernandes, Elma
APPLICANT: Li, Li
APPLICANT: Kekuda, Ramesh
APPLICANT: Liu, Xiahong
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
APPLICANT: Patuturajan, Meera
APPLICANT: Bialock, Angela
APPLICANT: Ballinger, Robert
APPLICANT: Tchernev, Velizar T
APPLICANT: Malyankar, Uriel M
APPLICANT: Gusev, Vladimir
APPLICANT: Rastcell, Luca
APPLICANT: Mezes, Peter S
APPLICANT: Ellerman, Karen
APPLICANT: Heyes, Melvin P
APPLICANT: Herrman, John
APPLICANT: Pena, Carol E A
APPLICANT: Shinkete, Richard A
APPLICANT: Taupler Jr, Raymond J
APPLICANT: Moore, No. US20040010119A111e
APPLICANT: Shenoy, Suresh
APPLICANT: Edinger, Shlomit
APPLICANT: Gunther, Erik
APPLICANT: Stone, Dave
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-269
CURRENT APPLICATION NUMBER: US/10/074,978A
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: 60/268,221
PRIOR FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/335,109
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 60/312,284
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: 60/268,496
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: 60/276,703
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/330,293
PRIOR FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 60/322,127
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/280,899
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/330,797
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/268,646
PRIOR FILING DATE: 2001-02-14
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 547
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 310
LENGTH: 73
TYPER: PRT
ORGANISM: Homo sapiens
US-10-074-978A-310

Query Match 91.7%; Score 33; DB 12; Length 73;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
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DB 46 LDYSWL 51

RESULT 15

US-10-074-978A-66
Sequence 66, Application US/10074978A
Publication No. US20040010119A1
GENERAL INFORMATION:
APPLICANT: Leite, Mario
APPLICANT: Spytek, Kimberly A
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Fernandes, Elma
APPLICANT: Li, Li
APPLICANT: Kekuda, Ramesh
APPLICANT: Liu, Xiahong
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
APPLICANT: Patuturajan, Meera
APPLICANT: Bialock, Angela
APPLICANT: Ballinger, Robert
APPLICANT: Tchernev, Corine
APPLICANT: Malyankar, Uriel M
APPLICANT: Gusev, Vladimir
APPLICANT: Rastcell, Luca
APPLICANT: Mezes, Peter S
APPLICANT: Ellerman, Karen
APPLICANT: Heyes, Melvin P
APPLICANT: Herrman, John
APPLICANT: Pena, Carol E A
APPLICANT: Shinkete, Richard A
APPLICANT: Taupler Jr, Raymond J
APPLICANT: Moore, No. US20040010119A111e
APPLICANT: Shenoy, Suresh
APPLICANT: Edinger, Shlomit
APPLICANT: Gunther, Erik
APPLICANT: Stone, Dave
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-269
CURRENT APPLICATION NUMBER: US/10/074,978A
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: 60/268,221
PRIOR FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/335,109
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 60/312,284
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: 60/268,496
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: 60/276,703
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/330,293
PRIOR FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 60/322,127
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/280,899

;; PRIOR FILING DATE: 2001-04-02
;; PRIOR APPLICATION NUMBER: 60/310,797
;; PRIOR FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: 60/268,646
;; PRIOR FILING DATE: 2001-02-14
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 547
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 66
;; LENGTH: 314
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-074-978A-66

Query Match 91.7%; Score 33; DB 12; Length 314;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDYSWL 6
Db 116 LDYTWL 121

Search completed: February 18, 2004, 15:41:59
Job time : 17.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	6	23	ABB08734
2	36	100.0	6	23	AAW48591
3	36	100.0	6	23	AAW48594
4	36	100.0	6	23	AAW48595
5	36	100.0	6	23	AAW48596
6	36	100.0	6	23	AAW48597
7	36	100.0	6	23	AAW48598
8	36	100.0	6	23	AAW48599
9	36	100.0	6	23	AAW48600

10	36	100.0	9	23	AAW48591	Anti-inflammatory
11	36	100.0	9	23	AAW48594	Anti-inflammatory
12	36	100.0	9	23	AAW48595	Anti-inflammatory
13	36	100.0	10	23	AAW48596	Anti-inflammatory
14	36	100.0	10	23	AAW48597	Anti-inflammatory
15	36	100.0	11	23	AAW48598	Anti-inflammatory
16	36	100.0	12	23	AAW48599	Anti-inflammatory
17	36	100.0	13	23	AAW48600	Anti-inflammatory
18	36	100.0	14	23	AAW48601	Anti-inflammatory
19	36	100.0	15	23	AAW48602	Anti-inflammatory
20	36	100.0	16	23	AAW48603	Anti-inflammatory
21	36	100.0	17	23	AAW48604	Anti-inflammatory
22	36	100.0	18	23	AAW48605	Anti-inflammatory
23	36	100.0	19	23	AAW48606	Anti-inflammatory
24	36	100.0	20	23	AAW48607	Anti-inflammatory
25	36	100.0	21	23	AAW48608	Anti-inflammatory
26	36	100.0	22	23	AAW48609	Anti-inflammatory
27	36	100.0	23	23	AAW48610	Anti-inflammatory
28	36	100.0	24	23	AAW48611	Anti-inflammatory
29	36	100.0	25	23	AAW48612	Anti-inflammatory
30	36	100.0	26	23	AAW48613	Anti-inflammatory
31	36	100.0	27	23	AAW48614	Anti-inflammatory
32	36	100.0	28	23	AAW48615	Anti-inflammatory
33	36	100.0	29	23	AAW48616	Anti-inflammatory
34	36	100.0	30	23	AAW48617	Anti-inflammatory
35	36	100.0	31	23	AAW48618	Anti-inflammatory
36	36	100.0	32	23	AAW48619	Anti-inflammatory
37	36	100.0	33	23	AAW48620	Anti-inflammatory
38	36	100.0	34	23	AAW48621	Anti-inflammatory
39	36	100.0	35	23	AAW48622	Anti-inflammatory
40	36	100.0	36	23	AAW48623	Anti-inflammatory
41	36	100.0	37	23	AAW48624	Anti-inflammatory
42	36	100.0	38	23	AAW48625	Anti-inflammatory
43	36	100.0	39	23	AAW48626	Anti-inflammatory
44	36	100.0	40	23	AAW48627	Anti-inflammatory
45	36	100.0	41	23	AAW48628	Anti-inflammatory

ALIGNMENTS

RESULT 1	ABB08734	standard; peptide; 6 AA.
XX	ABB08734	
XX	ABB08734	
DT	14-JUN-2002	(first entry)
XX		
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 12.	
XX		
XX	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
KW	kinase activation; leukocyte; inflammation; B-selectin; osteoclast;	
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KW	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KW	corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;	
KW	osteopathic; cytotoxic; nocitopic; neuroprotective; anti-HIV; human;	
KW	antiarteriosclerotic; vitinucide; antiasthmatic; antiallergic;	
KW	dermatological; antibacterial; antiparasitic; antineutrophic;	
KW	antiarthritic; osteopathic; antitumor; mutant; mutain.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference	3/ note= "Wildtype Trp substituted by Tyr"
PD	WO200183547-A2.	
XX	08-NOV-2001.	
XX		

PF 02-MAY-2001; 2001WO-US40654.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorder, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 PS Claim 23; Page 45; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkbppaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC polydermatitis. Also for Crohn's disease, ulcerative colitis,
 CC spondylarthritis. Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 QY
 Db 1 LDYSWL 6
 1 LDYSWL 6
 Query Match 100.0%; Score 36; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 2
 ID AAM48517 standard; Peptide; 6 AA.
 XX AAM48517;
 AC
 XX AAM48517;
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD mutant peptide SEQ ID NO 12.

XX
 XX Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;
 XX antirheumatic; antiarthritic; osteopathic; antibacterial; vitruide;
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 XX autoimmune disorder; multiple sclerosis; transplant rejection;
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 PD
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Flindeis MA, Phillips K;
 PI
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Example 6; Page 48; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, vitruide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 QY
 Db 1 LDYSWL 6
 1 LDYSWL 6
 Query Match 100.0%; Score 36; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 ID AAM48540 standard; Peptide; 6 AA.

XX	AA048540;	
AC		
XX	20-MAR-2002 (first entry)	
XX		
DE	Anti-inflammatory peptide SEQ ID NO 43.	
XX		
KM	Antiinflammatory; antiaesthetic; cyostatic; antiporiatic; nootropic;	
KM	antirheumatic; antiaesthetic; osteopathic; antibacterial; virucide;	
KM	immunopressive; dermatologic; neuroprotective; antiatherosclerotic;	
KM	antiallergic; membrane translocation domain; NEMO binding domain; eczema;	
KM	cyclokin; NFkBpab; IkappaB kinase beta; IKKbeta; cancer; psoriasis;	
KM	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;	
KM	autoimmune disorder; multiple sclerosis; transplant rejection;	
KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;	
KM	ataxia telangiectasia; allergy; anaphylaxis; arthritis.	
XX		
OS	Synthetic.	
XX		
FN	WO200183554-A2.	
XX		
PD	08-NOV-2001.	
XX		
PE	02-MAY-2001; 2001WO-US14346.	
XX		
PR	02-MAY-2000; 2000US-201261P.	
PR	22-AUG-2000; 2000US-0643260.	
XX		
PA	(PRAE-) PRAECS PHARM INC.	
PA	(UYIA) UNIV YALE.	
XX		
P1	May MJ, Ghosh S, Fandels MA, Phillips K;	
DR	WPI, 2002-121889/16.	
XX		
PT	Novel antiinflammatory compound comprising membrane translocation	
PT	domain fused to NEMO binding sequence, useful for blocking nuclear	
PT	factor kappaB activation, and for treating asthma, lung inflammation,	
PT	psoriasis	
XX		
PS	Claim 6; Page 61; 88pp; English.	
XX		
CC	The invention relates to an antiinflammatory compound (especially	
CC	AA048628-AA048645), comprising a membrane translocation domain	
CC	(AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15	
CC	amino acid residues, fused to a NEMO binding sequence	
CC	(AA048625-AA048619). The antiinflammatory compounds have antiaesthetic,	
CC	cyostatic, antiporiatic, antirheumatic, antiallergic, osteopathic,	
CC	antibacterial, immunopressive, dermatologic, neuroprotective,	
CC	nootropic, antiatherosclerotic, virucide and antiallergic activity. The	
CC	compounds act as selective inhibitors of cytokine-mediated NFkBpab	
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at	
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase	
CC	activation and subsequent decreased phosphorylation of IkappaB. The	
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,	
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,	
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,	
CC	bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,	
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;	
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia	
CC	telangiectasia. The compounds are also useful for treating	
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,	
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and	
CC	arthritis.	
XX		
XX	Sequence 6 AA;	
XX		
XX	Query Match 100.0%; Score 36; DB 23; Length 6;	
XX	Best Local Similarity 100.0%; Pred. No. 9.3e+05;	
XX	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
XX	1 LDYSWL 6	
XX		

Db 1 LDYSWL 6

RESULT 4
AAM48592
ID AAM48592 standard; Peptide; 6 AA.
XX
XX AAM48592;
AC
XX 20-MAR-2002 (first entry)
DT
XX
XX
XX Anti-inflammatory peptide SEQ ID NO 95.
DE
XX
XX Anti-inflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteoprotic; antibacterial; vincinide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; ecze-
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
OS
XX WO200183554-A2.
PN
XX
XX 08-NOV-2001.
PD
XX
XX 02-MAY-2001; 2001WO-US14346.
PF
XX
XX 02-MAY-2000; 2000US-201261P.
PR
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECTIS PHARM INC.
PA (UYVA) UNIV YALE.
XX
XX
PI May MJ, Ghosh S, Findels MA, Phillips K;
XX
XX WPI; 2002-121889/16.
DR
XX
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX
XX Claim 6; Page 62; 88pp; English.
PS
XX
XX The invention relates to an antiinflammatory compound (especially
CC AAM48620-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteoprotic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, vincinide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursts; autoimmune diseases such as lupus, polyarthritis, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX
XX Sequence 6 AA;

Query Match 100.0%; Score 36; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
| | | | |
Db 1 LDYSWL 6

RESULT 5
ABU08427 ID ABU08427 standard; peptide: 6 AA.

AC ABU08427;
XX
DT 12-JUN-2003 (first entry)
XX

DE Human NEMO binding site (NBD) mutant peptide #10.

XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
KW nuclear factor-kappaB induction; inflammatory disorder;
KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
KW atherosclerosis; viral infection; Ataxia telangiectasia;
KW translocation detection; immunosuppressive; osteopathic;
KW cytosolic; neutrotropic; antiatherosclerotic; virucide;
KW vasotropic; antirheumatic; antiarthritic; mutant; mucin.

XX Homo sapiens.
OS Synthetic.
XX

PN US200215600-A1.
XX

PD 24-OCT-2002.
XX

PE 02-MAY-2001; 2001US-0847940.
XX

PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.

XX (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
XX

PI May MJ, Ghosh S;
XX

DR WPI; 2003-209142/20.

XX Novel antiinflammatory peptide compounds comprising NEMO binding
PT domain, useful for modulating NF-kappaB induction in a cell and for
PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
PT psoriasis, vasculitis -

XX Claim 22; Page 17; 47pp; English.

XX The present invention relates to antiinflammatory compounds comprising
CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
CC in a cell, where the compounds are capable of blocking the interaction
CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
CC antiinflammatory compound further comprises at least one membrane
CC translocation domain. The compounds are useful for treating
CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
CC telangiectasia, and for translocation detection. The compounds of
CC the invention block NF-kappaB induction by IKK but do not inhibit
CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
CC NBD mutant peptides.

XX Sequence 6 AA;
SQ

Query Match 100.0%; Score 36; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
| | | | |
Db 1 LDYSWL 6

RESULT 6
AAM48596 ID AAM48596 standard; peptide: 7 AA.

AC AAM48596;
XX

DT 20-MAR-2002 (first entry)
XX

DE Anti-inflammatory peptide SEQ ID NO 99.

XX Antiinflammatory; antiaesthetic; cytostatic; antiproliferic; neutrotropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neutrotropic; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.
OS

PN WO200183554-A2.
XX

PD 08-NOV-2001.
XX

PE 02-MAY-2001; 2001WO-US14346.
XX

PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
XX

PI May MJ, Ghosh S, Finkelstein MA, Phillips K;
XX

DR WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -

XX Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
CC cytostatic, antiproliferic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neutrotropic,
CC neutrotropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC compound act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 36; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 1 LDYSWL 6
 RESULT 7
 ID AAM48589 standard; Peptide; 8 AA.
 XX AAM48589;
 AC
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 92.
 KW Anti-inflammatory; antiaesthetic; cytosolic; antiparietal; nootropic;
 KW antineumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findele MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 DR Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytosolic, antiparietal, antineumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 36; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 3 LDYSWL 8
 RESULT 8
 ID AAM48597 standard; Peptide; 8 AA.
 XX AAM48597;
 AC
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 100.
 KW Anti-inflammatory; antiaesthetic; cytosolic; antiparietal; nootropic;
 KW antineumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findele MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 DR Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytosolic, antiparietal, antineumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
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CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

CC Sequence 8 AA;

SO Query Match 100.0%; Score 36; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
 |||||
 Db 1 LDYSWL 6

RESULT 9
 ID AAM48588 standard; Peptide; 9 AA.
 AC AAM48588;
 XX 20-MAR-2002 (first entry)
 DT
 XX
 DE Anti-inflammatory peptide SEQ ID NO 91.
 XX
 KM Antinflammatory; antiaesthetic; cytosolic; antiprotic; nootropic;
 KM antineuritic; antiaesthetic; osteopathic; antibacterial; vitruide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.
 XX WO200183554-A2.
 PN 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX May MJ, Ghosh S, Flindels MA, Phillips K;
 PI WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
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 XX Claim 6, Page 62; 88pp; English.
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 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

CC Sequence 9 AA;

SO Query Match 100.0%; Score 36; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
 |||||
 Db 1 LDYSWL 6

RESULT 10
 ID AAM48591 standard; Peptide; 9 AA.
 AC AAM48591;
 XX 20-MAR-2002 (first entry)
 DT
 XX
 DE Anti-inflammatory peptide SEQ ID NO 94.
 XX
 KM Antinflammatory; antiaesthetic; cytosolic; antiprotic; nootropic;
 KM antineuritic; antiaesthetic; osteopathic; antibacterial; vitruide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.
 XX WO200183554-A2.
 PN 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX May MJ, Ghosh S, Flindels MA, Phillips K;
 PI WPI; 2002-121889/16.
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 PT domain fused to NEMO binding sequence, useful for blocking nuclear
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PR 22-AUG-2000; 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
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 PS Claim 6; Page 62; 88pp; English.
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 CC The invention relates to an antiinflammatory compound (especially
 CC AA48628-AA48645), comprising a membrane translocation domain
 CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
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 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
 CC cytoskeletal, antipneumatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virocidic and antiallergic activity. The
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 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 SQ Sequence 9 AA;
 XX
 Query Match 100.0%; Score 36; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 2 LDYSWL 7

RESULT 13
 AA48590
 ID AA48590 standard; Peptide: 10 AA.
 XX
 AC AA48590;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX
 DE Anti-inflammatory peptide SEQ ID NO 93.
 XX
 KM Antiinflammatory; antiasthmatic; cytoskeletal; antipneumatic; nootropic;
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 KM
 OS Synthetic.
 XX
 PN WO200183554-A2.

XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AA48628-AA48645), comprising a membrane translocation domain
 CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
 CC cytoskeletal, antipneumatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virocidic and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 SQ Sequence 10 AA;
 XX
 Query Match 100.0%; Score 36; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 2 LDYSWL 7

RESULT 14
 AA48593
 ID AA48593 standard; Peptide: 10 AA.
 XX
 AC AA48593;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX
 DE Anti-inflammatory peptide SEQ ID NO 96.
 XX
 KM Antiinflammatory; antiasthmatic; cytoskeletal; antipneumatic; nootropic;
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM

KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRACIS PHARM INC.
 PA (UYTA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virocidic and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 CC
 SQ Sequence 10 AA;
 XX
 XX
 Query Match 100.0%; Score 36; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.9; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 3 LDYSWL 8
 XX
 AC AAM48587;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 90.
 XX
 KM Antiinflammatory; antiasthmatic; cytostatic; antiproliferative; nootropic;

KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRACIS PHARM INC.
 PA (UYTA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virocidic and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 CC
 SQ Sequence 11 AA;
 XX
 XX
 Query Match 100.0%; Score 36; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.3; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 3 LDYSWL 8
 XX
 AC AAM48587;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 90.
 XX
 KM Antiinflammatory; antiasthmatic; cytostatic; antiproliferative; nootropic;

Search completed: February 18, 2004, 14:26:23
 Job time : 23.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDPSWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp Vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	179	11	Q8BZU5
2	35	100.0	315	13	Q91838
3	35	100.0	391	16	P95247
4	35	100.0	407	2	Q55047
5	35	100.0	414	2	Q960Y1
6	35	100.0	414	2	Q960Y1
7	35	100.0	415	16	Q8VJK7
8	35	100.0	1115	10	Q942A0
9	35	100.0	61	16	Q9PEJ5
10	33	94.3	144	16	Q8Z6L9
11	33	94.3	144	16	Q84950
12	33	94.3	253	16	Q24927
13	33	94.3	253	16	Q92MX2
14	33	94.3	518	16	Q9JYP7
15	33	94.3	518	16	Q9JYN9
16	33	94.3	1227	5	Q20129

17	32	91.4	208	17	Q28570	Q28570 archaeoglob
18	32	91.4	355	10	Q8RME1	Q8RME1 arabidopsis
19	32	91.4	371	10	Q81871	Q81871 arabidopsis
20	32	91.4	449	16	Q910V1	Q910V1 pseudomonas
21	32	91.4	467	16	Q92X93	Q92X93 rhizobium m
22	32	91.4	490	16	P96442	P96442 rhizobium m
23	31	88.6	44	4	Q96PA0	Q96PA0 homo sapien
24	31	88.6	54	16	Q8E977	Q8E977 shewanella
25	31	88.6	56	8	Q8WFM8	Q8WFM8 diadema pau
26	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
27	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
28	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
29	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
30	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
31	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
32	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
33	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
34	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
35	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
36	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
37	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
38	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
39	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
40	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
41	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
42	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
43	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
44	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
45	31	88.6	56	8	Q952H7	Q952H7 diadema ant

ALIGNMENTS

RESULT 1

Q8BZU5 PRELIMINARY; PRT; 179 AA.

AC Q8BZU5; Q8BZU5; 01-MAR-2003 (TRMBLrel. 23, Created)

DT 01-MAR-2003 (TRMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)

DE Hypothesis of the mouse transcriptome based on functional annotation of

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RP [1]

RC SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Colon;

RA MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs."

RT Nature 420:563-573(2002).

DR EMBL; AK033531; BAC28343.1; -

KW Hypothetical protein.

SQ SEQUENCE 179 AA; 21321 MW; CBF710227B0CDB18 CRC64;

Query Match 100.0%; Score 35; DB 11; Length 179;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6
|||||
Db 5 LDPSWL 10

RESULT 2

Q91838 PRELIMINARY; PRT; 315 AA.

AC Q91838; Q91838; 01-OCT-2000 (TRMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE Interferon regulatory factor 1 (interferon regulatory factor-1).
 GN IRF-1.
 OS *Coccurnix coccurnix* (Common quail), and
 OS *Coccurnix coccurnix japonica* (Japanese quail).
 OC *Ekaryota*; *Metazoa*; *Chordata*; *Cranialata*; *Vertebrata*; *Euteleostomi*;
 OC *Archosauria*; *Aves*; *Neognathae*; *Galliformes*; *Phasianidae*; *Phasianinae*;
 OC *Coccurnix*.
 NCBI_TaxID=9091, 93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=C.coccurnix;
 RA Zoeller B., Mueller I., Nanda I., Gutenbach M., Doseh E., Schmid M.,
 RA Jungwirth C.;
 RT "Sequence analysis of avian interferon regulatory factors (IRF)
 RT reveals close relation of the chicken and quail interferon induced
 RT transcriptional apparatus. Cytogenetic studies and sequence comparison
 RT of the avian IRF-1, ISBP and a MHC class II gene reveals that the
 RT avian cell line C-32 is derived from quail.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=C.coccurnix japonica; STRAIN=BREED.FRANZOSISCHE MASTWACHTEL;
 RA Zoeller B., Ingold R.M., Nanda I., Gutenbach M.;
 RT "Sequence comparison of avian interferon regulatory factors and
 RT identification of the avian CEC-32 cell as a quail cell line.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ271052; CAC01088.1; -.
 DR EMBL; AJ277743; CAB91630.1; -.
 DR HSP; PI5314; 11F1.
 DR InterPro; IPR001346; IRF.
 DR Pfam; PF00605; IRF.1.
 DR PRINTS; PR00267; INTERREGECT.
 DR ProDom; PD002355; IRF.1.
 DR SMART; SM00348; IRF.1.
 DR PROSITE; PS00601; IRF.1.
 SQ SEQUENCE 315 AA; 36257 MW; 7E32521A2D2D62D0 CRC64;
 Query Match 100.0%; Score 35; DB 13; Length 315;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDPSWL 6
 Db 297 LDPSWL 302
 RESULT 3
 ID P95247 PRELIMINARY; PRT; 391 AA.
 AC P95247;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, last annotation update)
 DE Hypothetical 37.4 kDa protein (PPE family protein).
 GN R23532C OR MTCY98.21C OR MT2419.
 OS *Mycobacterium tuberculosis*.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigemeier K., Gao S., Barry C.E. III, Tekala F.,
 RA Baccoc K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagsen K., Kelwell A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellon S., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
 RT complete genome sequence.";
 RL Nature 393:537-544 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,
 RA Bhat W.;
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z83860; CAB06149.1; -.
 DR EMBL; AE007082; AAK46712.1; -.
 DR TIGR; MT2419; -.
 DR R23532C; -.
 DR InterPro; IPR000030; Microbac_PPE.
 DR Pfam; PF00823; PPE.1.
 DR Hypothetical protein; Complete proteome.
 SQ SEQUENCE 391 AA; 37355 MW; 360B67EEF6CB46A CRC64;
 Query Match 100.0%; Score 35; DB 16; Length 391;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDPSWL 6
 Db 3 LDPSWL 8
 RESULT 4
 ID O55047 PRELIMINARY; PRT; 407 AA.
 AC O55047;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE Form I operon ORF protein genes, insertion sequence IS630
 DE protein.
 OS *Shigella sonnei*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 NCBI_TaxID=624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=53G;
 RA Hough H-S.;
 RT "Genetic analysis and identification of an IS630 element in the form I
 RT operon of *Shigella sonnei* 53G.";
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U34305; AAB4874.1; -.
 SQ SEQUENCE 407 AA; 47980 MW; 23BPAF09EBBD5D7 CRC64;
 Query Match 100.0%; Score 35; DB 2; Length 407;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDPSWL 6
 Db 175 LDPSWL 180
 RESULT 5
 ID O9S0Y1 PRELIMINARY; PRT; 414 AA.
 AC O9S0Y1;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE ORF5P (MBGV) (ORF5G).
 GN MBGV OR ORF5G.

OS *Plesiomonas shigelloides* (*Aeromonas shigelloides*), and
 OC *Shigella sonnei*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Plesiomonas*.
 RN NCBI_TaxID=703, 624;
 [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.shigelloides; STRAIN=SEROTYPE O17;
 RA Child T., Okamura N., Yoshida Y., Ohtani K., Arakawa E., Watanabe H.;
 RT "Complete DNA sequence of the O-antigen (rfb) gene cluster in
 RT *Plesiomonas shigelloides* serotype O17 having the same O-antigen as
 RT *Shigella sonnei*: comparison with that of *S. sonnei*.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.shigelloides; STRAIN=SEROTYPE O17;
 RX MEDLINE=99036814; PubMed=9817819;
 RA Houng H.H., Venkatesan M.M.;
 RT "Genetic analysis of *Shigella sonnei* form I antigen: identification of
 RT novel 16S30 as an essential element for the form I expression.";
 RL Microb. Pathog. 25:165-173(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.shigelloides; STRAIN=C27;
 RX PubMed=10992522;
 RA Shepherd J., Wang L., Reeves P.R.;
 RT "Comparison of the O antigen gene clusters of *Escherichia coli*
 RT (*Shigella*) *sonnei* and *Plesiomonas shigelloides* O17: *Sonnei* gained its
 RT current plasmid borne O antigen genes from *Plesiomonas shigelloides* in
 RT a recent event.";
 RL Infect. Immun. 68:6056-6061(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.sonnei;
 RA Xu D.Q., Clear J.O., Ambrose N. Jr., Burr D., Kopecko D.J.;
 RT "Molecular cloning and characterization of the O-antigen gene cluster
 RT of *Shigella sonnei*: genetic stability, proposed biosynthetic pathway
 RT and essential genes for expression of form I O polysaccharide in
 RT *Salmonella* vaccine vector strain.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB025970; BAA85010.1; -;
 DR EMBL; AF285970; AAG17412.1; -;
 DR EMBL; AF294823; AAK85169.1; -;
 SO SEQUENCE 414 AA; 49038 MW; E92985FE7F19D953 CRC64;
 Query Match 100.0%; Score 35; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDPSWL 6
 DB 175 LDPSWL 180
 RESULT 6
 ID 09F738 PRELIMINARY; PRT; 414 AA.
 AC 09F738;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE WbGV.
 GN WbGV.
 OS *Shigella sonnei*.
 OG Plasmid pInv.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Shigella*.
 OK NCBI_TaxID=624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=53G1;
 RX MEDLINE=20448976; PubMed=10992522;
 RA Shepherd J., Wang L., Reeves P.R.;

RT "Comparison of the O antigen gene clusters of *Escherichia coli*
 RT (*Shigella*) *sonnei* and *Plesiomonas shigelloides* O17: *Sonnei* gained its
 RT current plasmid borne O antigen genes from *Plesiomonas shigelloides* in
 RT a recent event.";
 RL Infect. Immun. 68:6056-6061(2000).
 DR EMBL; AF285971; AAG17422.1; -;
 KM Plasmid.
 SQ SEQUENCE 414 AA; 49034 MW; EA6CA44A19ACD8CD CRC64;
 Query Match 100.0%; Score 35; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDPSWL 6
 DB 175 LDPSWL 180
 RESULT 7
 ID 08VJK7 PRELIMINARY; PRT; 415 AA.
 AC 08VJK7;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE PPE family protein.
 GN MT2422.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OK NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / OshKosh;
 RA Fleischmann R.D., Alland P., Bisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE007082; AAK46715.1; -;
 DR TIGR; MT2422; -;
 DR InterPro; IPR000030; Microbac_PPE.
 DR Pfam; PF00823; PPE; 1.
 SQ SEQUENCE 415 AA; 40093 MW; 8B48C7671BFA521 CRC64;
 Query Match 100.0%; Score 35; DB 16; Length 415;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDPSWL 6
 DB 34 LDPSWL 39
 RESULT 8
 ID 0942A0 PRELIMINARY; PRT; 1115 AA.
 AC 0942A0;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Beta galactosidase-like protein.
 GN P0431G06.9.
 OS *Oryza sativa* (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; *Oryza*.
 OK NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 RT clone: P043106.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003683; BAB64698.1; -.
 DR Gramene; Q942A0; -.
 DR InterPro; IPR006101; Glyco_hydro_2.
 DR InterPro; IPR006102; Glyco_hydro_21g.
 DR InterPro; IPR006104; Glyco_hydro_25b.
 DR InterPro; IPR006103; Glyco_hydro_27tm.
 DR InterPro; IPR004200; Glyco_hydro_42c.
 DR InterPro; IPR004199; Glyco_hydro_42n.
 DR Pfam; PF02930; Bgal_small_N; 1.
 DR Pfam; PF02929; Bgal_small_N; 1.
 DR Pfam; PF00703; Glyco_hydro_2; 1.
 DR Pfam; PF02836; Glyco_hydro_2_C; 1.
 DR Pfam; PF02837; Glyco_hydro_2_N; 1.
 DR PRINTS; PR00132; GLHYDRLASE2.
 DR PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
 DR PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
 SQ SEQUENCE 1115 AA; 126078 MW; 1AABF6AA305CA8C5 CRC64;

Query Match 100.0%; Score 35; DB 10; Length 1115;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6
 DB 697 LDPSWL 702

RESULT 9
 OPEP35 PRELIMINARY; PRT; 61 AA.
 ID OPEP35
 AC OPEP35
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein Xf1033.
 GN Xf1033.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 CC Xanthomonadaceae; Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=985C;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barroo M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Faciniani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohne M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohelsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.B., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos W.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.V., Madelira A.M.B.N., Madelira H.M.F., Martino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorillo C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Queglio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva P.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silveira M.L.Z., Silveira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Teat S.M., Toubako M.H.,

RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Zeldin J., Zetbal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
 RL Nature 406:151-159 (2000).
 DR EMBL; AE003940; AAF83843.1; -.
 DR Hypothetical protein; Complete proteome.
 SQ SEQUENCE 61 AA; 6849 MW; 6CD0800BD7B8E107 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 61;
 Best Local Similarity 83.3%; Pred. No. 30;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6
 DB 2 MDPSWL 7

RESULT 10
 Q826L9 PRELIMINARY; PRT; 144 AA.
 ID Q826L9
 AC Q826L9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative pathogenicity island protein.
 GN SSCB OR STY1717.
 OS Salmonella typhi.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Mair J.,
 RA Churcher C., Kung'u K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies K., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.,
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852 (2001).
 DR EMBL; AL627271; CAD01962.1; -.
 DR InterPro; IPR001440; TPR.
 DR Pfam; PF00515; TPR; 2.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 144 AA; 16390 MW; ECD0DA7F08325B08 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 144;
 Best Local Similarity 83.3%; Pred. No. 72;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6
 DB 45 IDPSWL 50

RESULT 11
 O84950 PRELIMINARY; PRT; 144 AA.
 ID O84950
 AC O84950;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE SSCB (Secretion system chaparone).
 GN SSCB OR STM1403.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SL1344;
RA Cirillo D.M., Valdivia R.H., Monack D., Falkow S.;
RT "Microphage-dependent induction of the Salmonella pathogenicity island
  2 type III secretion system and its role in intracellular survival.";
RL Mol. Microbiol. 0:0-0(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RA MEDLINE=9900132; PubMed=9786193;
RA Hensel M., Shea J.E., Waterman R., Mundy R., Nikolaus T., Banks G.,
RA Vazquez-Torres A., Gleason C., Pang F.C., Holden D.W.;
RT "Genes encoding putative effector proteins of the type III secretion
  system of Salmonella pathogenicity island 2 are required for bacterial
  virulence and proliferation in macrophages.";
RL Mol. Microbiol. 30:163-174(1998).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RA MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Portolillo S., All J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan B., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
  LT2.";
RL Nature 413:852-856(2001).
DR EMBL; AF020808; AAC28884.1; -
DR EMBL; AJ224892; CA12190.1; -
DR EMBL; AB008761; AL20327.1; -
DR InterPro; IPR01440; TPR; 2.
DR Pfam; PF00515; TPR; 2.
KW Complete proteome.
SQ SEQUENCE 144 AA; 16375 MW; B60EDA7F0E325B0B CRC64;

Query Match 94.3%; Score 33; DB 16; Length 144;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6
Db 45 IDPSWL 50

RESULT 12
O24927 PRELIMINARY; PRT; 253 AA.
AC O24927;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein HP0101.
GN HP0101.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RA MEDLINE=9739467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter

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RT pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AB000532; AAD07180.1; -
DR TIGR; HP0101; -
DR InterPro; IPR002718; HP OMP.
DR Pfam; PF01856; HP OMP; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 253 AA; 29463 MW; C9A6BBE2C5A9003 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 253;
Best Local Similarity 83.3%; Pred. No. 1,3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6
Db 149 LDPSWI 154

RESULT 13
O9ZMX2 PRELIMINARY; PRT; 253 AA.
AC O9ZMX2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Putative.
GN JHP0093.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99120557; PubMed=99233682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Dolg P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Weisberg D., Mills S.D., Jiang Q., Taylor D.B., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
  gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
DR EMBL; AB001448; AAD05674.1; -
KW Complete proteome.
SQ SEQUENCE 253 AA; 29526 MW; 5C5F5239737B90AB CRC64;

Query Match 94.3%; Score 33; DB 16; Length 253;
Best Local Similarity 83.3%; Pred. No. 1,3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6
Db 149 LDPSWI 154

RESULT 14
O9JYP7 PRELIMINARY; PRT; 518 AA.
AC O9JYP7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein NMB1485.
GN NMB1485.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RA MEDLINE=2017575; PubMed=10710307;
RA Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.B.,

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RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Clecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
 RA Cotton M.D., Utterback T.R., Khoult H., Olin H., Yamahavan J.,
 RA Gill J., Scarlato V., Maignan V., Piza M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venier J.C.,
 RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain
 RT MC58.";
 RL Science 287:1809-1815(2000).
 DR EMBL: AE002498; AAF1841.1; -.
 DR TIGR: NMB1485; -.
 DR InterPro: IPR000644; CBS_domain.
 DR InterPro: IPR005170; CORC_HLYC.
 DR InterPro: IPR005496; Terc.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF03471; CORC_HLYC; 1.
 DR Pfam: PF03741; Terc; 1.
 DR SMART: SM00116; CBS; 2.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 518 AA; 57342 MW; CFP9324DA672DC96 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 518;
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDPSWL 6
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 Db 1 MDPSWL 6

RESULT 15

O9JTN9 PRELIMINARY; PRT; 518 AA.
 ID O9JTN9;
 AC O9JTN9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Conserved hypothetical integral membrane protein.
 GN NMA1694.
 OS *Neisseria meningitidis* (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / Serogroup A / Serotype 4A;
 RX MEDLINE=20222556; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S.,
 RA Jagsis K., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.;
 RT "Complete DNA sequence of a serogroup A strain of *Neisseria*
 RT *meningitidis* 22491.";
 RL Nature 404:502-506(2000).
 RL EMBL: AL162756; CAB84922.1; -.
 DR InterPro: IPR000644; CBS_domain.
 DR InterPro: IPR005170; CORC_HLYC.
 DR InterPro: IPR005496; Terc.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF03471; CORC_HLYC; 1.
 DR Pfam: PF03741; Terc; 1.
 DR SMART: SM00116; CBS; 2.
 KW Complete proteome.
 SQ SEQUENCE 518 AA; 57358 MW; 47PBC652664E3B80 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 518;
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDPSWL 6

Db 1 MDPSWL 6
 :|||||

Search completed: February 18, 2004, 14:35:50
 Job time : 19.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDPSWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127663 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127663

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	313	1	IRF1_CHICK
2	33	94.3	868	1	NI80_YEAST
3	31	88.6	121	1	YGD4_YEAST
4	31	88.6	224	1	PDXH_MYCTU
5	31	88.6	229	1	BCL2_BOVIN
6	31	88.6	236	1	BCL2_CRILLO
7	31	88.6	236	1	BCL2_MOUSE
8	31	88.6	236	1	BCL2_MOUSE
9	31	88.6	239	1	BCL2_MOUSE
10	31	88.6	444	1	GLGA_DEIRA
11	31	88.6	495	1	SYC_AQUAE
12	31	88.6	612	1	YNB8_YEAST
13	31	88.6	612	1	YNB8_YEAST
14	31	88.6	678	1	VID3_AGRRH
15	31	88.6	1343	1	VGR2_RAT
16	30	85.7	438	1	ELBL_ADECT
17	30	85.7	745	1	IKKA_HUMAN
18	30	85.7	745	1	IKKA_HUMAN
19	30	85.7	756	1	IKKB_HUMAN
20	30	85.7	757	1	IKKB_MOUSE
21	30	85.7	757	1	IKKB_MOUSE
22	30	85.7	926	1	MAY3_SCHCO
23	29	82.9	233	1	BCL2_CHICK
24	29	82.9	263	1	TRUA_BUCAR
25	29	82.9	304	1	YG78_PSEAE
26	29	82.9	308	1	CITR_BACSV
27	29	82.9	328	1	YCDU_ECOLI
28	29	82.9	362	1	SIAG_HUMAN
29	29	82.9	397	1	ARGJ_STRAP
30	29	82.9	401	1	HIS2_STY3
31	29	82.9	404	1	ADMR_HUMAN
32	29	82.9	477	1	GLGA_ECOLI
33	29	82.9	477	1	GLGA_SALTI

34	29	82.9	477	1	GLGA_SALTY	P05416 salmonella
35	29	82.9	494	1	DPOW_HUMAN	Q9N877 homo sapien
36	29	82.9	506	1	TDT_CHICK	P36195 gallus gall
37	29	82.9	518	1	TDT_MONDO	O02789 monodelphis
38	29	82.9	522	1	CPE4_RAT	P51869 rattus norv
39	29	82.9	529	1	TIMK_ECOLI	P08957 escherichia
40	29	82.9	529	1	TIM_SALPO	P07989 salmonella
41	29	82.9	529	1	TIM_SALTY	P40813 salmonella
42	29	82.9	530	1	TDT_MOUSE	P09838 mus muscula
43	29	82.9	561	1	Y423_MYCGE	P47662 mycoplasma
44	29	82.9	561	1	Y423_MYCPN	P75174 mycoplasma
45	29	82.9	630	1	Y242_MYCGE	P47484 mycoplasma

ALIGNMENTS

RESULT 1

ID IRF1_CHICK STANDARD; PRT; 313 AA.

AC Q90876; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Interferon regulatory factor 1 (IRF-1)

GN IRF1.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;

OC Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A. MEDLINE=95241453; PubMed=7536924;

RA Jungwirth C., Rebber M., Ozato K., Degen H.J., Schultz U.,

RA David I.B.;

RT "Chicken interferon consensus sequence-binding protein (ICSBP) and

RT interferon regulatory factor (IRF) 1 genes reveal evolutionary

RT conservation in the IRF gene family."

RL Proc. Natl. Acad. Sci. U.S.A. 92:3105-3109(1995).

CC -1- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF

CC TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON

CC CONSENSUS SEQUENCE (ICS) AND ACTIVATES THOSE GENES (BY

CC SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- SIMILARITY: Belongs to the IRF family.

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CC -----

DR EMBL: L39766; AAA62160.1; --

DR HSSP: P15314; IRF1.

DR InterPro: IPR001346; IRF.

DR Pfam: PF00605; IRF.1.

DR PRINTS: PR00267; INTERFERON.

DR ProDom: PD002355; IRF.1.

DR SMART: SM00348; IRF.1.

DR PROSITE: PS00601; IRF.1.

DR KX Transcription regulation; DNA-binding; Activator; Nuclear protein.

FT TRYPTOPHAN PENTAD REPEAT.

FT SEQUENCE 313 AA; 36009 MW; 0895FA3736FA7463 CRC64;

QY Query Match 100.0%; Score 35; DB 1; Length 313;

Best Local Similarity 100.0%; Pred. No. 7.4; Mismatches 0; Gaps 0;

Matches 6; Conservative 0; Indels 0; Gaps 0;

1 LDPSWL 6

Db 295 LDFSWL 300

RESULT 2

NI80 YEAST STANDARD; PRT; 866 AA.

AC P33420: 008917; Created

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE NIP80 protein (NIP100 protein).

GN NIP80 OR NIP100 OR YPL174C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RA SEQUENCE FROM N.A.

RA Schleutend G., Silver P.A.

RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.

RN REVISIONS.

RA Silver P.A.

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=5286C / AB972;

RX MEDLINE=9731271; PubMed=9169875;

RA Bussey H., Storm R.K., Ahmed A., Albermann K., Allen E., Ansgore W.,

RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

RA Bostein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,

RA Chung E., Churcher C.W., Coster F., Davis K., Davis R.W.,

RA Dietrich F.S., Dilius H., DiPaolo T., Dubois E., Duesthoeft A.,

RA Durcan M., Floeth H., Fortin N., Friesen J.D., Fitzer C., Goffeau A.,

RA Hall J., Hebling S., Hyman R., Johnston M., Kallman S., Klein K.,

RA Hunkle-Smith S., Hyman R., Johnston M., Kallman S., Klein K.,

RA Komp C., Kurdi O., Laekhari D., Lew H., Lin A., Lin D., Louis E.J.,

RA Marathe R., Messenguy F., Mewes H.-W., Miripacti S., Moestl D.,

RA Mueller-Auer S., Namath A., Newtich U., Oefner P., Pearson D.,

RA Petel F.X., Pohl T.M., Purnelle D., Schaefer M., Schaefer M.,

RA Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tetteil H.,

RA Uehara L.A., Uehinsky S., Vierendeels F., Vissers S., Voss H.,

RA Walsh S.V., Wambut R., Wang Y., Wedler E., Wedler H., Winnett E.,

RA Zhong W.W., Zollner A., Vo D.H., Hart J.

RL "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI."

RT Nature 367:103-105(1997).

CC -1- SIMILARITY: Contains 1 CAP-Gly domain.

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CC -----

DR EMBL: X72227; CAAS1030.1; -

DR EMBL: Z73330; CA97881.1; -

DR PIR: S65186; S65186.

DR SGD: S0006095; NIP100.

DR GO: GO:0005869; C:cytoskeleton; IDA.

DR GO: GO:0000982; P:mitotic anaphase B; IGI.

DR InterPro: IPR000938; CAP-Gly.

DR Pfam: PF01302; CAP_Gly_1.

DR PROSITE: PS00845; CAP_Gly_1; 1.

DR PROSITE: PS50245; CAP_Gly_2; 1.

KM Cyoskeleton; Coiled coil.

FT DOMAIN 34 84 CAP-Gly.

FT DOMAIN 101 175 COILED COIL (POTENTIAL).

FT DOMAIN 207 375 COILED COIL (POTENTIAL).

FT DOMAIN 445 776 COILED COIL (POTENTIAL).

SO SEQUENCE 866 AA; 100289 MW; A72EA9E338845081 CRC64;

Query Match 94.3%; Score 33; DB 1; Length 868;

Best Local Similarity 83.3%; Pred. No. 54;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 782 LDFSWL 787

Query 1 LDFSWL 6

Db 782 LDFSWL 787

RESULT 3

YGD4 YEAST STANDARD; PRT; 121 AA.

AC P33186;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Hypothetical 13.6 kDa protein in MIG1-AGA2 intergenic region.

GN YGL034C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RA Hedling U., Hofmann B., Dilius H.

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

CC -----

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CC -----

DR EMBL: Z72556; CA96735.1; -

DR PIR: S64036; S64036.

DR SGD: S0003002; YGL034C.

KM Hypothetical protein; ATP-binding.

FT NP_BIND 77 84 ATP (POTENTIAL).

SO SEQUENCE 121 AA; 13573 MW; 88D46FF50B67000F CRC64;

Query Match 88.6%; Score 31; DB 1; Length 121;

Best Local Similarity 83.3%; Pred. No. 17;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 40 LDFSWL 45

Query 1 LDFSWL 6

Db 40 LDFSWL 45

RESULT 4

PDXH MYCTU STANDARD; PRT; 224 AA.

AC 006207;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) (PNP/PMP oxidase)

DE (PNPOX).

GN PDXH OR RV2607 OR MT2682 OR MTCV1A10.26C.

OS Mycobacterium tuberculosis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1773;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H37Rv;

RX MEDLINE=9825987; PubMed=9634230;

RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,

RA Gordon S.V., Eiglsmeier K., Gas S., Barry C.B. III, Tekala F.,

RA Badcock K., Baaham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

RA Hornaby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultison J.E., Taylor K., Whitehead S., Barrett B.G.,
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.",
 RL Nature 393:537-544(1998).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L.,
 RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Blahut W.,
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.",
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: OXIDIZE PNP AND PNP INTO PYRIDOXAL 5'-PHOSPHATE (PLP)
 CC (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Pyridoxamine 5'-phosphate + H(2)O + O(2) =
 CC -1- COFACTOR: FMN (BY SIMILARITY).
 CC -1- PATHWAY: De novo synthesis of pyridoxine (vitamin B6) and
 CC pyridoxal phosphate
 CC -1- SIMILARITY: BELONGS TO THE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE
 CC FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: Z95387; CAB08633.1; -
 CC DR EMBL: AE007101; AAK4698.1; -
 CC DR FIR: F70570; F70570.
 CC DR HSSP: P28225; 1DNL.
 CC DR TIGR: MT2682; -
 CC DR TubercuList; RV2607; -
 CC DR InterPro: IPR000659; Pyridox_oxidase.
 CC DR Pfam: PF01243; Pyridox_oxidase; 1.
 CC DR ProDom: PD006312; Pyridox_oxidase; 1.
 CC DR TIGRFAme; TIGR00558; pdkH; 1.
 CC DR PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
 CC DR Pyridoxine biosynthesis; Oxidoreductase; Flavoprotein; FMN;
 CC KW Complete proteome.
 CC SQ SEQUENCE 224 AA; 25186 MW; 66ABCOAAACE90DC1 CRC64;
 CC
 CC Query Match 88.6%; Score 31; DB 1; Length 224;
 CC Best Local Similarity 83.3%; Pred. No. 32;
 CC Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 1 LDPSTL 6
 CC DB 32 LDPDWL 37
 CC
 CC RESULT 5
 CC BCL2_BOVIN STANDARD; PRT; 229 AA.
 CC ID BCL2_BOVIN
 CC AC 002718;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Apoptosis regulator Bcl-2.
 CC GN BCL2.
 CC OS Bos taurus (Bovine).
 CC OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Chariiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Holstein; TISSUE=Thymus;
 RA Reyes R.A., Cockrell G.L.,
 RT "Bovine leukemia virus associated-leukemogenesis is correlated
 RT with suppression of programmed cell death and increased expression
 RT of Bcl-2.",
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (APAF-1) (By similarity).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-x(L). Heterodimerization with BAX requires intrac BH1 and BH2
 CC domains, and is necessary for anti-apoptotic activity (By
 CC similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intercellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum (By
 CC similarity).
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 CC for interaction with RAIF-1 (By similarity).
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and
 CC occurs during the G2/M phase of the cell cycle (By similarity). In
 CC the absence of growth factors, Bcl2 appears to be phosphorylated
 CC by other protein kinases such as ERKs and stress-activated
 CC kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By
 CC similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
 CC activity, causes the release of cytochrome c into the cytosol
 CC promoting further caspase activity (By similarity).
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: U92434; AAB53319.1; -
 CC DR HSSP: Q07817; 1MAZ.
 CC DR InterPro: IPR000712; Bcl2_BH.
 CC DR InterPro: IPR003093; Bcl2_BH4.
 CC DR InterPro: IPR002475; BCL2_FAMILY.
 CC DR InterPro: IPR004725; Bcl2_reg.
 CC DR Pfam: PF00452; Bcl-2; 1.
 CC DR Pfam: PF02180; BH4; 1.
 CC DR SMART; SM00337; BCL; 1.
 CC DR SMART; SM00265; BH4; 1.
 CC DR TIGRFAme; TIGR00865; bcl-2; 1.
 CC DR PROSITE; PS50062; BCL2_FAMILY; 1.
 CC DR PROSITE; PS01080; BH1; 1.
 CC DR PROSITE; PS01258; BH2; 1.
 CC DR PROSITE; PS01259; BH3; 1.
 CC DR PROSITE; PS01260; BH4; 1.
 CC DR PROSITE; PS50063; BH4_2; 1.
 CC KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
 CC FT DOMAIN 10 30 BH4.
 CC FT DOMAIN 64 72 POLY-PRO.
 CC FT DOMAIN 69 78 POLY-ALA.
 CC FT DOMAIN 83 97 BH3.

FT DOMAIN 126 145 BH1.
 FT DOMAIN 177 192 BH2.
 FT TRANSMEM 202 223 POTENTIAL.
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
 FT MOD RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
 SQ SEQUENCE 229 AA; 25099 MW; ADIDDA98FFFLID CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 229;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DFSWL 6
 DB 201 DFSWL 205
 RESULT 6
 BCL2_CR10 STANDARD; PRT; 236 AA.
 AC Q9JVB8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2.
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 ON NCBI_TaxID=10030;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=20431763; PubMed=10973819;
 RA Tomicic M.T., Christmann M., Kaina B.;
 RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
 protein."
 RL Biochem. Biophys. Res. Commun. 275:899-903(2000).
 RN [2]
 RP SEQUENCE FROM N.A. AND CLEAVAGE BY CASPASES.
 RX MEDLINE=21092839; PubMed=1181062;
 RA Tomicic M.T., Kaina B.;
 RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
 and caspase-3."
 RL Biochem. Biophys. Res. Commun. 281:404-408(2001).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 permeability. Appears to function in a feedback loop system with
 caspases. Inhibits caspase activity either by preventing the
 release of cytochrome c from the mitochondria and/or by binding to
 the apoptosis-activating factor (APAF-1) (By similarity).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
 domains, and is necessary for anti-apoptotic activity (By
 similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 for interaction with RAIF-1 (By similarity).
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
 anti-apoptotic activity. Growth factor-stimulated phosphorylation
 on Ser-70 by PKC is required for the anti-apoptotic activity and
 occurs during the G2/M phase of the cell cycle (By similarity). In
 the absence of growth factors, Bcl2 appears to be phosphorylated
 by other protein kinases such as ERKs and stress-activated kinases
 (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
 (By similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
 cleaved protein, lacking the BH4 domain, has pro-apoptotic
 activity, causes the release of cytochrome c into the cytosol
 promoting further caspase activity.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----
 CC EMBL; AJ271720; CAB92245.1; -
 CC PIR; JC7383; JC7383.
 CC HSSP; O07817; IMAZ.
 CC InterPro; IPR000712; Bcl2_BH.
 CC InterPro; IPR003093; Bcl2_BH4.
 CC InterPro; IPR002475; Bcl2_family.
 CC InterPro; IPR004725; Bcl2_reg.
 CC Pfam; PF00452; Bcl-2_1.
 CC Pfam; PF02180; BH4_1.
 CC SMART; SM00337; BCL; 1.
 CC SMART; SM00265; BH4; 1.
 CC TIGRFAMs; TIGR00865; bcl-2_1.
 CC PROSITE; PS0062; BCL2_FAMILY; 1.
 CC PROSITE; PS01080; BH1; 1.
 CC PROSITE; PS01258; BH2; 1.
 CC PROSITE; PS01259; BH3; 1.
 CC PROSITE; PS01260; BH4_1; 1.
 CC PROSITE; PS0063; BH4_2; 1.
 CC K0 Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
 FT DOMAIN 10 30 BH4.
 FT DOMAIN 90 104 BH3.
 FT DOMAIN 133 152 BH1.
 FT DOMAIN 184 199 BH2.
 FT TRANSMEM 209 230 POTENTIAL.
 FT SITE 64 65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
 FT MOD RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
 SQ SEQUENCE 236 AA; 26491 MW; BECADFIEF337228 CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 236;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DFSWL 6
 DB 208 DFSWL 212
 RESULT 7
 BCL2_MOUSE STANDARD; PRT; 236 AA.
 ID BCL2_MOUSE
 AC P10417; P10418;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2 OR BCL-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A. (ISOPFORMS ALPHA AND BETA).
 RC STRAIN=BA1B/C; TISSUE=Liver;
 RX MEDLINE=87187643; PubMed=3032455;
 RA Negrint M., Siliu E., Kozak C., Tsujimoto Y., Croce C.M.;
 RT "Molecular analysis of mbcl-2: structure and expression of the murine
 RT gene homologous to the human gene involved in follicular lymphoma."
 RL Cell 49:455-463(1987).
 RN [2]
 RP REVISIONS TO 221-222.

RA MEDLINE=92375724; PubMed=1508712;
 RA Eguuchi Y., Ewert D.L., Tsujimoto Y.;
 RT "Isolation and characterization of the chicken bcl-2 gene: expression
 RT in a variety of tissues including lymphoid and neuronal organs in
 RT adult and embryo.";
 RL Nucleic Acids Res. 20:4187-4192(1992).
 CC [3]
 RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.
 RX MEDLINE=97277291; PubMed=9115213;
 RA Ito T., Deng X., Carr B., May W.S. Jr.;
 RT "Bcl-2 phosphorylation required for anti-apoptosis function.";
 RL J. Biol. Chem. 272:11671-11673(1997).
 CC [4]
 RP DEPHOSPHORYLATION BY PP2A.
 RX MEDLINE=99069407; PubMed=9852076;
 RA Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;
 RT "Reversible phosphorylation of Bcl2 following interleukin 3 or
 RT bryostatin 1 is mediated by direct interaction with protein
 RT phosphatase 2A.";
 RL J. Biol. Chem. 273:34157-34163(1998).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (APAF-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
 CC domains, and is necessary for anti-apoptotic activity (by
 CC similarity). Also interacts with APAF-1 and RAF-1.
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Alpha;
 CC IsoId=PI0417-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=PI0417-2; Sequence=VSP 000513;
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 CC for interaction with RAF-1.
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and
 CC occurs during the G2/M phase of the cell cycle. In the absence of
 CC growth factors, Bcl2 appears to be phosphorylated by other protein
 CC kinases such as ERKs and stress-activated kinases.
 CC Dephosphorylated by protein phosphatase 2A (PP2A).
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
 CC activity, causes the release of cytochrome c into the cytosol
 CC promoting further caspase activity.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC -----
 DR EMBL: L31532; AAA37282.1; JOINED.
 DR EMBL: M16506; AAA37282.1; JOINED.
 DR EMBL: M16506; AAA37281.1; --
 DR PIR: B25960; TMSB1.
 DR HSSP: C07817; IMAZ.
 DR MCD: MGI:88138; Bcl2.

DR GO: GO:0008189; F:apoptosis inhibitor activity; IDA.
 DR GO: GO:0005515; F:protein binding activity; IPI.
 DR GO: GO:0006915; F:apoptosis; IDA.
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR003093; Bcl2_BH4.
 DR InterPro: IPR002475; Bcl2_family.
 DR InterPro: IPR004725; Bcl2_reg.
 DR Pfam: PF00452; Bcl-2; 1.
 DR Pfam: PF02180; BH4; 1.
 DR SMART: SM00337; BCL; 1.
 DR SMART: SM00265; BH4; 1.
 DR TIGRfam: TIGR00865; bcl-2; 1.
 DR PROSITE: PS00862; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS01260; BH4; 1.
 DR PROSITE: PS00663; BH4_2; 1.
 KW Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;
 KW Phosphorylation.
 KW DOMAIN 10 30 BH4.
 FT DOMAIN 90 104 BH3.
 FT DOMAIN 133 152 BH1.
 FT DOMAIN 184 199 BH2.
 FT TRANSMEM 209 230 POTENTIAL.
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
 FT MOD_RSS 70 70 PHOSPHORYLATION (BY PKC).
 FT VASPLIC 193 236 DAPFLYGPSRPLPDPSPSLKTLTSLALVGACITLGAVL
 FT /FTId=VSP 000513.
 FT /FTId=VSP 000513.
 SQ SEQUENCE 236 AA; 26425 MW; AA85EP6B0766BBE0A CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 236;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Cy 2 DFWL 6
 Db 208 DFWL 212
 RESULT 8
 BCL2_RAT STANDARD; PRT; 236 AA.
 AC P49950; Q62837; Q64032;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2 OR BCL-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94193015; PubMed=8144041;
 RA Sato T., Irie S., Krajewski S., Reed J.C.;
 RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
 RL Gene 140:291-292(1994).
 CC [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
 RX MEDLINE=95129487; PubMed=7828536;
 RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
 RT "Expression of members of the bcl-2 gene family in the immature rat
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
 RT cell apoptosis is associated with decreased bax and constitutive
 RL Endocrinology 136:232-241(1995).
 RN [3]
 RP SEQUENCE OF 19-172 FROM N.A.

RX MEDLINE=9505917; PubMed=7969891;
 RA Castrén E., Ohga Y., Berzagli M.P., Tzimagiorgis G., Thoenen H.,
 RA Lindholm D.;
 RT "bcl-2 messenger RNA is localized in neurons of the developing and
 RT adult rat brain."
 RL Neuroscience 61:165-177(1994).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (Apaf-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
 CC domains, and is necessary for anti-apoptotic activity (By
 CC similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with
 CC highest levels in reproductive tissues. In the adult brain,
 CC expression is localized in mitral cells of the olfactory bulb,
 CC granule and pyramidal neurons of hippocampus, pontine nuclei,
 CC cerebellar granule neurons, and in ependymal cells. In prenatal
 CC brain, expression is higher and localized in the neuroepithelium
 CC and in the cortical plate.
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 CC for interaction with RAIF-1 (By similarity).
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
 CC on Ser-70 by PKC is required for the anti-apoptotic activity and
 CC occurs during the G2/M phase of the cell cycle. In the absence of
 CC growth factors, Bcl2 appears to be phosphorylated by other protein
 CC kinases such as ERKs and stress-activated kinases.
 CC Phosphorylated by protein phosphatase 2A (PP2A) (By similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
 CC activity, causes the release of cytochrome c into the cytosol
 CC promoting further caspase activity (By similarity).
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC
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 CC
 CC -----
 DR EMBL: U14680; AAA53662.1; -;
 DR EMBL: U14680; AAA53662.1; -;
 DR EMBL: S74122; -; NOT_ANNOTATED_CDS.
 DR PIR: I53744; I53744.
 DR PIR: I67432; I67432.
 DR HSP: Q07817; IMAZ.
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR002475; Bcl2_FAMILY.
 DR InterPro: IPR004725; Bcl2_Reg.
 DR Pfam: PF00452; Bcl-2; 1.
 DR Pfam: PF02180; Bcl-2; 1.
 DR SMART: SM00337; BCL; 1.
 DR SMART: SM00265; BH4; 1.
 DR TIGRfam: TIGR00865; bcl-2; 1.
 DR PROSITE: PS00062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS01260; BH4; 1; 1.

DR PROSITE: PS00063; BH4_2; 1.
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
 FT DOMAIN 10 30
 FT DOMAIN 90 104 BH4.
 FT DOMAIN 133 152 BH1.
 FT DOMAIN 184 199 BH2.
 FT TRANSMEM 209 230
 FT SITE 34 35
 FT MOD RES 70 70
 FT CONFLICT 42 42
 FT CONFLICT 157 157
 FT CONFLICT 164 164
 FT CONFLICT 212 212
 SQ SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 236;
 Best local similarity 100.0%; Pred. No. 34;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DFSWL 6
 Db 208 DFSWL 212
 RESULT 9
 BCL2 HUMAN STANDARD; PRT; 239 AA.
 AC P10415; P10416; Q13842; Q16197;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN BCL2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
 RA MEDLINE=86259760; PubMed=3523487;
 RX Tsujimoto Y., Croce C.M.;
 RT "Analysis of the structure, transcripts, and protein products of
 RT bcl-2, the gene involved in human follicular lymphoma."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
 RN [2]
 RP REVISIONS TO 96; 110 AND 237.
 RX MEDLINE=92375724; PubMed=1508712;
 RA Buchl Y., Ewert D.L., Tsujimoto Y.;
 RT "Isolation and characterization of the chicken bcl-2 gene: expression
 RT in a variety of tissues including lymphoid and neuronal organs in
 RT adult and embryo."
 RL Nucleic Acids Res. 20:4187-4192(1992).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RA MEDLINE=87002488; PubMed=2875799;
 RX Cleary M.L., Smith S.D., Sklar J.;
 RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
 RT 2/immunoglobulin transcript resulting from the t(14;18)
 RT translocation."
 RL Cell 47:19-28(1986).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=88196071; PubMed=2834157;
 RA Seto M., Jaeger U., Hockett R.D., Gruninger W., Bennett S.,
 RA Goldman P., Korsmeyer S.J.;
 RT "Alternative promoters and exons, somatic mutation and deregulation
 RT of the Bcl-2-ig fusion gene in lymphoma."
 RL EMBO J. 7:123-131(1988).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haib F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohilyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Millar S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RP SEQUENCE OF 1-131 FROM N.A. (ISOPHORM ALPHA), AND VARIANTS
 RP NON-HODGKIN'S LYMPHOMA SER-59 AND ILE-93.
 RX MEDLINE=92096610; PubMed=1339299;
 RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.,
 RT "Frequent incidence of somatic mutations in translocated BCL2
 RT oncogenes of non-Hodgkin's lymphomas.";
 RL Blood 79:229-237(1992).
 [7]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=91066924; PubMed=2250705;
 RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.,
 RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
 RT programmed cell death.";
 RL Nature 348:334-336(1990).
 [8]
 RP MUTAGENESIS.
 RX MEDLINE=94239528; PubMed=8183370;
 RA Yin X.-M., Oliva Z.N., Korsmeyer S.J.,
 RT "Bhl and Bhl domains of Bcl-2 are required for inhibition of
 RT apoptosis and heterodimerization with Bax.";
 RL Nature 369:321-323(1994).
 [9]
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.
 RX MEDLINE=98057466; PubMed=9395403;
 RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
 RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
 RL Science 278:1966-1988(1997).
 [10]
 RP REVIEW ON PHOSPHORYLATION.
 RX MEDLINE=21260650; PubMed=1368354;
 RA Ruvoilo P.P., Deng X., May W.S.,
 RT "Phosphorylation of Bcl2 and regulation of apoptosis.";
 RL Leukemia 15:515-522(2001).
 [11]
 RP PHOSPHORYLATION BY ASK1/JNK1.
 RX MEDLINE=20036804; PubMed=10567572;
 RA Yamamoto K., Ichijo H., Korsmeyer S.J.,
 RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal
 RT protein kinase pathway normally activated at G(2)/M.";
 RL Mol. Cell. Biol. 19:8469-8478(1999).
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (Apaf-1).
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC domains, and is necessary for anti-apoptotic activity (By
 CC similarity). Also interacts with Apaf-1 and Raf-1.
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular

CC membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named Isoforms=2;
 CC Name=Alpha;
 CC IsoId=PI0415-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=PI0415-2; Sequence=VSP 000512;
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.
 CC -1- DOMAIN: The BHL domain is required for anti-apoptotic activity and
 CC for interaction with Raf-1.
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and
 CC occurs during the G2/M phase of the cell cycle. In the absence of
 CC growth factors, Bcl2 appears to be phosphorylated by other protein
 CC kinases such as ERKs and stress-activated kinases.
 CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleaved protein, lacking the BHL domain, has pro-apoptotic
 CC activity, causes the release of cytochrome c into the cytosol
 CC promoting further caspase activity.
 CC -1- DISEASE: Involved in follicular lymphoma (FL) (also known as type
 CC II chronic lymphocytic leukemia) by a chromosomal translocation
 CC t(14;18)(q32;q21) which involves BCL2 and immunoglobulin gene
 CC regions. BCL2 mutations found in non-Hodgkin's lymphomas carrying
 CC the chromosomal translocation could be attributed to the Ig
 CC somatic hypermutation mechanism resulting in nucleotide
 CC translocations.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -1- DATABASE: NAME=Alta Gene. Cytogene. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chromcancer/Genes/BCL2ID9.html".
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 CC -----
 CC DR EMBL, M13994; AAAS181.1; ALT_SEQ.
 CC DR EMBL, M13995; AAAS181.1; ALT_SEQ.
 CC DR EMBL, M14745; AAAS591.1; -.
 CC DR EMBL, X06487; CAA29778.1; -.
 CC DR EMBL, BC027258; AAH27258.1; -.
 CC DR EMBL, S72602; AAD1411.1; ALT_SEQ.
 CC DR PIR, C37332; TVHUAL.
 CC DR PDB, 1GSM; 21-MAR-01.
 CC DR PDB, 1GCH; 13-JUN-01.
 CC DR Genew; HGNC:990; BCL2.
 CC DR MIM, 151430; -.
 CC DR GO; GO:0005743; C:mitochondrial inner membrane; TAS.
 CC DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
 CC DR GO; GO:0008916; F:anti-apoptosis; TAS.
 CC DR GO; GO:0008959; F:humoral immune response; TAS.
 CC DR GO; GO:0008285; F:negative regulation of cell proliferation; TAS.
 CC DR GO; GO:0007049; P:oncogenesis; TAS.
 CC DR GO; GO:0000074; P:regulation of cell cycle; TAS.
 CC DR InterPro; IPR00712; Bcl2 BH.
 CC DR InterPro; IPR003093; Bcl2 BH4.
 CC DR InterPro; IPR00475; Bcl2 Family.
 CC DR InterPro; IPR004725; Bcl2_Fam.
 CC DR Pfam; PF00452; Bcl-2; 1.
 CC DR Pfam; PF02180; BH4; 1.
 CC DR SMART; SM00337; BCL; 1.
 CC DR SMART; SM00265; BH4; 1.
 CC DR TIGRFam; TIGR00865; bcl-2; 1.
 CC DR PROSITE; PS5062; BCL2_FAMILY; 1.
 CC DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 KM Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;
 KM Mitochondrion; Phosphorylation; Chromosomal translocation;
 KM Polymorphism; Disease mutation; 3D-structure.

Query Match 88.6%; Score 31; DB 1; Length 239;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 DFSWL 6
 Db 211 DFSWL 215

RESULT 10

GLGA_DEIRA STANDARD; PRT; 444 AA.
 AC Q9RWS1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glycogen synthase (EC 2.4.1.21) (Starch [bacterial glycogen]
 synthase).
 GN GLGA OR DRO594.
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxId=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 radiodurans R1.";
 RT Science 286:1571-1577(1999).
 RU CC
 CC -1- FUNCTION: Synthesizes alpha-1,4-glucan chains using ADP-glucose.
 CC -1- CATALYTIC ACTIVITY: ADP-glucose + (1,4)-alpha-D-glucosyl(N) =
 CC ADP + (1,4)-alpha-D-glucosyl(N+1).
 CC -1- PATHWAY: Glycogen biosynthesis; second step.
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.
 CC Bacterial/plant glycogen synthase subfamily.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AB001917; AAF10170.1; ALT_INTL.
 DR TIGR; DR0594; -; 1.
 DR HAMAP; MF_00484; -; 1.
 DR InterPro; IPR001296; Glyco_trans_1.
 DR Pfam; PF00534; Glyco_transf_1; 1.
 KM Glycogen biosynthesis; Transferase; Glycosyltransferase;
 KM Complete proteome.
 FT BINDING 15 ADP-GLUCOSE (BY SIMILARITY).
 SQ SEQUENCE 444 AA; 48457 MW; 767605781A915302 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 444;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDFSW 5
 Db 426 LDFSW 430

RESULT 11

STC_AQUAE STANDARD; PRT; 495 AA.
 ID -SYC_AQUAE
 AC O67163;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cysteineyl-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase)
 DE (Cyarks).
 GN CYSS OR AQ_1068.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxId=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RX MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjey M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus.";
 RT Nature 392:353-358(1998).
 RL CC
 CC -1- CATALYTIC ACTIVITY: ATP + L-cysteine + tRNA(Cys) = AMP +
 CC diphosphate + L-cysteineyl-tRNA(Cys).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
 CC Strong, to methionyl-tRNA synthetase.
 CC
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 CC
 CC EMBL; AB000721; AAC07125.1; -;
 DR PIR; H70391; H70391.
 DR HAMAP; MF_00041; -; 1.
 DR InterPro; IPR002308; Cys_tRNA-synt_1a.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR Pfam; PF01406; tRNA-synt_1e; 1.
 DR PRINTS; PR00963; TRNASYNTHCS.
 DR TIGRPFAM; TIGR00435; CysS; 1.
 DR PROSITE; PS00178; AA TRNA_LIGASE_I; FALSE NEG.
 KM Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KM Complete proteome.
 FT SITE 31 "HIGH" REGION.
 FT SITE 266 "RMSK" REGION.
 FT BINDING 269 ATP (BY SIMILARITY).
 SQ SEQUENCE 495 AA; 57135 MW; A45458B2BBA8BA4 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 495;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LDFSW 5
 Db 302 LDFSW 306

RESULT 12
 YNB8_YEAST STANDARD; PRT; 612 AA.
 ID YNB8_YEAST
 AC P53976;

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Hypothetical 69.6 kDa protein in HDAL-FUBI intergenic region.
 GN YNL018C OR N2831.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Andre B., Iraqi Housaini I., Urrestarazu L.A., Vlassers S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO YEAST YNL034W.
 CC -----
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 CC -----
 DR EMBL: Z71294; CAA95880.1; -.
 DR PIR: S62930; S62930.
 DR SGD: S0004963; YNL018C.
 KW Hypothetical protein.
 SQ SEQUENCE 612 AA; 69551 MW; E655B2D96317FC62 CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 612;
 Best Local Similarity 83.3%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 Db 17 LDFQWL 22
 RESULT 13
 ID YND4 YEAST STANDARD; PRT; 612 AA.
 AC P53963;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 69.4 kDa protein in NCE3-HRT intergenic region.
 GN YNL034W OR N2740.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,
 RA Hilbert H., Moestl D.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO YEAST YNL018C.
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 CC -----
 DR EMBL: Z71310; CAA95897.1; -.
 DR PIR: S62956; S62956.
 DR SGD: S0004979; YNL034W.
 KW Hypothetical protein.
 SQ SEQUENCE 612 AA; 69373 MW; E39B7080BDE0285 CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 612;

Best Local Similarity 83.3%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 Db 17 LDFQWL 22
 RESULT 14
 ID VID3 AGRH STANDARD; PRT; 678 AA.
 AC P13463;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein VID3.
 GN VID3.
 OS Agrobacterium rhizogenes.
 OC Plasmid pRiA4b.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 NCBI_TaxID=359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A4;
 RX MEDLINE=89039712; PubMed=3185501;
 RA Hirayama T., Muranaka T., Ohkawa H., Oka A.;
 RT "Organization and characterization of the vird genes from
 RT Agrobacterium rhizogenes";
 RL Mol. Gen. Genet. 213:225-237 (1988).
 CC -----
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 CC -----
 DR EMBL: X12667; CAA1352.1; -.
 DR PIR: S12456; S12456.
 DR Crown gall tumor; Plasmid.
 SQ SEQUENCE 678 AA; 72777 MW; A5BCBA58AC26532 CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DPFSL 6
 Db 418 DFWL 422
 RESULT 15
 ID VGR2 RAT STANDARD; PRT; 1343 AA.
 AC O08775;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
 DE (VEGFR-2) (Protein-Tyrosine Kinase receptor fkr-1) (Fetal liver kinase
 DE 1).
 GN KDR OR FLK1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RA Wen Y., Edelman J.L., De Vries G.W., Sachs G.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

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OM protein - protein search, using bw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)

87.531 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDPSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96166682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76:*

2: PIR 2:*

3: PIR 3:*

4: PIR 4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	391	2 A70663	probable PPE prote
2	35	100.0	414	2 T44513	hypothetical prote
3	33	94.3	61	2 D82732	hypothetical prote
4	33	94.3	144	2 A10698	probable pathogeni
5	33	94.3	253	2 D71975	hypothetical prote
6	33	94.3	253	2 E64532	hypothetical prote
7	33	94.3	518	2 A81865	conserved hypotet
8	33	94.3	518	2 C81077	conserved hypotet
9	33	94.3	868	2 S65186	NIP80 protein - ye
10	33	94.3	1214	2 T21915	hypothetical prote
11	32	91.4	208	1 F69462	hypothetical prote
12	32	91.4	371	2 T04971	hypothetical prote
13	32	91.4	449	2 F83328	hypothetical prote
14	32	91.4	467	2 E95850	probable sodium/AI
15	32	91.4	490	2 G95953	probable amino aci
16	31	88.6	121	2 S64036	probable membrane
17	31	88.6	150	2 S74754	hypothetical prote
18	31	88.6	199	2 F82836	hypothetical prote
19	31	88.6	219	2 T30439	hypothetical prote
20	31	88.6	224	2 F70570	transforming prote
21	31	88.6	236	1 TWMSA1	transforming prote
22	31	88.6	236	2 I53744	gene bel-2 protein
23	31	88.6	236	2 JC7383	B-cell lymphoma 2
24	31	88.6	239	1 TYVUA1	transforming prote
25	31	88.6	247	2 C96594	unknown protein, 7
26	31	88.6	253	2 S65170	hypothetical prote
27	31	88.6	262	2 G72694	hypothetical prote
28	31	88.6	262	2 T31582	hypothetical prote
29	31	88.6	331	2 B95880	conserved hypotet

30	31	88.6	338	2 A82890	hypothetical prote
31	31	88.6	387	2 D88968	protein T27B7.3 f1
32	31	88.6	401	2 T44831	probable emulsan r
33	31	88.6	440	2 B71153	hypothetical prote
34	31	88.6	461	2 B83601	probable transport
35	31	88.6	467	2 A81892	hypothetical prote
36	31	88.6	472	2 B75501	glycogen synthase
37	31	88.6	484	2 T33504	hypothetical prote
38	31	88.6	495	2 H70391	cyteline-CRNA 11ga
39	31	88.6	516	2 AC1892	hypothetical prote
40	31	88.6	544	2 T45498	hypothetical prote
41	31	88.6	611	2 G83177	probable sodium/hy
42	31	88.6	612	2 S62930	hypothetical prote
43	31	88.6	612	2 S62956	hypothetical prote
44	31	88.6	641	2 AG2794	hypothetical prote
45	31	88.6	641	2 F97573	hypothetical prote

ALIGNMENTS

RESULT 1

A70663 probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: A70663

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, J.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentile, S.; Hamlin, N.; Holtroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellern, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; PMID:98295987; PMID:9634230

A:Accession: A70663

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-391 <COL>

A:Cross-references: GB:283860; GB:AL133456; NID:G3261681; PIDN:CAB06149.1; PID:e290759;

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: PPE

Query Match	100.0%	Score 35;	DB 2;	Length 391;
Best Local Similarity	100.0%	Pred. No. 21;		
Matches	6;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

RESULT 2

T44513 hypothetical protein 5P [imported] - Pleistomonas shigelloides

C:Species: Pleistomonas shigelloides

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C:Accession: T44513

R:Chida, T.; Okamura, N.; Yoshida, Y.; Ohtani, K.; Arakawa, E.; Watanabe, H.

submitted to the EMBL Data Library, April 1999

A:Description: Complete DNA sequence of the O-antigen (rfb) gene cluster in Pleistomonas

A:Reference number: Z22786

A:Accession: T44513

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-414 <CHI>

A:Cross-references: EMBL:AB025970; PIDN:BA85010.1

A:Experimental source: ATCC 14029

Query Match	100.0%	Score 35;	DB 2;	Length 414;
Best Local Similarity	100.0%	Pred. No. 22;		
Matches	6;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

QY 1 LDPSWL 6
 DB 175 LDPSWL 180

RESULT 3

D82732
 hypothetical protein XP1033 [imported] - *Xylella fastidiosa* (strain 945c)
 C/Species: *Xylella fastidiosa*
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C/Accession: D82732
 R:Anonymous. The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing
 Nature 406, 151-157, 2000
 A/Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A/Reference number: A82515; PMID:20365717; PMID:10910347
 A/Note: for a complete list of authors see reference number A59328 below
 A/Accession: D82732
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-61 <STM>
 A/Cross-references: GB:AE003940; GB:AE003849; NID:99105966; PIDN:AA83843.1; GSPDB:GN001
 A/Experimental source: strain 945c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Agencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.F.; Ferreira, A.J.S.
 submitted to Genbank, June 2000
 A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laizy
 Chado, M.A.; Madeira, A.M.B.N.; Medeiros, W.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 R.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaasak
 A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva
 M.; Teuhako, M.H.; Vallada, H.; Van Sluyt, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A/Reference number: A59328
 A/Content: annotation
 C/Genetics:
 A/Gene: XP1033

Query Match 94.3%; Score 33; DB 2; Length 61;
 Best Local Similarity 83.3%; Pred. No. 6.9;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

A10698
 probable pathogenicity island protein sbcB [imported] - *Salmonella enterica* subsp. enter
 C/Species: *Salmonella enterica* subsp. *enterica* serovar Typh
 A/Note: this species has also been called *Salmonella typhi*
 C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C/Accession: A10698
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 Th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skellton, J.; Stevens, K.;
 A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
 A/Reference number: AB0502; MUID:21534947; PMID:11677608
 A/Accession: A10698
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-144 <PAR>
 A/Cross-references: GB:AL513382; PIDN:CAD01962.1; PID:G16502804; GSPDB:GN00176
 C/Genetics:
 A/Gene: sbcB

Query Match 94.3%; Score 33; DB 2; Length 144;
 Best Local Similarity 83.3%; Pred. No. 17;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6
 DB 45 LDPSWL 50

RESULT 5

D71975
 hypothetical protein jhp0093 - *Helicobacter pylori* (strain J99)
 C/Species: *Helicobacter pylori*
 A/Variety: strain J99
 C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
 C/Accession: D71975
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.R
 Ives, C.; Gibson, R.; Merberg, D.; Miller, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999
 A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric pa
 A/Reference number: A71800; MUID:99120557; PMID:9923682
 A/Accession: D71975
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-253 <ARN>
 A/Cross-references: GB:AE001448; GB:AE001439; NID:94154594; PIDN:AAD05674.1; PID:94154
 A/Experimental source: strain J99
 C/Genetics:
 A/Gene: jhp0093

Query Match 94.3%; Score 33; DB 2; Length 253;
 Best Local Similarity 83.3%; Pred. No. 32;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

B64532
 hypothetical protein HP0101 - *Helicobacter pylori* (strain 26695)
 C/Species: *Helicobacter pylori*
 C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
 C/Accession: B64532
 R:Tomb, J.F.; White, O.; Kesteven, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khajak, H.G.; Glodek, A.; McKen
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Welden, J.M.; Fujii, C.; Bowman, C.; Watney, J
 Nature 388, 539-547, 1997
 A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C
 A/Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
 A/Reference number: A64520; MUID:97394467; PMID:9252185
 A/Accession: B64532
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-253 <TOM>
 A/Cross-references: GB:AE000532; GB:AE000511; NID:92313184; PIDN:AAD07180.1; PID:92313;
 C/Genetics:
 A/Start codon: TTG

Query Match 94.3%; Score 33; DB 2; Length 253;
 Best Local Similarity 83.3%; Pred. No. 32;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 7

AB1865
 conserved hypothetical integral membrane protein NMA1694 [imported] - *Neisseria mening*:
 C/Species: *Neisseria meningitidis*
 C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C/Accession: AB1865
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mori

Holroyd, S.; Jagels, K.; Leather, S.; Moile, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
 A>Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A:Reference number: A81775; MUID:2022556; PMID:10761919
 A:Accession: A81865
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-518 <PAR>
 A:Cross-references: GB:AL62756; GB:AL57959; NID:G7380091; PIDN:CA884922.1; PID:G738033
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA1694

Query Match 94.3%; Score 33; DB 2; Length 518;
 Best Local Similarity 83.3%; Pred. No. 70;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6
 Db 1 MDPSWL 6

RESULT 8

conserved hypothetical protein NMB1485 (imported) - *Neisseria meningitidis* (strain MC58
 C:Species: *Neisseria meningitidis*
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C:Accession: C81077
 R:Retcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizzi, M.
 Science 287, 1899-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Frazer, C.M.; Moxon, E.R.; Rappuoli, R.; VE
 A>Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755; PMID:10710307
 A:Accession: C81077
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-518 <TEP>
 A:Cross-references: GB:AE002498; GB:AE002098; NID:G7226724; PIDN:AAFA1841.1; PID:G722672
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB1485

Query Match 94.3%; Score 33; DB 2; Length 518;
 Best Local Similarity 83.3%; Pred. No. 70;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6
 Db 1 MDPSWL 6

RESULT 9

NIP80 protein - yeast (*Saccharomyces cerevisiae*)
 A:Alternate names: protein P2279; protein YPL174c
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 05-Dec-1997
 C:Accession: S65186; S34343
 R:Benes, V.; Rehm, S.; Nentwich, U.; Vogt, H.; Ansoyge, W.
 submitted to the Protein Sequence Database, May 1996
 A:Reference number: S65183
 A:Accession: S65186
 A:Molecule type: DNA

A:Residues: 1-868 <BEN>
 A:Cross-references: EMBL:Z73530; NID:G1370366; PID:6246907; PID:G1370367; MIPS:YPL174c
 A:Experimental source: strain S288C (AB872)
 R:Schlueder, G.; Silver, P.A.
 submitted to the EMBL Data Library, May 1993
 A:Reference number: S34342
 A:Accession: S34343
 A:Molecule type: DNA

A:Residues: 169-429, 'V', 431-868 <SCH>
 A:Cross-references: EMBL:X72227
 C:Genetics:
 A:Gene: SGD:NIP100; NIP80
 A:Cross-references: MIPS:YPL174c; SGD:S0006095
 A:Map position: 16L
 C:Keywords: transmembrane protein
 F:574-590/Domain: transmembrane #status predicted <TMM>

Query Match 94.3%; Score 33; DB 2; Length 868;
 Best Local Similarity 83.3%; Pred. No. 1,2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6
 Db 782 IDPSWL 787

RESULT 10

hypothetical protein F37D6.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T21915
 R:McMurray, A.

submitted to the EMBL Data Library, June 1996
 A:Reference number: Z19487
 A:Accession: T21915

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1214 <WIL>
 A:Cross-references: EMBL:Z75540; PIDN:CAA9847.1; GSPDB:GN00019; CESP:F37D6.1

A:Experimental source: clone F37D6

C:Genetics:
 A:Gene: CESP:F37D6.1

A:Map position: 1
 A:Intons: 43/1; 59/3; 103/3; 149/2; 230/3; 278/3; 313/1; 439/2; 489/3; 571/1; 625/2; 6

Query Match 94.3%; Score 33; DB 2; Length 1214;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6
 Db 772 LDPSWI 777

RESULT 11

hypothetical protein AF1703 - *Archaeoglobus fulgidus*
 C:Species: *Archaeoglobus fulgidus*
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: F69462
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodex, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Springs, T.; Attiach, P.; Kaine, B.P.; Sykes, S
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: F69462

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-208 <KLE>
 A:Cross-references: GB:AE000986; GB:AE000782; NID:G2689309; PIDN:AA889558.1; PID:G26488

C:Superfamily: Mechanobacterium thermoautotrophicum conserved hypothetical protein MTH1

Query Match 91.4%; Score 32; DB 1; Length 208;
 Best Local Similarity 83.3%; Pred. No. 41;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6

Db 155 LDFPWL 160

RESULT 12

hypothetical protein T16L1.30 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000

C:Accession: T04971

R:Bevan, M.; Obermaier, B.; Deutschenbaue, S.; Piravandi, E.; Hohetzel, J.; Mewes, H.W.;

submitted to the Protein Sequence Database, November 1998

A:Reference number: 215393

A:Accession: T04971

A:Molecule type: DNA

A:Residues: 1-371 <BEV>

A:Cross-references: EMBL:AL031394

A:Experimental source: cultivar Columbia; BAC clone T16L1

C:Genetics:

A:Map position: 4

A:Initiation: 69/1; 83/3; 123/3; 176/2; 201/2; 224/3; 275/3; 312/1; 333/1

A:Note: T16L1.30

C:Superfamily: Arabidopsis thaliana hypothetical protein T16L1.30

Query Match

Best Local Similarity 91.4%; Score 32; DB 2; Length 371;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFPWL 6
Db 325 LDFPWL 330

RESULT 13

F83328

probable sodium/alanine symporter PA2533 [imported] - Pseudomonas aeruginosa (strain PAO

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: F83328

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuochi, S.D.; Warren, P.; Hickey, M.J.; Bz

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: F83328

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-449 <STO>

A:Cross-references: GB:AE004681; GB:AE004091; NID:9948587; PIDN:AA005921.1; GSPDB:GN001

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: PA2533

C:Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 91.4%; Score 32; DB 2; Length 449;
Best Local Similarity 83.3%; Pred. No. 95;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFPWL 6
Db 407 LDFPWL 412

RESULT 14

E95850

probable amino acid carrier protein [imported] - Sinorhizobium meliloti (strain 1021) me

C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C:Accession: E95850

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmeier, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo

A:Reference number: A95842; MUID:21396508; PMID:11481431

A:Accession: E95850

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-467 <KUR>

A:Cross-references: GB:AL591985; PIDN:CA048469.1; PID:G15139941; GSPDB:GN00167

A:Experimental source: strain 1021, megaplasmid pSymb

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpiet, N.A.; Fisher, R.F.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure

hebaulic, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, I

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: Smb20069

A:Genome: plasmid

C:Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 91.4%; Score 32; DB 2; Length 467;
Best Local Similarity 83.3%; Pred. No. 99;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFPWL 6
Db 407 LDFPWL 412

RESULT 15

G95953

probable membrane-anchored protein [imported] - Sinorhizobium meliloti (strain 1021) m

C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C:Accession: G95953

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmeier, J.; Chain, P.; Vorholter, F.J.; Hern

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing en

A:Reference number: A95842; MUID:21396508; PMID:11481431

A:Accession: G95953

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-490 <KUR>

A:Cross-references: GB:AL591985; PIDN:CA049295.1; PID:G15140781; GSPDB:GN00167

A:Experimental source: strain 1021, megaplasmid pSymb

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpiet, N.A.; Fisher, R.F.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure

hebaulic, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, I

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: expA1; Smb21319

A:Genome: plasmid

Query Match 91.4%; Score 32; DB 2; Length 490;
Best Local Similarity 83.3%; Pred. No. 1402;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFPWL 6
Db 466 VDFPWL 471

Search completed: February 18, 2004, 14:38:46
Job time : 8.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDFSWL 6

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters:

801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	10	US-09-847-940B-11
2	35	100.0	6	11	US-09-847-946A-11
3	35	100.0	6	11	US-09-847-946A-42
4	35	100.0	6	11	US-09-847-946A-84
5	35	100.0	7	11	US-09-847-946A-88
6	35	100.0	8	11	US-09-847-946A-81
7	35	100.0	8	11	US-09-847-946A-89
8	35	100.0	9	11	US-09-847-946A-80
9	35	100.0	9	11	US-09-847-946A-83
10	35	100.0	9	11	US-09-847-946A-86
11	35	100.0	9	11	US-09-847-946A-87
12	35	100.0	10	11	US-09-847-946A-82
13	35	100.0	10	11	US-09-847-946A-85
14	35	100.0	11	11	US-09-847-946A-79
15	33	94.3	265	10	US-09-881-752A-368

16	33	94.3	868	12	US-10-369-493-22465	Sequence 22465, A
17	32	91.4	6	10	US-09-847-940B-12	Sequence 12, Appl
18	32	91.4	6	11	US-09-847-946A-12	Sequence 95, Appl
19	32	91.4	7	11	US-09-847-946A-95	Sequence 99, Appl
20	32	91.4	8	11	US-09-847-946A-99	Sequence 92, Appl
21	32	91.4	8	11	US-09-847-946A-92	Sequence 100, App
22	32	91.4	8	11	US-09-847-946A-100	Sequence 91, Appl
23	32	91.4	9	11	US-09-847-946A-91	Sequence 94, Appl
24	32	91.4	9	11	US-09-847-946A-94	Sequence 5624, Ap
25	32	91.4	9	11	US-09-847-946A-97	Sequence 11, Appl
26	32	91.4	9	11	US-09-847-946A-98	Sequence 96, Appl
27	32	91.4	10	11	US-09-847-946A-93	Sequence 90, Appl
28	32	91.4	10	11	US-09-847-946A-96	Sequence 5624, Ap
29	32	91.4	11	11	US-09-847-946A-90	Sequence 5, Appl
30	31	88.6	106	12	US-09-864-408A-5624	Sequence 12, Appl
31	31	88.6	236	15	US-10-277-693A-11	Sequence 2, Appl
32	31	88.6	239	8	US-08-726-211-5	Sequence 12, Appl
33	31	88.6	239	12	US-10-141-618-12	Sequence 21, Appl
34	31	88.6	239	12	US-10-053-665A-21	Sequence 5, Appl
35	31	88.6	239	12	US-10-387-961A-5	Sequence 12, Appl
36	31	88.6	239	15	US-10-101-482-12	Sequence 10, Appl
37	31	88.6	239	15	US-10-277-693A-10	Sequence 23432, A
38	31	88.6	239	15	US-10-072-830-2	Sequence 11, Appl
39	31	88.6	472	12	US-10-369-493-23432	Sequence 11, Appl
40	31	88.6	662	10	US-09-924-358-11	Sequence 6, Appl
41	31	88.6	662	12	US-10-410-764-11	Sequence 2, Appl
42	31	88.6	1398	12	US-10-021-571-6	Sequence 33, Appl
43	30	85.7	6	10	US-09-847-940B-2	
44	30	85.7	6	11	US-09-847-946A-2	
45	30	85.7	6	11	US-09-847-946A-33	

ALIGNMENTS

RESULT 1
US-09-847-940B-11
Sequence 11, Application US/09847940B
Patent No. US2002015600A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847, 940B
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643, 260
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-11

Query Match 100.0%; Score 35; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
DB 1 LDFSWL 6

RESULT 2
US-09-847-946A-11
Sequence 11, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J

```
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-11
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Query Match          100.0%; Score 35; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDFSWL 6
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Db      1 LDFSWL 6
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RESULT 3
US-09-847-946A-42
; Sequence 42, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
```

```
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-42
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```
Query Match          100.0%; Score 35; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 LDFSWL 6
        |||||
Db      1 LDFSWL 6
```

```
RESULT 4
US-09-847-946A-84
; Sequence 84, Application US/09847946A
; Publication No. US20030054999A1
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```
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 84
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-84
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Query Match          100.0%; Score 35; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 LDFSWL 6
        |||||
Db      1 LDFSWL 6
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```
RESULT 5
US-09-847-946A-88
; Sequence 88, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 88
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-88
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Query Match          100.0%; Score 35; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 LDFSWL 6
        |||||
Db      1 LDFSWL 6
```

```
RESULT 6
```

US-09-847-946A-81
; Sequence 81, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-81

Query Match 100.0%; Score 35; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6
Db 3 LDFSWL 8

RESULT 7
US-09-847-946A-89
; Sequence 89, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-89

Query Match 100.0%; Score 35; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6
Db 1 LDFSWL 6

RESULT 8
US-09-847-946A-80
; Sequence 80, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-80

Query Match 100.0%; Score 35; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6
Db 1 LDFSWL 6

RESULT 9
US-09-847-946A-83
; Sequence 83, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-83

Query Match 100.0%; Score 35; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6
|||||
Db 1 LDFSWL 6

RESULT 10

US-09-847-946A-86
; Sequence 86, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hamnig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-86

Query Match Best Local Similarity 100.0%; Score 35; DB 11; Length 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6
|||||
Db 3 LDFSWL 8

RESULT 11

US-09-847-946A-87
; Sequence 87, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hamnig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-87

Query Match Best Local Similarity 100.0%; Score 35; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6
|||||
Db 2 LDFSWL 7

RESULT 12

US-09-847-946A-82
; Sequence 82, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hamnig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-82

Query Match Best Local Similarity 100.0%; Score 35; DB 11; Length 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6
|||||
Db 2 LDFSWL 7

RESULT 13

US-09-847-946A-85
; Sequence 85, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hamnig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-85

Query Match Best Local Similarity 100.0%; Score 35; DB 11; Length 10;

US-09-847-946A-85

Query Match 100.0%; Score 35; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSWL 6
|||
DB 3 LDFSWL 8

RESULT 14

US-09-847-946A-79
Sequence 79, Application US/09847946A
Publication No. US2003005499A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sanjay
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 79
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NEMO binding
US-09-847-946A-79

Query Match 100.0%; Score 35; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSWL 6
|||
DB 3 LDFSWL 8

RESULT 15

US-09-881-752A-368
Sequence 368, Application US/09881752A
Patent No. US20020115078A1
GENERAL INFORMATION:
APPLICANT: Kleantous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in the
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 368
LENGTH: 265
TYPE: PRT
ORGANISM: Helicobacter pylori

US-09-881-752A-368

Query Match 94.3%; Score 33; DB 10; Length 265;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSWL 6
|||
DB 161 LDFSWI 166

Search completed: February 18, 2004, 15:41:58
Job time : 16.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDRSWL 6

Scoring table: BLASTUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
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10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	ABB08733	Mutated IKKbeta NB
2	35	100.0	6	AA48516	NBD mutant peptide
3	35	100.0	6	AA48539	Anti-inflammatory
4	35	100.0	6	AA48581	Anti-inflammatory
5	35	100.0	6	ABU08426	Human NEMO binding
6	35	100.0	7	AA48585	Anti-inflammatory
7	35	100.0	8	AA48578	Anti-inflammatory
8	35	100.0	8	AA48586	Anti-inflammatory
9	35	100.0	9	AA48577	Anti-inflammatory

10	35	100.0	9	23	AA48580	Anti-inflammatory
11	35	100.0	9	23	AA48583	Anti-inflammatory
12	35	100.0	9	23	AA48584	Anti-inflammatory
13	35	100.0	10	23	AA48579	Anti-inflammatory
14	35	100.0	10	23	AA48582	Anti-inflammatory
15	35	100.0	11	23	AA48576	Anti-inflammatory
16	35	100.0	11	23	ABF77296	Human IKKbeta
17	35	100.0	14	21	AAV70582	Salmonella Pathogen
18	33	94.3	253	19	AAV11039	H. pylori ORF 068
19	33	94.3	265	19	AAV98384	N. gonorrhoeae anti
20	33	94.3	528	24	ABP79808	Mutated IKKbeta NB
21	32	91.4	6	23	ABB08734	NBD mutant peptide
22	32	91.4	6	23	AA48517	Anti-inflammatory
23	32	91.4	6	23	AA48540	Anti-inflammatory
24	32	91.4	6	23	AA48592	Anti-inflammatory
25	32	91.4	6	24	ABU08427	Human NEMO binding
26	32	91.4	7	23	AA48596	Anti-inflammatory
27	32	91.4	8	23	AA48589	Anti-inflammatory
28	32	91.4	8	23	AA48597	Anti-inflammatory
29	32	91.4	8	23	AA48588	Anti-inflammatory
30	32	91.4	9	23	AA48591	Anti-inflammatory
31	32	91.4	9	23	AA48594	Anti-inflammatory
32	32	91.4	9	23	AA48595	Anti-inflammatory
33	32	91.4	10	23	AA48590	Anti-inflammatory
34	32	91.4	10	23	AA48593	Anti-inflammatory
35	32	91.4	11	23	AA48587	Anti-inflammatory
36	32	91.4	11	23	AA48587	Anti-inflammatory
37	32	91.4	11	23	AA48587	Anti-inflammatory
38	31	88.6	23	20	AA487823	Human IKKbeta
39	31	88.6	23	20	AA487823	Human IKKbeta
40	31	88.6	25	22	AA487440	Bax epitope #10.
41	31	88.6	25	22	AA487446	Bax epitope #16.
42	31	88.6	42	21	AA483437	Human secreted pro
43	31	88.6	46	24	ABU07218	Matze SIII C-term
44	31	88.6	87	22	ABG10985	Novel human diapo
45	31	88.6	106	22	AA488387	Human immune/haemo

ALIGNMENTS

RESULT 1
ABB08733
ID ABB08733 standard; peptide, 6 AA.
XX
AC ABB08733;
XX
DT 14-JUN-2002 (first entry)
XX
DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 11.
XX
XX IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
XX kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
XX autoimmune disease; transplant rejection; osteoporosis; cancer;
XX Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
XX rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
XX corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
XX osteopathic; cytotoxic; nocotropic; neuroprotective; anti-HIV; human;
XX antiarteriosclerotic; vincristine; antiasthmatic; antiallergic;
XX dermatological; antibacterial; antipsoriatic; antipneumatic;
XX antirheumatic; osteopathic; antitumor; mutant; mutcin.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 3 /note= "Wildtype Trp substituted by Phe"
XX WO200183547-A2.
XX
XX 08-NOV-2001.
XX

PF	02-MAY--2001; 2001WO-US40654.
XX	
PR	02-MAY--2000; 2000US-201261P.
PR	22-AUG--2000; 2000US--0643260.
XX	
PA	(UYVA) UNIV YALE.
XX	
P1	May MJ, Ghosh S;
XX	
DR	WPI, 2002-179350/23.
XX	
PT	Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT	inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT	cell with an anti-inflammatory compound comprising at least one NEMO
XX	binding domain -
PS	Claim 23; Page 44; 82pp; English.
XX	
CC	The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC	comprises contacting a cell with an anti-inflammatory compound
CC	(ABB08725-ABB08742) comprising at least one NEMO binding domain
CC	(AAB877113). The compound has acts through selective inhibition of
CC	cyclooxygenase-mediated NF-kB activation by blocking the interaction of NEMO
CC	with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC	interaction results in inhibition of IKKalpha kinase activation and
CC	subsequent decreased phosphorylation of Ikbappab. The compound may also
CC	act (directly or indirectly) by blocking the recruitment of leukocytes
CC	into sites of acute and chronic inflammation, by down-regulating the
CC	expression of E-selectin on leukocytes or by blocking osteoclast
CC	differentiation. The compound is useful in treating NF-kB mediated
CC	conditions, where the condition is an inflammatory disorder, an
CC	autoimmune disease, transplant rejection, osteoporosis, cancer,
CC	Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC	telangiectasias. The inflammatory disorder is asthma, allergies,
CC	urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC	rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC	bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC	bursitis. The inflammatory disorder may also be dermatitis, eczema,
CC	psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC	spondyloarthritis. Also for Crohn's disease, ulcerative colitis,
CC	polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC	cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC	caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC	diseases include HIV and influenza. The compound may also be useful for
CC	treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC	sunburn or aging. The compound may be used to replace corticosteroids in
CC	any application in which corticosteroids are used, including
CC	immunosuppression in transplants and cancer therapy. Also for identifying
CC	antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC	The compound may be administered alone or in combination with other known
CC	anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC	binding domain of IKKbeta.
XX	
SQ	Sequence 6 AA;
XX	
DY	Query Match 100.0%; Score 35; DB 23; Length 6;
DB	Best Local Similarity, 100.0%; Pred. No. 9.3e+05;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 LDFSWL 6
Db	1 LDFSWL 6
RESULT 2	
ID	AAM48516
AA	AAM48516 standard; Peptide; 6 AA.
XX	AAM48516;
DT	20-MAR--2002 (first entry)
XX	NBD mutant peptide SEQ ID NO 11.
DE	

KX	Antiinflammatory; antiasthmatic; cytoprotic; antipneumatic; nocotropic;
KW	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KM	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KV	anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW	Cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; atherosclerosis; viral infection;
KW	osteoporosis; Alzheimer's disease; rheumatoid arthritis; viral infection;
KX	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS	Synthetic.
PN	WO200183554-A2.
PP	
PD	08-NOV-2001.
XX	
PF	02-MAY-2001; 2001WO-US14346.
XX	
PR	02-MAY-2000; 2000US-201261P.
PR	22-APR-2000; 2000US-0643260.
XX	
PA	(PARA-) PRACIS PHARM INC.
PI	(OTTA) UNIV YALE.
PI	May MJ, Ghosh S, Findels MA, Phillips K,
XX	
XX	WPI; 2002-121889/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PS	psoriasis -
XX	
XX	Example 6; Page 47; 88pp; English.
CC	The invention relates to an antiinflammatory compound (especially
CC	AAM48628-AAM48645), comprising a membrane translocation domain
CC	(AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC	cytoprotic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
CC	
XX	
SQ	Sequence 6 AA;
Query Match	100.0%; Score 35; DB 23; Length 6;
Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 LDRSWM 6
Db	1 LDRSWM 6
AA	AA
ID	AA

XX
AC AAM48539;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 42.
XX
KM Anti-inflammatory; antiasthmatic; cytoskeletal; antiproliferative; neurotrophic;
KM antiinflammatory; antiarthritic; osteopathic; antibacterial; virucide;
KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM autoimmune disorder; multiple sclerosis; transplant rejection;
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
XX
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Pindels MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Claim 6; Page 61; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48519). The antiinflammatory compounds have antiasthmatic,
CC cytoskeletal, antiproliferative, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neurotrophic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 35; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 LDPSWL 6
RESULT 4
ID AAM48581
XX AAM48581 standard; Peptide; 6 AA.
XX
AC AAM48581;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 84.
XX
KM Anti-inflammatory; antiasthmatic; cytoskeletal; antiproliferative; neurotrophic;
KM antiinflammatory; antiarthritic; osteopathic; antibacterial; virucide;
KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM autoimmune disorder; multiple sclerosis; transplant rejection;
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
XX
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Pindels MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Claim 6; Page 62; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48519). The antiinflammatory compounds have antiasthmatic,
CC cytoskeletal, antiproliferative, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neurotrophic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDPSWL 6
 Db 1 LDPSWL 6

RESULT 5
 ABU08426
 ID ABU08426 standard; peptide; 6 AA.
 AC ABU08426;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human NEMO binding site (NBD) mutant peptide #9.
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW translocation detection; immunosuppressive; osteopathic;
 KW cytostatic; nocrotropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antirheumatic; antiasthmatic; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2002156000-A1.
 PD 24-OCT-2002.
 XX
 PF 02-MAY-2001; 2001US-0847940.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (MAYM/) MAY M J.
 PA (GHOSH/) GHOSH S.
 XX
 PI May MJ, Ghosh S;
 PT
 DR WPI; 2003-209142/20.
 XX
 PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX
 PS Claim 22; Page 17; 47pp; English.
 XX
 CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for translocation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 CC
 CC Sequence 6 AA;
 CC
 CC Query Match 100.0%; Score 35; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDPSWL 6
 Db 1 LDPSWL 6

RESULT 6
 AAM48585
 ID AAM48585 standard; Peptide; 7 AA.
 AC AAM48585;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 88.
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nocrotropic;
 KW antirheumatic; antiasthmatic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 OS
 XX
 PN WO200183554-A2.
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA-) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 PT
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiasthmatic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nocrotropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g., asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC arthritis, autoimmune diseases such as lupus, polyarthritis, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 35; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 1 LDFSWL 6
 Db 1 LDFSWL 6
 RESULT 7
 AAM48578
 ID AAM48578 standard; Peptide; 8 AA.
 XX
 AC AAM48578;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 81.
 XX
 KM Anti-inflammatory; antiaesthetic; cytostatic; antiporiatic; nootropic;
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antiporiatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 35; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 3 LDFSWL 8
 Db 3 LDFSWL 8
 RESULT 8
 AAM48586
 ID AAM48586 standard; Peptide; 8 AA.
 XX
 AC AAM48586;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 89.
 XX
 KM Anti-inflammatory; antiaesthetic; cytostatic; antiporiatic; nootropic;
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antiporiatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

Query Match	Similarity	Score	DB	Length
Best Local	100.0%	100.0%	Pred. No. 9.3e+05	
Matches	6	Conservative	0	Mismatches 0; Indels 0; Gaps 0
Oy	1	LDPFWL 6		
Db	1	LDPFWL 6		
RESULT 9				
ID	AA048577	standard; Peptide; 9 AA.		
XX	AA048577;			
AC	20-MAR-2002	(first entry)		
XX	Anti-inflammatory peptide SEQ ID NO 80.			
DE	Anti-inflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic; antirheumatic; antiaesthetic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antithrombotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.			
XX	Synthetic.			
OS	WO200183554-A2.			
PN	08-NOV-2001.			
XX	02-MAY-2001; 2001WO-US14346.			
PD	02-MAY-2000; 2000US-201261P.			
XX	22-AUG-2000; 2000US-0643260.			
PR	(PRAE-) PRAECS PHARM INC.			
XX	(UYVA) UNIV YALE.			
PA	May MJ, Ghosh S, Fandels MA, Phillips K;			
XX	WPI, 2002-121889/16.			
DR	Novel anti-inflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,			
XX	psoriasis			
PT	Claim 6; Page 62; 89pp; English.			
PS	The invention relates to an anti-inflammatory compound (especially			
CC	AA048628-AA046645), comprising a membrane translocation domain			

CC	(AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence
CC	(AAM48525-AAM48619). The anti-inflammatory compounds have antiaesthetic, cytoskeletal, antiproliferative, antineuritic, antiallergic, osteoprotective, antibacterial, immunosuppressive, dermatological, neuroprotective, CC nootropic, antithrombotic, virocidic and anti-allergic activity. The compounds act as selective inhibitors of cytokine-mediated NF-kappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The CC compound are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, CC granulomatosis, multiple sclerosis; transplant rejection; and ataxia telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, angina and drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.
CC	
XX	
SQ	Sequence 9 AA;
Query Match	100.0%; Score 35; DB 23; Length 9;
Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Matches 6;	Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 LDFSWL 6 1 LDFSWL 6
Dd	
RESULT 10	
ID	AAM48580
AA	AAM48580 standard; Peptide: 9 AA.
XX	
AC	AAM48580;
XX	
DT	20-MAR-2002 (first entry)
DE	Anti-inflammatory peptide SEQ ID NO 83.
XX	
KM	Antinflammatory; antiaesthetic; cytoskeletal; antiproliferative; nootropic; antineuritic; antiallergic; osteoprotective; antibacterial; virocidic; immunosuppressive; dermatological; neuroprotective; antithrombotic; CC antifungal; membrane translocation domain; NEMO binding domain; eczema; cyclokinase; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmunity disorder; multiple sclerosis; transplant rejection; CC osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; amyotrophy; arthritis.
KM	
OS	Synthetic.
XX	
MO	WO200183554-A2.
XX	
PD	08-NOV-2001.
XX	
PE	02-MAY-2001; 2001WO-US14346.
XX	
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
PA	(UYIA) UNIV YALE.
XX	
P1	May MU, Ghosh S, Findeis MA, Phillips K;
XX	
DR	WPI; 2002-121889/16.
XX	
PT	Novel antinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis -
 XX Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48620-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteoprotective,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antithrombotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC burns; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 SQ Sequence 9 AA;
 XX
 XX
 Query Match 100.0%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 1 LDFSWL 6
 DB 1 LDFSWL 6
 RESULT 11
 AAM48583
 ID AAM48583 standard; Peptide; 9 AA.
 XX
 AC AAM48583;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 86.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antiproliferative; neurotropic;
 KW antirheumatic; antiarthritic; osteoprotective; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Fandels MA, Phillips K;

XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48620-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteoprotective,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antithrombotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC burns; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 SQ Sequence 9 AA;
 XX
 XX
 Query Match 100.0%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 1 LDFSWL 6
 DB 3 LDFSWL 8
 RESULT 12
 AAM48584
 ID AAM48584 standard; Peptide; 9 AA.
 XX
 AC AAM48584;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 87.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antiproliferative; neurotropic;
 KW antirheumatic; antiarthritic; osteoprotective; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.
XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
XX
XX
PI May MJ, Ghosh S, Findels MA, Phillips K;
XX WPI; 2002-121889/16.
DR
XX
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
PS
XX Claim 6; Page 62; 88pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 35; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSWL 6
Db 2 LDFSWL 7
RESULT 13
AAM48579
ID AAM48579 standard; Peptide; 10 AA.
XX
AC AAM48579;
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 82.
XX
XX Antiinflammatory; antiasthmatic; cytoskeletal; antibacterial; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; inflammatory bowel disease;
XX osteoporosis; Alzheimer's disease; atherosclerosis; transplant rejection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
XX
XX
PN W0200183554-A2.

XX
PD 08-NOV-2001.
XX
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX
XX 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
XX
XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S, Findels MA, Phillips K;
XX WPI; 2002-121889/16.
DR
XX
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
PS
XX Claim 6; Page 62; 88pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 35; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSWL 6
Db 2 LDFSWL 7
RESULT 14
AAM48582
ID AAM48582 standard; Peptide; 10 AA.
XX
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 85.
XX
XX Antiinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX

KW		osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XV		ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	Synthetic.	
OS		
XX	WO200183554-A2.	
PX		
PN		
PD	08-NOV-2001.	
XX		
PF	02-MAY-2001; 2001WO-US14346.	
PR		
XX	02-MAY-2000; 2000US-201261P.	
PR	22-AUG-2000; 2000US-0643260.	
PA	(PRAE-) PRAECIS PHARM INC.	
PA	(UYTA) UNIV YALE.	
PI		
PI	May MJ, Ghosh S, Findels MA, Phillips K;	
XX		
XX	WPI: 2002-121889/16.	
DR		
PT		
PT	Novel antiinflammatory compound comprising membrane translocation	
PT	domain fused to NEMO binding sequence, useful for blocking nuclear	
PT	factor kappaB activation, and for treating asthma, lung inflammation,	
XX	psoriasis -	
PS		
PS	Claim 6; Page 62; 88pp; English.	
XX		
XX	The invention relates to an antiinflammatory compound (especially	
CC	AAM48628-AAM48645), comprising a membrane translocation domain	
CC	(AAM48620-AAM48637 or AAM48646-AAM48651) which comprises from 6-15	
CC	amino acid residues, fused to a NEMO binding sequence	
CC	(AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,	
CC	Cyclostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,	
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,	
CC	nocrotropic, antiatherosclerotic, virucide and antiallergic activity. The	
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB	
CC	activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at	
CC	the NEMO binding domain that results in inhibition of IKKbeta Kinase	
CC	activation and subsequent decreased phosphorylation of IkkappaB. The	
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,	
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,	
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,	
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,	
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;	
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia	
CC	telangiectasia. The compounds are also useful for treating	
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,	
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and	
CC	arthritis.	
XX		
XX	Sequence 10 AA;	
XX		
Query Match	100.0%; Score 35; DB 23; Length 10;	
Best Local Similarity	100.0%; Pred. No. 5.1;	
Matches 6; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
QY	1 LDFSWL 6 	
Db	3 LDFSWL 8	
RESULT 15		
ID	AAM48576 standard; Peptide; 11 AA.	
XX		
AC	AAM48576;	
XX		
DT	20-MAR-2002 (first entry)	
XX		
DE	Anti-inflammatory peptide SEQ ID NO 79.	
XX		
XM	Antinflammatory; antiaesthetic; cyclostatic; antipsoriatic; nocrotropic;	

KM antiinflammatory; antiarthritic; osteopathic; antibacterial; virucide;
KM immunosuppressive; dermatological; neuroprotective; antithrombotic;
KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KM cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM autoimmune disorder; multiple sclerosis; transplant rejection;
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PP 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALR.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI, 2002-121899/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX Claim 6; Page 62; 8pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
CC AA48638-AA48645), comprising a membrane translocation domain
CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AA48525-AA48519). The antiinflammatory compounds have antiaesthetic,
CC cytosarctic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antithrombotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of Ikappab kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of Ikappab. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursts; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 11 AA;

Query Match Similarity 100.0%; Score 35; DB 23; Length 11;
Best Local 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conserved 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSM 6
Db 3 LDFSM 8

Search completed: February 18, 2004, 14:26:22
Job time : 22.7763 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-10

Perfect score: 33
Sequence: 1 LDASWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	518	5	Q968Y8
2	33	100.0	521	11	Q968Y8
3	33	100.0	535	5	Q968Y7
4	31	93.9	908	16	Q82A04
5	31	93.9	535	17	Q27987
6	31	93.9	763	10	Q96U25
7	30	90.9	187	2	Q9JRL8
8	30	90.9	187	2	Q9JRL9
9	30	90.9	187	2	Q9JRL5
10	30	90.9	187	2	Q9JRL0
11	30	90.9	187	2	Q9JRL7
12	30	90.9	205	16	Q8BBG1
13	30	90.9	221	16	Q9A120
14	30	90.9	221	16	Q8B239
15	30	90.9	225	17	Q8BRL0
16	30	90.9	245	2	Q68096

17	30	90.9	261	4	Q9P012	Q9P012 homo sapien
18	30	90.9	261	11	Q99K13	Q99K13 mus musculus
19	30	90.9	290	2	Q9F238	Q9F238 xanthomonas
20	30	90.9	290	2	Q9RB02	Q9RB02 xanthomonas
21	30	90.9	290	2	Q9RB03	Q9RB03 xanthomonas
22	30	90.9	290	2	Q51899	Q51899 xanthomonas
23	30	90.9	293	16	Q8PFB8	Q8PFB8 xanthomonas
24	30	90.9	307	11	Q9CXJ5	Q9CXJ5 mus musculus
25	30	90.9	316	16	Q9BIR6	Q9BIR6 rhizobium 1
26	30	90.9	317	4	Q9BRA3	Q9BRA3 homo sapien
27	30	90.9	332	2	Q9RA30	Q9RA30 vibrio mari
28	30	90.9	344	11	Q8R306	Q8R306 mus musculus
29	30	90.9	442	10	Q9S232	Q9S232 arabidopsis
30	30	90.9	461	10	Q9M0J8	Q9M0J8 arabidopsis
31	30	90.9	500	11	Q8CHX7	Q8CHX7 mus musculus
32	30	90.9	563	4	Q8B510	Q8B510 homo sapien
33	30	90.9	688	9	Q9PRZ2	Q9PRZ2 mycoplasma
34	30	90.9	810	16	Q8ZKN4	Q8ZKN4 salmoneilla
35	30	90.9	810	16	Q8Z226	Q8Z226 salmoneilla
36	30	90.9	906	16	Q8YXK2	Q8YXK2 anabaena sp
37	30	90.9	997	2	Q68533	Q68533 pseudomonas
38	29	87.9	69	10	Q43289	Q43289 arabidopsis
39	29	87.9	125	16	Q8DUJ9	Q8DUJ9 streptococc
40	29	87.9	150	16	Q9HTX9	Q9HTX9 pseudomonas
41	29	87.9	151	5	Q77003	Q77003 biophila
42	29	87.9	156	4	Q96G14	Q96G14 homo sapien
43	29	87.9	162	8	Q94Z49	Q94Z49 neolepidape
44	29	87.9	162	8	Q94Z27	Q94Z27 profundiver
45	29	87.9	175	16	Q8PQ04	Q8PQ04 xanthomonas

ALIGNMENTS

RESULT 1	ID	Q968Y8	PRELIMINARY	PRT	518 AA.
AC	Q968Y8	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)				
DE	Hypothetical protein T28B4.1b.				
GN	T28B4.1 OR T28B4.1b.				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;				
OC	Rhabditidae; Pelodierinae; Caenorhabditis.				
OX	NCBI_TaxID=6239;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Briscot N2;				
RX	MEDLINE=99069613; PubMed=9851916;				
RA	None;				
RT	"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.",				
RL	Science 282:2012-2018 (1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Briscot N2;				
RA	Wilson R., Greco T., Sansone J.;				
RT	"The sequence of C. elegans cosmid T28B4.",				
RL	Submitted (Oct-1997) to the EMBL/Genbank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Briscot N2;				
RA	Waterston R.;				
RT	Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.				
RL	EMBL, AF026206; AA039308.1; --				
DR	Wormep; T28B4.1b; CE27216.				
DR	Interp; IP001810; F-box.				
DR	Pfam; PF00646; F-box; 1.				
DR	SMART; SM00256; FBOX; 1.				
DR	PROSITE; PS50181; FBOX; 1.				
SQ	SEQUENCE 518 AA, 60125 MW; A8A30C911618BD47 CRC64;				

Query Match 100.0%; Score 33; DB 5; Length 518;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 |||||
 DB 323 LDASWL 328

RESULT 2

08CAD5 PRELIMINARY; PRT; 521 AA.

AC 08CAD5; (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=CS7BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851;
 RA the FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK082517; BAC38515.1; -.
 KW Hypothetical protein.

FT NON TER 1
 SQ SEQUENCE 521 AA; 57719 MW; D4CF39CB2512D5 CRC64;

Query Match 100.0%; Score 33; DB 11; Length 521;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 |||||
 DB 283 LDASWL 288

RESULT 3

0968Y7 PRELIMINARY; PRT; 535 AA.

AC 0968Y7; (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE T28B4.1a protein.
 GN T28B4.1 OR T28B4.1A.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelioidinae; Caenorhabditis.
 CX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;
 RA Wilson R.; Greco T.; Sansone J.;
 RT "The sequence of C. elegans cosmid T28B4.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF026206; AAK39309.1; -.
 DR WormPep; T28B4.1a; CE27215.
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.
 DR SMART; SM00256; FBOX; 1.
 DR PROSITE; PS50181; FBOX; 1.
 SQ SEQUENCE 535 AA; 62557 MW; CFEA8794E188C104 CRC64;

Query Match 100.0%; Score 33; DB 5; Length 535;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 |||||
 DB 340 LDASWL 345

RESULT 4

08ZAJ4 PRELIMINARY; PRT; 308 AA.

AC 08ZAJ4; (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE High-affinity branched-chain amino acid transport system,
 DE protein (high-affinity branched-chain amino acid ABC transport system
 DE membrane permease).
 GN LIVH OR YPO3807 OR Y0423.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 CX NCBI_TaxId=632;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J.; Wren B.W.; Thomson N.R.; Titchell R.W.; Holden M.T.G.;
 RA Prentice M.B.; Sebatilla M.; James K.D.; Churcher C.; Mungall K.L.;
 RA Baker S.; Basham D.; Bentley S.D.; Brooks K.; Cerdano-rarraga A.M.;
 RA Chillingworth T.; Cronin A.; Davies R.M.; Davis P.; Dougan G.;
 RA Felwell T.; Hamlin N.; Holtroyd S.; Jegerle K.; Karlyshev A.V.;
 RA Leather S.; Moule S.; Oyston P.C.F.; Quail M.; Rutherford K.;
 RA Simmonds M.; Skelton J.; Stevens K.; Whitehead S.; Barrell B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
 RL Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=KIMS / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W.; Burland V.; Plunkett G. III; Boutin A.; Mayhew G.F.; Lise P.;
 RA Perna N.T.; Rose D.J.; Muu B.; Zhou S.; Schwartz D.C.;
 RA Retcherston J.D.; Lindler L.E.; Brubaker R.R.; Plano G.V.;
 RA Straley S.C.; McDonough K.A.; Niles M.L.; Watson J.S.; Blattner F.R.;
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).

DR EMBL; AJ414159; CAC93274.1; -.
 DR EMBL; AB013643; AAM84012.1; -.
 DR InterPro; IPR001851; Bac_inmem_transp.
 DR Pfam; PF02653; BPD_transp_2; 1.
 KW Complete proteome.

SQ SEQUENCE 308 AA; 33042 MW; 9C2527B553063A7 CRC64;

Query Match 93.9%; Score 31; DB 16; Length 308;
 Best Local Similarity 83.3%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 |||||

Db 66 IDASWL 71

RESULT 5

027987 PRELIMINARY; PRT; 535 AA.

AC 027987; PRT; 535 AA.

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Cytochrome oxidase, subunit I (CYDA-2).

GN AF2297.

OS Archaeoglobus fulgidus.

OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;

OC Archaeoglobaceae; Archaeoglobus.

OX NCBI_TaxID=2234;

RN [1] IDASWL 71

RP SEQUENCE FROM N.A.

RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE=98049343; PubMed=9389475;

RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyriplides N.C.,

RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,

RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,

RA Sadov P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

RA Venter J.C.,

RT "The complete genome sequence of the hyperthermophilic, sulphate-

RT reducing archaeon Archaeoglobus fulgidus."

RL Nature 390:364-370(1997).

DR EMBL; AE000946; AAB8960.1; -

DR TIGR; AF2297; -

DR InterPro; IPR002585; Bac_Ubq_Cox.

DR InterPro; IPR000515; BPD_transp.

DR Pfam; PF01654; Bac_Ubq_Cox; 1.

DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; 1.

KW Hypothetical protein; Complete proteome.

SO SEQUENCE 535 AA; 57605 MW; 68C821D58A11EE96 CRC64;

Query Match 93.9%; Score 31; DB 17; Length 535;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDASWL 6

Db 8 IDASWL 13

RESULT 6

09SUZ5 PRELIMINARY; PRT; 763 AA.

AC 09SUZ5;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical 65.2 kDa protein.

GN F4F15.210.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC euroside II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1] IDASWL 6

RP SEQUENCE FROM N.A.

RA Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W., Lemcke K.,

RA Mayer K.F.X., Quelet F., Salanoubat M.,

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RN [2] IDASWL 6

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL049711; CAB41330.1; -

DR InterPro; IPR001965; Znf_PHD.

DR InterPro; IPR001941; Znf_PHD.

DR SMART; SM00249; PHD; 2.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS50016; ZF_PHD_2; 1.

DR PROSITE; PS50089; ZF_RING_2; 1.

KW Hypothetical protein.

SO SEQUENCE 763 AA; 85199 MW; 92BB47843D5314F9 CRC64;

Query Match 93.9%; Score 31; DB 10; Length 763;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDASWL 6

Db 613 IDASWL 618

RESULT 7

09JRL8 PRELIMINARY; PRT; 187 AA.

AC 09JRL8;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Metallo-beta-lactamase 3 (Fragment).

GN MBL3.

OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas

OS maltophilia).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Stenotrophomonas.

OX NCBI_TaxID=40324;

RN [1] IDASWL 6

RP SEQUENCE FROM N.A.

RC STRAIN=U152;

RA Walker R.A., Higgins P., Payne D.J., Ames S.G.,

RT "A biochemical and molecular assessment of the heterogeneity of the

RT metallo-beta-lactamases from clinical Stenotrophomonas maltophilia

RT isolates."

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ289083; CAB94702.1; -

DR HSP; P52700; ISML.

DR InterPro; IPR001018; Beta_lactamase_B.

DR InterPro; IPR001379; Blactamase-like.

DR Pfam; PF00753; lactamase_B; 1.

DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.

FT NON_TER 187

FT 187

SO SEQUENCE 187 AA; 19931 MW; F07D49B4C88043 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;

Best Local Similarity 83.3%; Pred. No. 3.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDASWL 6

Db 12 IDASWL 17

RESULT 8

09JRL9 PRELIMINARY; PRT; 187 AA.

AC 09JRL9;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Metallo-beta-lactamase 2 (Fragment).

GN MBL2.

OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas

OS maltophilia).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Stenotrophomonas.
 OX NCBI_TaxID=40324;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0062;
 RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;
 RT "A biochemical and molecular assessment of the heterogeneity of the metallo-beta-lactamase from clinical Stenotrophomonas maltophilia isolates."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ289082; CAB94701.1; -.
 DR HSSP; P52700; ISML.
 DR InterPro; IPR001018; Beta_lactamase_B.
 DR InterPro; IPR001279; Blactamase-1like.
 DR Pfam; PF00753; lactamase_B; 1.
 DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
 FT NON_TER 1 187
 FT NON_TER 1 187
 SQ SEQUENCE 187 AA; 19960 MW; 877D49E4B4C698F4 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
 Db 12 VDASWL 17

RESULT 9

Q9JRL5 PRELIMINARY; PRT; 187 AA.
 AC Q9JRL5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Metallo-beta-lactamase 511 (Fragment).
 GN MBL511 OR MBL5.
 OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).
 OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Stenotrophomonas.
 OX NCBI_TaxID=40324;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=511, and 37;
 RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;
 RT "A biochemical and molecular assessment of the heterogeneity of the metallo-beta-lactamase from clinical Stenotrophomonas maltophilia isolates."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ289086; CAB94705.1; -.
 DR EMBL; AJ289085; CAB94704.1; -.
 DR HSSP; P52700; ISML.
 DR InterPro; IPR001018; Beta_lactamase_B.
 DR InterPro; IPR001279; Blactamase-1like.
 DR Pfam; PF00753; lactamase_B; 1.
 DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
 FT NON_TER 1 187
 FT NON_TER 1 187
 SQ SEQUENCE 187 AA; 19811 MW; 7A2B11372028E5FE CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
 Db 12 VDASWL 17

RESULT 10

Q9JRM0 PRELIMINARY; PRT; 187 AA.
 AC Q9JRM0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Metallo-beta-lactamase 1 (Fragment).
 GN MBL1.
 OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).
 OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Stenotrophomonas.
 OX NCBI_TaxID=40324;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GEL;
 RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;
 RT "A biochemical and molecular assessment of the heterogeneity of the metallo-beta-lactamase from clinical Stenotrophomonas maltophilia isolates."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ289081; CAB94700.1; -.
 DR HSSP; P52700; ISML.
 DR InterPro; IPR001018; Beta_lactamase_B.
 DR InterPro; IPR001279; Blactamase-1like.
 DR Pfam; PF00753; lactamase_B; 1.
 DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
 FT NON_TER 1 187
 FT NON_TER 1 187
 SQ SEQUENCE 187 AA; 19901 MW; 72B8515412892A08 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
 Db 12 VDASWL 17

RESULT 11

Q9JRL7 PRELIMINARY; PRT; 187 AA.
 AC Q9JRL7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Metallo-beta-lactamase 4 (Fragment).
 GN MBL4.
 OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).
 OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Stenotrophomonas.
 OX NCBI_TaxID=40324;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Q2323;
 RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;
 RT "A biochemical and molecular assessment of the heterogeneity of the metallo-beta-lactamase from clinical Stenotrophomonas maltophilia isolates."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ289084; CAB94703.1; -.
 DR HSSP; P52700; ISML.
 DR InterPro; IPR001018; Beta_lactamase_B.
 DR InterPro; IPR001279; Blactamase-1like.
 DR Pfam; PF00753; lactamase_B; 1.
 DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
 FT NON_TER 1 187
 FT NON_TER 1 187
 SQ SEQUENCE 187 AA; 19900 MW; D3C749B4B6C3F18 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;

Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
Db 12 VDASWL 17

RESULT 12

Q8EBG1 PRELIMINARY; PRT; 205 AA.
AC Q8EBG1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN S03557.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
CX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eilen J.A., Sehnadi R., Ward N., Meche B., Clayton R.A.,
RA Meyer T., Tsaplin A., Scott J., Beaman M., Brinac L., Daugherty S.,
RA Deboy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill U., Utterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AB015792; AAN56548.1; -
DR TIGR; S03557; -
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 205 AA; 23686 MW; 3A301AC03E782334 CRC64;

Query Match 90.9%; Score 30; DB 16; Length 205;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
Db 194 LDSSWL 199

RESULT 13

Q9A120 PRELIMINARY; PRT; 221 AA.
AC Q9A120;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative NAD(P)H-flavin oxidoreductase.
GN SPY0512.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferreretti J.J., Meshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu Y., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

DR EMBL; AE006509; AAK33511.1; -
DR InterPro; IP000415; Nitroreductase.
DR Pfam; PF00881; Nitroreductase; 1.
KM Complete proteome.
SQ SEQUENCE 221 AA; 25283 MW; 724C1A54FC72C85 CRC64;

Query Match 90.9%; Score 30; DB 16; Length 221;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
Db 36 LDAAWL 41

RESULT 14

Q8P239 PRELIMINARY; PRT; 221 AA.
AC Q8P239;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Putative NAD(P)H-flavin oxidoreductase.
GN SPYM18 0570 OR SPYM3 0360.
OS Streptococcus pyogenes (serotype M18), and
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxID=186103, 198466;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes; STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.B., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
RN [2]

RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes; STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=2133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlivert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus;
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
DR EMBL; AB009993; AAL97264.1; -
DR EMBL; AB014143; AAL78967.1; -
DR InterPro; IPR000415; Nitroreductase.
DR Pfam; PF00881; Nitroreductase; 1.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 221 AA; 25269 MW; A929A147EB0027D6 CRC64;

Query Match 90.9%; Score 30; DB 16; Length 221;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
Db 36 LDAAWL 41

RESULT 15

Q8TR10 PRELIMINARY; PRT; 225 AA.
AC Q8TR10;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein MA1374.
 GN MA1374.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 NC NCBI_TaxID=2214;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZA / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238;
 RA Galagan J.E., Nussbaum C., Roy A., Endrizzi M.G., MacDonald P.,
 RA Fitzhugh W., Calvo S., Engels R., Smitrov S., Alnoor D., Brown A.,
 RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
 RA Lincon L., McEwan P., McKernan K., Talamaas J., Turrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
 RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.;
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity."
 RL Genome Res. 12:532-542(2002).
 DR EMBL; AB010607; AA004790.1; -
 DR InterPro; IPR005237; Cons. hypoth289.
 DR InterPro; IPR002764; DUF71.
 DR Pfam; PF01902; DUF71.1.
 DR TIGRPM; TIGR00289; MJ0570_dom; 1.
 DR TIGRPM; TIGR00289; TIGR00289; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 225 AA; 25146 MW; A573D46D1DDFB9D1 CRC64;

Query Match 90.9%; Score 30; DB 17; Length 225;
 Best Local Similarity 83.3%; Pred. NO. 4.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASWL 6
 ||:||||
 Db 149 LDSSWL 154

Search completed: February 18, 2004, 14:35:48
 Job time : 19.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-10

Perfect score: 33

Sequence: 1 LDASWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing filter 45 summaries

Database : PIR 76: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	419	T32441	hypothetical prote
2	31	93.9	535	AF0463	high-affinity bran
3	31	93.9	535	A69537	cytochrome oxidase
4	31	93.9	763	T49089	hypothetical prote
5	30	90.9	245	T03533	probable precorrin
6	30	90.9	290	T48880	beta-lactamase (EC
7	30	90.9	290	S45349	L1 metallo-beta-la
8	30	90.9	332	T44337	aminodeoxychorism
9	30	90.9	442	T04815	hypothetical prote
10	30	90.9	461	D85312	probable homeodoma
11	30	90.9	810	AH0937	bifunctional aspar
12	30	90.9	906	AG1957	hypothetical prote
13	30	90.9	919	OYFKG	phosphoenolpyruvat
14	29	87.9	150	C82994	conserved hypochet
15	29	87.9	177	B41377	cytochrome c-L pre
16	29	87.9	243	G83450	hypothetical prote
17	29	87.9	252	C83837	hypothetical prote
18	29	87.9	255	G75626	probable 3-alpha-h
19	29	87.9	264	F84612	hypothetical prote
20	29	87.9	264	D84504	probable VSF-1-like
21	29	87.9	269	A75397	probable signal pe
22	29	87.9	274	B83444	probable transcrip
23	29	87.9	277	T29979	hypothetical prote
24	29	87.9	278	H82759	cell division prot
25	29	87.9	282	E70890	hypothetical prote
26	29	87.9	286	A48399	probable oxidoredu
27	29	87.9	286	A85739	probable dehydroge
28	29	87.9	286	H90879	probable dehydroge
29	29	87.9	289	A37209	thiosulfate sulfur

30	29	87.9	295	2	G15081	thiosulfate sulfur
31	29	87.9	296	1	ROHU	thiosulfate sulfur
32	29	87.9	296	1	AH2327	hypothetical prote
33	29	87.9	297	1	ROBO	thiosulfate sulfur
34	29	87.9	297	2	JC4398	thiosulfate sulfur
35	29	87.9	297	2	UC5286	thiosulfate sulfur
36	29	87.9	301	2	G83182	hypothetical prote
37	29	87.9	316	2	P89791	peptidoglycan hyd
38	29	87.9	318	2	T52663	thiosulfate sulfur
39	29	87.9	326	2	B99790	hypothetical prote
40	29	87.9	329	2	A86300	hypothetical prote
41	29	87.9	333	2	F70678	probable transposa
42	29	87.9	359	2	S15305	rtbg protein - Sal
43	29	87.9	359	2	AH0766	CDPglucose 4,6-deh
44	29	87.9	360	2	T26037	hypothetical prote
45	29	87.9	360	2	S32695	mtc-2 protein - Ca

ALIGNMENTS

RESULT 1
T32441
hypothetical protein T2884.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T32441
R:Wilson, R.; Greco, T.; Sansone, J.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid T2884.
A:Reference number: Z2168
A:Accession: T32441
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Cross-references: EMBL:AF026206; PIDN:ABJ7262.1; GSPDB:GN00028; CESP:T2884.1
A:Experimental source: strain Bristol N2; clone T2884
A:Gene: CESP:T2884.1
A:Map position: X
A:Introns: 47/3; 68/3; 102/3; 153/1; 207/1; 296/1

Query Match 100.0%; Score 33; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 340 LDASWL 345

RESULT 2
AF0463
high-affinity branched-chain amino acid transport system, permease protein 11vH (import
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
R:Parthill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.E
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
J., M.; Rutherford, K.; Stimpson, M.; Skelton, J.; Stevens, K.; Mitchell, S.; Barrett,
Nature 413, 523-527, 2001
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0463
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <KUP>
A:Cross-references: GB:AU590842; PIDN:CA93274.1; PID:G15981721; GSPDB:GN00175
A:Gene: 11vH
C:Superfamily: leucine transport protein 11vH

Query Match 93.9%; Score 31; DB 2; Length 308;

Best Local Similarity 83.3%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
:|||||
Db 66 LDASWL 71

RESULT 3
A69537
cytochrome oxidase, subunit I (cydA-2) homolog - Archaeoglobus fulgidus

C/Species: Archaeoglobus fulgidus
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000

C/Accession: A69537

R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.P.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997

A/Authors: Overbeek, R.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.

A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A/Reference number: A69537; PMID:98049343; PMID:9389475

A/Accession: A69537

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-535 <KE>

A/Cross-references: GB:AE000946; GB:AE000782; NID:92669269; PIDN:AA88960.1; PID:g264822
C/Superfamily: cytochrome d complex terminal oxidase chain I

Query Match
Best Local Similarity 83.3%; Pred. No. 1.6e+02; Length 535;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
:|||||
Db 8 LDASWL 13

RESULT 4
T49089
hypothetical protein F4F15.210 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C/Accession: T49089

R/Altman, J.P.; Clabault, G.; Cortez, A.; Maché, R.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence Database, April 2000

A/Reference number: 225015

A/Accession: T49089

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-763 <ALC>

A/Cross-references: EMBL:AL049711; GSPDB:GN00061; ATSP:F4F15.210

A/Experimental source: cultivar Columbia; BAC clone F4F15

A/Genes: ATSP:F4F15.210

A/Map position: 3

A/Insertions: 11/2; 124/3; 183/1; 199/3; 230/3; 274/1; 297/3; 325/2; 351/3; 478/1; 641/2; 6

Query Match
Best Local Similarity 83.3%; Pred. No. 2.3e+02; Length 763;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
:|||||
Db 613 LDASWL 618

RESULT 5
T03533
probable precorrin-2 methyltransferase (BC 2.1.1.-) - Rhodobacter capsulatus

C/Species: Rhodobacter capsulatus
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 18-Feb-2000

C/Accession: T03533

R/Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Hasek, R.; Fomstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997

A/Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB101

A/Reference number: Z14955; PMID:97404404; PMID:9256491

A/Accession: T03533

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-245 <VLC>

A/Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AA016186.1; PID:g3128334

C/Genetics:

A/Map position: 1

C/Superfamily: precorrin-3 methylase

C/Keywords: methyltransferase

Query Match
Best Local Similarity 83.3%; Pred. No. 1.2e+02; Length 245;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
:|||||
Db 197 LDASWL 202

RESULT 6
T48880

beta-lactamase (EC 3.5.2.6) L-1 precursor (validated) - Pseudomonas maltophilia

N/Alternate names: L-1 metallo-beta-lactamase

C/Species: Pseudomonas maltophilia

C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C/Accession: T48880

R/Sanchez, R.; Dufresne, J.; Levesque, R.C.
Antimicrob. Agents Chemother. 42, 1245-1248, 1998

A/Title: Molecular heterogeneity of the L-1 metallo-beta-lactamase family from Stenotri

A/Reference number: 224841; PMID:98253990; PMID:9593158

A/Accession: T48880

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-290 <SAN>

A/Cross-references: EMBL:AF010282; PIDN:AA021590.1

A/Experimental source: strain GNI2873

C/Genetics:

A/Function:

A/Description: catalyzes the hydrolysis of an amide bond in the beta-lactam ring of the

C/Keywords: antibiotic resistance; hydrolase

F/1-33/Domain: signal sequence #status predicted <SIG>

F/34-290/Product: L-1 metallo-beta-lactamase #status predicted <MAT>

Query Match
Best Local Similarity 83.3%; Pred. No. 1.4e+02; Length 290;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
:|||||
Db 34 LDASWL 39

RESULT 7
S45349

L1 metallo-beta-lactamase - Xanthomonas maltophilia

C/Species: Xanthomonas maltophilia

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997

C/Accession: S45349

R/Walsh, T.R.; Hall, L.; Absinder, S.J.; Nichols, W.W.; Cartwright, S.J.; MacGowan, A.I

Biochim. Biophys. Acta 1218, 199-201, 1994

A/Title: Sequence analysis of the L1 metallo-beta-lactamase from Xanthomonas maltophil

A/Reference number: S45349; PMID:94289479; PMID:8018721

A/Accession: S45349

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-290 <WAL>

Query Match
Best Local Similarity 83.3%; Pred. No. 1.4e+02; Length 290;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
:|||||
Db 34 VDASWL 39

RESULT 8

T44437

aminoacylcholine esterase lyase homolog [imported] - Moritella marina
C:Species: Moritella marina
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000

C:Accession: T44437
R:Morita, N.; Ueno, A.; Tanaka, M.; Ohgita, S.; Hoshino, T.; Kawasaki, K.; Yumoto, I.; I
Biotechnol. Lett. 21, 641-646, 1999
A>Title: Cloning and sequencing of clustered genes involved in fatty acid biosynthesis
A:Reference number: 222768

A:Accession: T44437
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-332 <MOR>

A:Cross-references: EMBL:AB021978; PIDN:BAA85259.1
A:Experimental source: ATCC 15381
C:Genetics:
A:Note: pADC
C:Superfamily: yceG protein

Query Match 90.9%; Score 30; DB 2; Length 332;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
:|||||
Db 187 LDASWL 192

RESULT 9

T04815

hypothetical protein F10M23.260 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999

C:Accession: T04815
R:Bevan, M.; Lecharny, A.; Chedford, F.; Krivitzky, M.; Kreis, M.; Hohnel, J.; Mewes, H
submitted to the Protein Sequence Database, February 1999
A:Reference number: 215385
A:Accession: T04815
A:Molecule type: DNA
A:Residues: 1-442 <BEV>

A:Cross-references: EMBL:AL035440
A:Experimental source: cultivar Columbia; BAC clone F10M23
C:Genetics:
A:Map position: 4
A:Introns: 140/3; 165/3; 236/1; 358/3
A:Note: F10M23.260

Query Match 90.9%; Score 30; DB 2; Length 442;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
:|||||
Db 128 VDASWL 133

RESULT 10

D85312

probable homeodomain protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C:Accession: D85312
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999

A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: AB0001; MUID:20083488; PMID:10617198
A:Accession: D85312

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-461 <STO>
A:Cross-references: GB:NC_001268; NID:g7269545; PIDN:CA879547.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4G26920
A:Map position: 4

Query Match 90.9%; Score 30; DB 2; Length 461;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
:|||||
Db 128 VDASWL 133

RESULT 11

AH0937

bifunctional aspartokinase II/homoserine dehydrogenase II can I write [imported] - Salmo
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: This species has also been called Salmonella typh
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AH0937
R:Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
S.; Moller, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serc
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0937

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-810 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD09522.1; PID:g16504639; GSPDB:GN00176
A:Genetics:
A:Gene: STY3768
C:Superfamily: thra bifunctional enzyme; aspartate kinase homolog; homoserine dehydrog

Query Match 90.9%; Score 30; DB 2; Length 810;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
:|||||
Db 146 LDASWL 151

RESULT 12

AG1957

hypothetical protein all1210 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AG1957
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Iritani
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takasawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG1957
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-906 <KUM>

A:Cross-references: GB:BA000019; PIDN:BA873167.1; PID:g17130557; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1210

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds

(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-10

Sequence: 1 LDASWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications AA:*
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15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	6	10 US-09-847-940B-10	Sequence 10, Appl1
2	33	100.0	6	11 US-09-847-946A-10	Sequence 10, Appl1
3	33	100.0	105	10 US-09-738-626-6278	Sequence 6278, Ap
4	30	90.9	191	12 US-10-291-265-782	Sequence 782, App
5	30	90.9	221	15 US-10-169-048-2	Sequence 2, Appl1
6	30	90.9	261	9 US-09-765-205-14	Sequence 14, Appl1
7	30	90.9	261	12 US-10-360-849A-12	Sequence 12, Appl1
8	30	90.9	261	12 US-10-360-849A-15	Sequence 15, Appl1
9	30	90.9	261	12 US-10-360-849A-18	Sequence 18, Appl1
10	30	90.9	277	12 US-10-291-265-310	Sequence 310, App
11	30	90.9	919	10 US-09-738-626-6970	Sequence 6970, Ap
12	30	90.9	935	9 US-09-784-208-3	Sequence 3, Appl1
13	30	90.9	935	12 US-10-077-745-1	Sequence 1, Appl1
14	30	90.9	935	12 US-10-338-915-1	Sequence 1, Appl1
15	30	90.9	935	14 US-10-078-107-1	Sequence 1, Appl1

16	30	90.9	935	14	US-10-077-751-1	Sequence 1, Appl1
17	30	90.9	935	15	US-10-315-023-3	Sequence 3, Appl1
18	30	90.9	935	15	US-10-315-023-8	Sequence 8, Appl1
19	29	87.9	136	10	US-09-738-973-123	Sequence 123, App
20	29	87.9	136	10	US-09-854-133-123	Sequence 123, App
21	29	87.9	136	15	US-10-144-649A-123	Sequence 123, App
22	29	87.9	238	12	US-10-108-608A-3740	Sequence 3740, App
23	29	87.9	269	12	US-10-369-493-592	Sequence 592, App
24	29	87.9	277	12	US-10-369-493-5377	Sequence 5377, App
25	29	87.9	278	12	US-10-369-493-7867	Sequence 7867, App
26	29	87.9	279	12	US-10-369-493-11783	Sequence 11783, A
27	29	87.9	279	12	US-10-369-493-14664	Sequence 14664, A
28	29	87.9	279	12	US-10-369-493-15142	Sequence 15142, A
29	29	87.9	285	12	US-10-369-493-7936	Sequence 7936, App
30	29	87.9	286	12	US-10-369-493-821	Sequence 821, App
31	29	87.9	293	12	US-10-369-493-11834	Sequence 21834, A
32	29	87.9	297	10	US-09-981-353-90	Sequence 90, Appl1
33	29	87.9	305	9	US-09-815-242-12482	Sequence 12482, A
34	29	87.9	314	10	US-09-738-626-6011	Sequence 6011, App
35	29	87.9	322	9	US-09-815-242-5327	Sequence 5327, App
36	29	87.9	397	14	US-10-029-180-40	Sequence 40, Appl1
37	29	87.9	437	15	US-10-145-415-101	Sequence 101, Appl1
38	29	87.9	465	15	US-10-156-761-10355	Sequence 10355, A
39	29	87.9	491	12	US-10-369-493-23656	Sequence 23656, A
40	29	87.9	501	12	US-10-094-749-1887	Sequence 1887, App
41	29	87.9	512	12	US-10-320-797-3205	Sequence 3205, App
42	29	87.9	571	12	US-10-369-493-3747	Sequence 3747, App
43	29	87.9	854	11	US-09-770-107-2	Sequence 2, Appl1
44	29	87.9	865	12	US-10-347-470A-17	Sequence 17, Appl1
45	29	87.9	1066	15	US-10-128-714-3190	Sequence 3190, App

ALIGNMENTS

RESULT 1
US-09-847-940B-10
Sequence 10, Application US/09847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PRI-117CP
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-10

Query Match
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OR 1 LDASWL 6
Db 1 LDASWL 6

RESULT 2
US-09-847-946A-10
Sequence 10, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hamms, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PFI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 10
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NBD peptide
US-09-847-946A-10

Query Match 100.0%; Score 33; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 LDASWL 6
Db 1 LDASWL 6

RESULT 3
US-09-738-626-6278
; Sequence 6278, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: MAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIRO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASARO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6278
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6278

Query Match 100.0%; Score 33; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 48 LDASWL 53

RESULT 4
US-10-291-265-782
; Sequence 782, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: NO. US20030232054A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 782
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-782

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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 161 LDASWL 166

RESULT 5
US-10-169-048-2
; Sequence 2, Application US/10169048
; Publication No. US20030072769A1
; GENERAL INFORMATION:
; APPLICANT: Clarke, Edna Elizabeth
; APPLICANT: Zhou, Liqing
; APPLICANT: Shea, Jacqueline Elizabeth
; APPLICANT: Feldman, Robert Graham
; APPLICANT: Holden, David William
; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their Use
; FILE REFERENCE: G1E-97
; CURRENT APPLICATION NUMBER: US/10/169,048
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: PCT/GB00/04997
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-169-048-2

Query Match 90.9%; Score 30; DB 15; Length 221;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 36 LDASWL 41

RESULT 6
US-09-765-205-14
; Sequence 14, Application US/09765205
; Patent No. US20020034800A1

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; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 261
; TYPE: PRT
; ORGANISM: human
; US-09-765-205-14

Query Match          90.9%; Score 30; DB 9; Length 261;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASWL 6
        |||||:
        161 LDASWV 166

Db

RESULT 7
; US-10-360-849A-12
; Sequence 12, Application US/10360849A
; Publication No. US20030220249A1
; GENERAL INFORMATION:
; APPLICANT: Discovery Genomics, Inc.
; APPLICANT: Hackett, Perry
; APPLICANT: Nasevicius, Aldas
; APPLICANT: Essner, Jeffrey
; APPLICANT: Clark, Karl
; APPLICANT: Larson, Jon
; APPLICANT: Ekker, Stephen
; APPLICANT: Roberg-Perez, Sharon
; APPLICANT: Wadman, Shannon
; TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
; FILE REFERENCE: 3021.05US02
; CURRENT APPLICATION NUMBER: US/10/360,849A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/354,978
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 261
; TYPE: PRT
; ORGANISM: danio rerio
; US-10-360-849A-12

Query Match          90.9%; Score 30; DB 12; Length 261;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASWL 6
        |||||:
        161 LDASWV 166

Db

RESULT 8
; US-10-360-849A-15
; Sequence 15, Application US/10360849A
; Publication No. US20030220249A1
; GENERAL INFORMATION:
; APPLICANT: Discovery Genomics, Inc.
; APPLICANT: Hackett, Perry
; APPLICANT: Nasevicius, Aldas
; APPLICANT: Essner, Jeffrey
; APPLICANT: Clark, Karl
```

```

; APPLICANT: Larson, Jon
; APPLICANT: Ekker, Stephen
; APPLICANT: Roberg-Perez, Sharon
; APPLICANT: Wadman, Shannon
; TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
; FILE REFERENCE: 3021.05US02
; CURRENT APPLICATION NUMBER: US/10/360,849A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/354,978
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 261
; TYPE: PRT
; ORGANISM: mus musculus
; US-10-360-849A-15

Query Match          90.9%; Score 30; DB 12; Length 261;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASWL 6
        |||||:
        161 LDASWV 166

Db

RESULT 9
; US-10-360-849A-18
; Sequence 18, Application US/10360849A
; Publication No. US20030220249A1
; GENERAL INFORMATION:
; APPLICANT: Discovery Genomics, Inc.
; APPLICANT: Hackett, Perry
; APPLICANT: Nasevicius, Aldas
; APPLICANT: Essner, Jeffrey
; APPLICANT: Clark, Karl
; APPLICANT: Larson, Jon
; APPLICANT: Ekker, Stephen
; APPLICANT: Roberg-Perez, Sharon
; APPLICANT: Wadman, Shannon
; TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
; FILE REFERENCE: 3021.05US02
; CURRENT APPLICATION NUMBER: US/10/360,849A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/354,978
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PRT
; ORGANISM: home sapiens
; US-10-360-849A-18

Query Match          90.9%; Score 30; DB 12; Length 261;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASWL 6
        |||||:
        161 LDASWV 166

Db

RESULT 10
; US-10-291-265-310
; Sequence 310, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseed, Inc.
; APPLICANT: Tang et al
```

```

; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FaecSeq for Windows Version 3.0
; SEQ ID NO 310
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-310
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Query Match          90.9%; Score 30; DB 12; Length 277;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDASWL 6
        |||:|
Db       161 LDASWV 166
```

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RESULT 11
US-09-738-626-6970
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; Sequence 6970, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIO
; APPLICANT: IKEDA, MASARO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6970
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6970
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```

Query Match          90.9%; Score 30; DB 10; Length 919;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDASWL 6
        |||:|
Db       105 LDATWL 110
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RESULT 12
US-09-784-208-3
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; Sequence 3, Application US/09784208
; Patent No. US20010019836A1
; GENERAL INFORMATION:
; APPLICANT: IZUI, HIROSHI
; APPLICANT: ONO, Eiji
; APPLICANT: MATSUI, Kazuhiko
; APPLICANT: MORIYA, Mika
; APPLICANT: ITO, Hisao
; APPLICANT: HARA, Yoshihiko
; TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR
; TITLE OF INVENTION: PRODUCING L-GLUTAMIC ACID
; FILE REFERENCE: 0010-0989-0
; CURRENT APPLICATION NUMBER: US/09/784,208
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/271,438
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: JP 10-69068
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: JP 10-297129
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-09-784-208-3
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Query Match          90.9%; Score 30; DB 9; Length 935;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDASWL 6
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Db       10 LDSSWL 15
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RESULT 13
US-10-077-745-1
; Sequence 1, Application US/10077745
; Publication No. US20030172698A1
; GENERAL INFORMATION:
; APPLICANT: KODA, TAKAYUKI
; APPLICANT: SATO, KAZUHIRO
; TITLE OF INVENTION: ORGANIC NITROGEN-CONTAINING COMPOSITION AND FERTILIZER COMPRISIN
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 219843U50
; CURRENT APPLICATION NUMBER: US/10/077,745
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: JP 2001-044137
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-10-077-745-1
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Query Match          90.9%; Score 30; DB 12; Length 935;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDASWL 6
        |||:|
Db       10 LDSSWL 15
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RESULT 14
US-10-338-915-1
; Sequence 1, Application US/10338915
; Publication No. US20030190713A1
; GENERAL INFORMATION:
```



```

; APPLICANT: Ueda, Hiroshi
; APPLICANT: Koda, Takayuki
; APPLICANT: Sato, Masakazu
; TITLE OF INVENTION: METHOD FOR PRODUCING L-GLUTAMIC ACID
; FILE REFERENCE: 232696USOCONT
; CURRENT APPLICATION NUMBER: US/10/338,915
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 10/077,999
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: JP 2001-044136
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-10-338-915-1

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```

Query Match          90.9%; Score 30; DB 12; Length 935;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LDASWL 6
        ||:||||
Db      10 LDSSWL 15

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```

RESULT 15
US-10-078-107-1
; Sequence 1, Application US/10078107
; Publication No. US20020182688A1
; GENERAL INFORMATION:
; APPLICANT: IZUI, HIROSHI
; APPLICANT: HARA, YOSHIHIKO
; APPLICANT: SATO, MASAKAZU
; APPLICANT: AKIYOSHI, NAOKI
; TITLE OF INVENTION: METHOD FOR PRODUCING L-GLUTAMIC ACID
; FILE REFERENCE: 219846USO
; CURRENT APPLICATION NUMBER: US/10/078,107
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: JP 2001-044134
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-10-078-107-1

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Query Match          90.9%; Score 30; DB 14; Length 935;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LDASWL 6
        ||:||||
Db      10 LDSSWL 15

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Job time : 17.7529 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-10

Perfect score: 33

Sequence: 1 LDASWL 6

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158725573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	6	23	ABB08732
2	33	100.0	6	23	AAW48515
3	33	100.0	6	24	ABU08425
4	33	100.0	105	22	AAW92524
5	33	100.0	756	23	ABW77295
6	31	93.9	618	21	AAW32182
7	31	93.9	676	21	AAW32181
8	31	93.9	763	21	AAW32180
9	30	90.9	117	22	ABG20551

10	30	90.9	119	21	AAW42606	Human ORF2370
11	30	90.9	156	22	AAW03936	Human gene 39 enco
12	30	90.9	189	22	AAW03978	Human gene 39 enco
13	30	90.9	191	22	AAW14439	Human novel protei
14	30	90.9	221	22	AAW03119	Streptococcus pyog
15	30	90.9	221	23	ABW77441	Streptococcus poly
16	30	90.9	261	21	AAW53628	A bone marrow bact
17	30	90.9	261	21	AAW52388	Human transmembran
18	30	90.9	277	22	AAW14203	Human novel protei
19	30	90.9	431	22	ABG20554	Novel human diagno
20	30	90.9	919	11	AAW05512	Phosphoenolpyruvat
21	30	90.9	919	17	AAW95580	Bacterial phosphoe
22	30	90.9	919	19	AAW68151	Phosphoenolpyruvat
23	30	90.9	919	20	AAW9634	Phosphoenolpyruvat
24	30	90.9	919	22	AAW93216	C glutamic prote
25	30	90.9	924	20	AAW79297	Corynebacterium gl
26	30	90.9	935	20	AAW11987	Alpha-ketoglutarat
27	30	90.9	935	22	AAW0224	Succinate dehydrog
28	30	90.9	935	23	ABW71283	Enterobacter agglu
29	30	90.9	935	23	ABW9311	Enterobacter agglu
30	30	90.9	935	23	AAW09312	E. agglomerans L-9
31	30	90.9	935	23	ABW70588	Human KRPI cryptic
32	29	87.9	12	23	ABW61529	Novel human diagno
33	29	87.9	12	23	ABW62926	Human secreted pro
34	29	87.9	121	21	AAW02267	Human lung tumour
35	29	87.9	122	22	AAW69910	Human lung tumour
36	29	87.9	136	20	AAW9543	Human lung tumour
37	29	87.9	136	21	AAW44455	Human lung tumour
38	29	87.9	136	22	AAW13796	Novel human diagno
39	29	87.9	146	22	ABW5119	Novel human diagno
40	29	87.9	168	22	ABW3169	Human phospholipas
41	29	87.9	183	23	AAW22840	Bordetella pertuss
42	29	87.9	220	21	AAW14119	Herbicidally activ
43	29	87.9	256	23	ABW91837	Human protein SEQ
44	29	87.9	297	22	AAW78633	Staphylococcus aur
45	29	87.9	305	22	AAW6889	

ALIGNMENTS

RESULT 1	ABB08732	standard; peptide: 6 AA.
ID	ABB08732	
XX	ABB08732;	
XX	14-JUN-2002	(first entry)
DE	Mutated IKKdelta NEMO binding domain peptide SEQ ID NO 10.	
XX	IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
XX	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
XX	autoimmune disease; transplant rejection; osteoporosis; cancer;	
XX	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
XX	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
XX	corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;	
XX	osteopontin; cyclostatin; neotropic; neuroprotective; anti-HIV; human;	
XX	antiartherosclerotic; vincristine; antipneumatic; antiallergic;	
XX	dermatological; antibacterial; antiparasitic; antineoplastic;	
XX	antiarthritic; osteopontin; antitumor; mutant; muten.	
XX	Homo sapiens.	
XX	Synthetic.	
XX	Key	Location/Qualifiers
XX	Misc-difference	/note= "Wildtype Trp substituted by Ala"
XX	WO200183547-A2.	
XX	08-NOV-2001.	

PF 02-MAY-2001; 2001WO-US40654.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S,
XX
DR WPI, 2002-179350/23.
XX
XX
PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT cell with an anti-inflammatory compound comprising at least one NEMO
PT binding domain -
XX
XX
PS Claim 23; Page 44; 82pp; English.
XX
XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC comprises contacting a cell with an anti-inflammatory compound
CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
CC (ABB077313). The compound has acts through selective inhibition of
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC interaction results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of Ikbppab. The compound may also
CC act (directly or indirectly) by blocking the recruitment of leukocytes
CC into sites of acute and chronic inflammation, by down-regulating the
CC expression of E-selectin on leukocytes or by blocking osteoclast
CC differentiation. The compound is useful in treating NF-kB mediated
CC conditions, where the condition is an inflammatory disorder, an
CC autoimmune disease, transplant rejection, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC telangiectasia. The inflammatory disorder is asthma, allergies,
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammation
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC diseases include HIV and influenza. The compound may also be useful for
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC binding domain of IKKbeta.
XX
SQ Sequence 6 AA;
QY
Db 1 LDASWL 6
1 LDASWL 6
Query Match 100.0%; Score 33; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
XX Anti-inflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200193554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI, 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX Example 6; Page 47; 88pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
CC AAM48625-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IKkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis, transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 6 AA;
QY
Db 1 LDASWL 6
1 LDASWL 6
Query Match 100.0%; Score 33; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
ABU08425
ID ABU08425 standard; peptide; 6 AA.

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XX AC ABU08425;
XX XX 12-JUN-2003 (first entry)
XX DT
XX DE Human NEMO binding site (NBD) mutant peptide #8.
XX XX
XX KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
XX KW Ikappab kinase-beta; Ikappab kinase-alpha; IKKalpha; NF-kappab;
XX KW nuclear factor-kappaB induction; inflammatory disorder;
XX KW autoimmunity disease; osteoporosis; cancer; Alzheimer's disease;
XX KW atherosclerosis; viral infection; Ataxia telangiectasia;
XX KW transplantation detection; immunosuppressive; osteopathic;
XX KW cytoskeletal; neuroprotective; antiatherosclerotic; virucide;
XX KW vasotropic; antineumatic; antithrombotic; mutant; mutein.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX PN US2002156000-A1.
XX XX
XX PD 24-OCT-2002.
XX XX
XX PP 02-MAY-2001; 2001US-0847940.
XX XX
XX PR 02-MAY-2000; 2000US-201261P.
XX PR 22-AUG-2000; 2000US-0643260.
XX XX
XX PA (MAYM/) MAY M J.
XX PA (GHOS/) GHOSH S.
XX XX
XX PI May MJ, Ghosh S;
XX XX
XX DR WPI; 2003-209142/20.
XX XX
XX PT Novel antiinflammatory peptide compounds comprising NEMO binding
XX PT domain, useful for modulating NF-kappaB induction in a cell and for
XX PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
XX PT psoriasis, vasculitis -
XX XX
XX PS Claim 22; Page 17; 47pp; English.
XX XX
XX CC The present invention relates to antiinflammatory compounds comprising
XX CC NEMO binding domain (NBD) peptides. The NEMO binding domain are
XX CC found on Ikappab kinase-beta (IKKbeta) and Ikappab kinase-alpha
XX CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
XX CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
XX CC in a cell, where the compounds are capable of blocking the interaction
XX CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
XX CC antiinflammatory compound further comprises at least one membrane
XX CC translocation domain. The compounds are useful for treating
XX CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
XX CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
XX CC telangiectasia, and for transplantation detection. The compounds of
XX CC the invention block NF-kappaB induction by IKK but do not inhibit
XX CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
XX CC NBD mutant peptides.
XX XX
XX SQ Sequence 6 AA;

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Query Match 100.0%; Score 33; DB 24; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

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QY 1 LDASWL 6
DB 1 LDASWL 6

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RESULT 4
AAG92524
ID AAG92524 standard; Protein; 105 AA.

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AC AC AAG92524;
XX XX 26-SEP-2001 (first entry)
XX DT
XX DE C glucanidum protein fragment SEQ ID NO: 6278.
XX XX
XX KW Corynebacterium; amino acid synthesis; vitamin; saccharide;
XX KW organic acid synthesis.
XX XX
XX OS Corynebacterium glucanidum.
XX OS
XX PN Bp108790-A2.
XX XX
XX PD 20-JUN-2001.
XX XX
XX PP 18-DEC-2000; 2000EP-0127688.
XX XX
XX PR 16-DEC-1999; 99JP-0377484.
XX PR 07-APR-2000; 2000JP-0159152.
XX PR 03-AUG-2000; 2000JP-0280988.
XX XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX XX
XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX XX
XX DR WPI; 2001-376931/40.
XX DR N-PSDB; AAH67743.
XX XX
XX PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
XX PT mutation point of a gene, measuring expression of a gene, analysing
XX PT expression profile or pattern of a gene and identifying homologous gene
XX PT
XX PS Claim 17; SEQ ID NO: 6278; 246pp + sequence listing; English.
XX XX
XX CC The present invention provides a number of nucleotide and protein
XX CC sequences from the Corynebacterium bacteria Corynebacterium glutamicum. These
XX CC are useful for identifying the mutation point of a gene derived from a
XX CC mutant of corynebacterium bacterium, measuring expression amount and
XX CC analysing the expression profile or expression pattern of a gene derived
XX CC from Corynebacterium bacterium, and identifying a homologue of a gene derived
XX CC from corynebacterium bacterium. Corynebacterium bacteria are useful for producing
XX CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
XX CC particularly L-lysine. The present sequence is a protein described
XX CC in the exemplification of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from the
XX CC European Patent Office.
XX XX
XX SQ Sequence 105 AA;

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Query Match 100.0%; Score 33; DB 22; Length 105;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LDASWL 6
DB 48 LDASWL 53

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RESULT 5
ABB77295
ID ABB77295 standard; protein; 756 AA.

```

AC ABB77295;
XX XX
XX DT 14-JUN-2002 (first entry)
XX DE Human IKKbeta mutant W739A.
XX XX
XX KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
XX KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
XX KW

```

KM autoimmune disease; transplant rejection; osteoporosis; cancer;
 KM Alzheimer's disease; viral; infection; aschma; anaphylaxis; psoriasis;
 KM rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KM corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
 KM osteopathic; cytostatic; nocrotic; neuroprotective; anti-HIV; human;
 KM antiarteriosclerotic; vincristine; antiasplastic; antiallergic;
 KM dermatological; antibacterial; antipsoriatic; antineumatic;
 KM antirheumatic; osteopathic; antitumor; mutant; mutagen.
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 739 /note= "Wildtype Trp substituted by Ala"
 PN MO200183547-A2.
 PD 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001MO-US40654.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (UTYA) UNIV YALE.
 PA
 XX May MJ, Ghosh S;
 PI
 DR WPI, 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 XX Example 11; Page -; 82pp; English.
 PS
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkbppaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections,
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta
 CC mutant, useful in examples of the invention.
 CC Note: The present sequence is not given in the specification but is

CC derived from Genbank Accession No. 014920 (ABB772294).
 XX
 XX Sequence 756 AA;
 SQ
 Query Match 100.0%; Score 33; DB 23; Length 756;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASWL 6
 DB 737 LDASWL 742
 RESULT 6
 AAG32182
 ID AAG32182 standard; Protein; 618 AA.
 XX
 XX AAG32182;
 AC
 XX 17-OCT-2000 (first entry)
 DT
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 38774.
 DE
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.
 XX
 XX Arabidopsis thaliana.
 OS
 XX EP1033405-A2.
 PN
 XX
 PD 06-SEP-2000.
 XX
 XX 25-FEB-2000; 2000EP-0301439.
 PF
 XX
 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
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 PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.
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PR 31-AUG-1999; 99US-0151438.
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Query Match 93.9%; Score 31; DB 21; Length 618;
Beet local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
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DB 468 LDASWI 473

RESULT 7
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ID AACG32181 standard; Protein; 676 AA.
XX
XX AACG32181;
AC
XX
DT 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 38773.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147415.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.

PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0148368.
PR 17-AUG-1999; 99US-0148175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 93.9%; Score 31; DB 21; Length 676;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 526 LDASWI 531

RESULT 8

AA32180
ID AA32180 standard; Protein; 763 AA.
XX
AC AA32180;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38772.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126284.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 04-MAY-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134758.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136382.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138504.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139482.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.

[illegible]

Human; open reading frame; ORF; detection; cytosolic; hepatotropic; vulnerability; antipariatic; antiparkinsonian; neurotropic; neuroprotective; anticonvulsant; osteopathic; antiallergic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antineuritic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.

OS Homo sapiens.

PN WO200058473-A2.

PP 05-OCT-2000.

PR 31-MAR-2000; 2000WO-US08621.

PR 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

XX (CUBA-) CUBAGEN CORP.

XX Shinkels RA, Leach M;

XX MPI; 2000-602362/57.

XX N-PSDB; AAC76815.

XX Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

XX Claim 11; Page 3920; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORF open reading frames 1 to 3161. The ORF sequences have activities such as: cytostatic; hepatotropic; vulnerability; antipariatic; antiparkinsonian; neurotropic; neuroprotective; osteopathic; anticonvulsant; antiallergic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antineuritic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORF-associated disorder. The nucleic acids can be used to express ORF proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 119 AA;

XX Query Match 90.9%; Score 30; DB 21; Length 119;

XX Best Local Similarity 83.3%; Pred. No. 3.9e+02;

XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX 1 LDASWL 6

XX 29 LDASWL 34

CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancers, tumours, foetal and developmental
 CC abnormalities, hematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiotensin disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention.

XX Sequence 189 AA;

Query Match 90.9%; Score 30; DB 22; Length 189;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 Db 164 LDASWV 169

RESULT 13

AAU14439
 ID AAU14439 standard; Protein; 191 AA.

AC AAU14439;

DT 24-OCT-2001 (first entry)

DE Human novel protein #310.

XX Human; novel protein; Antianemic; osteopathic; antiinflammatory;
 KW immunomodulatory; cytoskeletal; neuroprotective; vulnery; nocotropic;
 KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
 KW antibacterial; antiallergic; dermatological; hemostatic; antiaesthetic;
 KW chondrolytic; immunogen; antibody; gene therapy; neurological disorder;
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 KW tissue regeneration; immune disorder.

XX Homo sapiens.

OS WO200155437-A2.

PN 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02623.

PF 25-JAN-2000; 2000US-0491404.

PR (HSE-) HSEQ INC.

PA Tang YT, Liu C, Drmanac RT,

XX WPI; 2001-451939/48.

DR N-PSDB; AA822744.

XX Isolated polypeptides useful for treating anti-inflammatory diseases,
 PT nervous system disorders, and for regenerating bone and cartilage -

XX Example 4; Page 816; 894p; English.

XX The invention relates to polynucleotides encoding novel human

CC proteins or their active domains. The polypeptides, polynucleotides and
 CC antibodies raised against the polypeptides are used in a method of
 CC treatment of a mammal and prevention of disorders caused by the aberrant
 CC protein expression or activity. The polypeptides can be used as
 CC molecular weight markers, food supplements, and in antibody production.
 CC The polypeptides are used to identify compounds which bind to the
 CC polypeptides. Polynucleotides of the invention are used as probes and
 CC primers, for sequencing, for chromosome or gene mapping, in the
 CC production of recombinant proteins, and in generating anti-gene DNA or
 CC RNA and in gene therapy. Polypeptides of the invention can be used to
 CC target drugs to a tumour, in assays to determine biological activity, to
 CC raise antibodies/elicite an immune response, to determine quantitative
 CC protein levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.

XX The present sequence represents a protein of the invention.

Query Match 90.9%; Score 30; DB 22; Length 191;
 Best Local Similarity 83.3%; Pred. No. 6.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 Db 161 LDASWV 166

RESULT 14

AAU03119
 ID AAU03119 standard; Protein; 221 AA.

AC AAU03119;

DT 23-OCT-2001 (first entry)

DE Streptococcus pyogenes virulence protein #1.

XX Virulence; attenuated microorganism; Streptococcal infection;
 KW Gram-positive bacteria; antimicrobial; impetigo; pneumonia.

XX Streptococcus pyogenes.

OS WO200148208-A2.

PN 05-JUL-2001.

XX 22-DEC-2000; 2000WO-GB04997.

PF 23-DEC-1999; 99GB-0030462.

PR 23-DEC-1999; 99GB-0030463.

PR 23-DEC-1999; 99GB-0030464.

PR 23-DEC-1999; 99GB-0030466.

PR 23-DEC-1999; 99GB-0030467.

PR 23-DEC-1999; 99GB-0030469.

PR 23-DEC-1999; 99GB-0030471.

PR 23-DEC-1999; 99GB-0030472.

PR 23-DEC-1999; 99GB-0030473.

PR 17-FEB-2000; 2000GB-0003725.

PR 17-FEB-2000; 2000GB-0003726.

PR 17-FEB-2000; 2000GB-0003727.

PR 17-FEB-2000; 2000GB-0003728.

PR 17-FEB-2000; 2000GB-0003729.

PR 17-FEB-2000; 2000GB-0003730.

PR 17-FEB-2000; 2000GB-0003731.
 PR 17-FEB-2000; 2000GB-0003732.
 PR 17-FEB-2000; 2000GB-0003733.
 PR 02-MAY-2000; 2000GB-0010585.
 PR 02-MAY-2000; 2000GB-0010587.
 XX
 PA (MICR-) MICROSCIENCE LTD.
 XX
 PI Clarke BE, Zhou L, Shea JE, Feldman RG, Holden DW;
 XX
 DR WPI; 2001-418285/44.
 DR N-PSDB; AAS06351.
 XX
 PT Novel peptide obtained from Streptococcus pyogenes useful for treating
 PT or preventing a condition associated with infection by Streptococcal or
 PT Gram-positive bacteria, preferably pneumonia -
 XX
 PS Claim 4; Page 26-27; 91pp; English.
 XX
 CC AAU03119-AAU03149 represent novel Streptococcus pyogenes virulence
 CC proteins #1-31. The S. pyogenes virulence genes can be used to
 CC produce attenuated microorganisms comprising a mutation that disrupt
 CC the expression of the virulence protein. The virulence genes, proteins
 CC or an attenuated microorganism are useful for therapeutic or diagnostic
 CC purposes. DNA encoding the virulence proteins, the proteins themselves,
 CC an attenuated microorganism or a vaccine comprising the virulence
 CC protein are useful for the manufacture of a medicament for use in
 CC the treatment or prevention of a condition associated with infection
 CC by Streptococcal or Gram-positive bacteria, for veterinary treatment,
 CC and in a screening assay for the identification of an antimicrobial
 CC drug. Disorders which can be treated using S. pyogenes virulence
 CC polynucleotide and polypeptide sequences include non-invasive infections
 CC and invasive infections e.g. impetigo, pharyngitis, necrotising
 CC fasciitis, bacteraemia, streptococcal toxic shock syndrome (STSS),
 CC pneumonia and rheumatic fever. The virulence proteins are also useful
 CC in the preparation of antibodies.
 CC
 SQ Sequence 221 AA;
 XX
 Query Match 90.9%; Score 30; DB 22; Length 221;
 Best Local Similarity 83.3%; Pred. No. 7.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASWL 6
 Db 36 LDAAWL 41
 RESULT 15
 ABP27441
 ID ABP27441 standard; Protein; 221 AA.
 XX
 AC ABP27441;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DB Streptococcus polypeptide SEQ ID NO 4058.
 XX
 KM Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus pyogenes.
 XX
 PN MO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PP 29-OCT-2001; 2001WO-GB04789.
 XX
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640;

XX (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Maignani V, Margalit Ros YI, Grandi G, Fraser C;
 PI Tettelein H;
 XX
 DR WPI; 2002-352536/38.
 DR N-PSDB; ABN68072.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 XX
 PS Claim 1; Page 3561; 4525pp; English.
 XX
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.
 CC
 SQ Sequence 221 AA;
 XX
 Query Match 90.9%; Score 30; DB 23; Length 221;
 Best Local Similarity 83.3%; Pred. No. 7.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASWL 6
 Db 36 LDAAWL 41
 Search completed: February 18, 2004, 14:26:22
 Job time : 23.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds

(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-9

Perfect score: 40

Sequence: 1 LNWSWL 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	10 US-09-847-940B-9	Sequence 9, Appl1
2	40	100.0	6	11 US-09-847-946A-9	Sequence 9, Appl1
3	36	90.0	117	11 US-09-809-391-360	Sequence 360, App
4	36	90.0	117	12 US-09-882-171-360	Sequence 360, App
5	36	90.0	117	12 US-10-108-260A-2963	Sequence 2963, Ap
6	36	90.0	464	9 US-09-815-242-10647	Sequence 10647, A
7	36	90.0	9	US-09-815-242-4997	Sequence 10997, Ap
8	36	90.0	864	12 US-10-436-715-29	Sequence 82, Appl1
9	36	90.0	864	12 US-10-436-715-82	Sequence 82, Appl1
10	35	87.5	6	10 US-09-847-940B-2	Sequence 2, Appl1
11	35	87.5	6	11 US-09-847-946A-2	Sequence 2, Appl1
12	35	87.5	6	11 US-09-847-946A-3	Sequence 33, Appl1
13	35	87.5	7	11 US-09-847-946A-37	Sequence 37, Appl1
14	35	87.5	8	11 US-09-847-946A-30	Sequence 30, Appl1
15	35	87.5	8	11 US-09-847-946A-38	Sequence 38, Appl1

16	35	87.5	9	11 US-09-847-946A-29	Sequence 29, Appl1
17	35	87.5	9	11 US-09-847-946A-32	Sequence 32, Appl1
18	35	87.5	9	11 US-09-847-946A-35	Sequence 35, Appl1
19	35	87.5	9	11 US-09-847-946A-36	Sequence 36, Appl1
20	35	87.5	10	11 US-09-847-946A-31	Sequence 31, Appl1
21	35	87.5	10	11 US-09-847-946A-34	Sequence 34, Appl1
22	35	87.5	11	11 US-09-847-946A-28	Sequence 28, Appl1
23	35	87.5	11	11 US-09-847-946A-132	Sequence 132, Appl1
24	35	87.5	11	11 US-09-847-946A-140	Sequence 140, App
25	35	87.5	13	11 US-09-847-946A-143	Sequence 143, App
26	35	87.5	13	11 US-09-847-946A-145	Sequence 145, App
27	35	87.5	13	11 US-09-847-946A-147	Sequence 147, App
28	35	87.5	13	11 US-09-847-946A-148	Sequence 148, App
29	35	87.5	17	11 US-09-847-946A-141	Sequence 141, App
30	35	87.5	17	11 US-09-847-946A-142	Sequence 142, App
31	35	87.5	17	11 US-09-847-946A-146	Sequence 146, App
32	35	87.5	17	11 US-09-847-946A-147	Sequence 147, App
33	35	87.5	18	11 US-09-847-946A-131	Sequence 131, App
34	35	87.5	18	11 US-09-847-946A-135	Sequence 135, App
35	35	87.5	18	11 US-09-847-946A-136	Sequence 136, App
36	35	87.5	22	11 US-09-847-946A-134	Sequence 134, App
37	35	87.5	22	11 US-09-847-946A-137	Sequence 137, App
38	35	87.5	22	11 US-09-847-946A-139	Sequence 139, App
39	35	87.5	22	11 US-09-847-946A-141	Sequence 141, App
40	35	87.5	28	10 US-09-847-940B-18	Sequence 18, Appl1
41	35	87.5	28	10 US-09-847-940B-18	Sequence 18, Appl1
42	35	87.5	222	10 US-09-771-161A-141	Sequence 141, App
43	35	87.5	745	9 US-09-796-872-2	Sequence 2, Appl1
44	35	87.5	745	10 US-09-844-908-10	Sequence 10, Appl1
45	35	87.5	745	10 US-09-844-908-10	Sequence 10, Appl1

ALIGNMENTS

RESULT 1
US-09-847-940B-9
Sequence 9, Application US/09847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
TITLE OR INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PFI-117CP
CURRENT APPLICATION NUMBER: US/09/847, 940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-9
Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LNWSWL 6
Db 1 LNWSWL 6
RESULT 2
US-09-847-946A-9
Sequence 9, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J

```
APPLICANT: Ghosh, Sankar
APPLICANT: Fındeıs, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hamid, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PRI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-647-946A-9
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Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 LNMSWL 6
        |||||
Db       1 LNMSWL 6
```

```
RESULT 3
US-09-809-391-360
Sequence 360, Application US/09809391
Publication No. US20030049618A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 360
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-809-391-360
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Query Match          90.0%; Score 36; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 LNMSW 5
        |||||
Db       30 LNMSW 34
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RESULT 4
US-09-882-171-360
Sequence 360, Application US/09882171
Publication No. US2003015858A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/809,391
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/149,476
PRIOR FILING DATE: 1998-09-08
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PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/038,621
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,626
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,334
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,336
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,163
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/047,600
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,615
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,597
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,502
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,633
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,583
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,617
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,618
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,503
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,592
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,581
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,584
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,500
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,587
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,492
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,598
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,613
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,582
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,596
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,612
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,632
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,601
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043,580
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,568
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,314
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,569
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,311
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,671
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,674
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PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,669
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,312
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,313
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,672
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,315
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/048,974
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/056,886
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,877
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,889
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,893
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,630
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,878
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,662
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,872
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,882
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,637
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,903
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,888
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,879
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,880
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,894
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,911
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,636
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,874
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,910
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,864
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,631
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,845
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,892
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/057,761
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/047,595
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,599
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,588
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,585
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,586
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,590
PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 60/047,594
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,589
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,593
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,614
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043,578
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,576
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/047,501
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043,670
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/056,632
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,664
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,876
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,881
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,909
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,875
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,862
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,887
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,908
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/048,964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/057,650
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/057,669
PRIOR FILING DATE: 1997-09-05

Query Match 90.0%; Score 36; DB 12; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSW 5
Db 30 LNWSW 34

RESULT 5
US-10-108-260A-2983
Sequence 2983, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2983
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-10-108-260A-2983

Query Match 90.0%; Score 36; DB 12; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6
Db 20 NWSWL 24

RESULT 6
US-09-815-242-10647
Sequence 10647, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Hagelbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyckind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10647
LENGTH: 464
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-815-242-10647

Query Match
Best Local Similarity 100.0%; Score 36; DB 9; Length 464;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6
Db 422 NWSWL 426

RESULT 7
US-09-815-242-4997
Sequence 4997, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Hagelbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyckind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4997
LENGTH: 467
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-815-242-4997

Query Match
Best Local Similarity 100.0%; Score 36; DB 9; Length 467;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6
Db 425 NWSWL 429

RESULT 8
US-10-436-715-29
Sequence 29, Application US/10436715
Publication No. US20040018976A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
FILE REFERENCE: D0262 NP
CURRENT APPLICATION NUMBER: US/10/436,715
CURRENT FILING DATE: 2003-05-13
PRIOR APPLICATION NUMBER: U.S. 60/380,336
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 471
SOFTWARE: Patencin version 3.2
SEQ ID NO 29
LENGTH: 864
TYPE: PRT
ORGANISM: Fugu rubripes
US-10-436-715-29

Query Match
Best Local Similarity 83.3%; Score 36; DB 12; Length 864;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNWOWL 6
Db 481 LNWOWL 486

RESULT 9
US-10-436-715-82
Sequence 82, Application US/10436715
Publication No. US20040018976A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
FILE REFERENCE: D0262 NP
CURRENT APPLICATION NUMBER: US/10/436,715
CURRENT FILING DATE: 2003-05-13
PRIOR APPLICATION NUMBER: U.S. 60/380,336

;; PRIOR FILING DATE: 2002-05-14
;; NUMBER OF SEQ ID NOS: 471
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 82
;; LENGTH: 864
;; TYPE: PRT
;; ORGANISM: Fugu rubripes
US-10-436-715-82

Query Match 90.0%; Score 36; DB 12; Length 864;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNWSWL 6
|:||||
Db 481 LNWQWL 486

RESULT 10
US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2

Query Match 87.5%; Score 35; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
|:||||
Db 1 LDMWSWL 6

RESULT 11
US-09-847-946A-2
; Sequence 2, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-2

Query Match 87.5%; Score 35; DB 11; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
|:||||
Db 1 LDMWSWL 6

RESULT 12
US-09-847-946A-33
; Sequence 33, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD binding
US-09-847-946A-33

Query Match 87.5%; Score 35; DB 11; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
|:||||
Db 1 LDMWSWL 6

RESULT 13
US-09-847-946A-37
; Sequence 37, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37

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; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-37
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Query Match      87.5%; Score 35; DB 11; Length 7;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LNWSQL 6
        |||||
DB      1 LDWSQL 6
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RESULT 14

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US-09-847-946A-30
; Sequence 30, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-30
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Query Match      87.5%; Score 35; DB 11; Length 8;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LNWSQL 6
        |||||
DB      3 LDWSQL 8
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RESULT 15

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US-09-847-946A-38
; Sequence 38, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
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; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-38
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Query Match      87.5%; Score 35; DB 11; Length 8;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LNWSQL 6
        |||||
DB      1 LDWSQL 6
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Search completed: February 18, 2004, 15:41:57
Job time : 17.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignment)
41.814 Million cell updates/sec

Title: US-09-643-260-9

Perfect score: 40
Sequence: 1 LMSWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	23	ABB08731
2	40	100.0	6	23	AAW48514
3	40	100.0	6	24	ABU08424
4	40	100.0	22	22	ABB62034
5	40	100.0	22	22	ABB77304
6	38	95.0	20	20	AAV76530
7	37	92.5	130	22	AAW85139
8	37	92.5	464	21	AAW53151
9	36	90.0	117	23	ABG95220

10	36	90.0	464	22	AAU35054	Enterococcus faeca
11	36	90.0	467	22	AAU35301	Enterococcus faeca
12	36	90.0	767	23	ABP65725	Bifidobacterium 10
13	35	87.5	6	23	ABB08725	IKKbeta NEMO bindi
14	35	87.5	6	23	AAW48530	Anti-inflammatory
15	35	87.5	6	23	AAW48555	NBD mutant peptide
16	35	87.5	6	24	ABU08418	Human NEMO binding
17	35	87.5	7	23	AAW48534	Anti-inflammatory
18	35	87.5	8	23	AAW48527	Anti-inflammatory
19	35	87.5	8	23	AAW48535	Anti-inflammatory
20	35	87.5	9	20	AAW6182	IKK-alpha polypep
21	35	87.5	9	23	AAW48526	Anti-inflammatory
22	35	87.5	9	23	AAW48529	Anti-inflammatory
23	35	87.5	9	23	AAW48532	Anti-inflammatory
24	35	87.5	9	23	AAW48533	Anti-inflammatory
25	35	87.5	10	23	ABB77313	IKKbeta NEMO bindi
26	35	87.5	10	23	AAW48528	Anti-inflammatory
27	35	87.5	10	23	AAW48531	Anti-inflammatory
28	35	87.5	11	23	ABB77311	Human NBD peptide
29	35	87.5	11	23	AAW48506	Human IKKbeta pep
30	35	87.5	11	23	AAW48525	Anti-inflammatory
31	35	87.5	11	23	AAW48525	NBD peptide. Sync
32	35	87.5	13	23	AAW48633	Anti-inflammatory
33	35	87.5	13	23	AAW48640	Anti-inflammatory
34	35	87.5	13	23	AAW48641	Anti-inflammatory
35	35	87.5	13	23	AAW48642	Anti-inflammatory
36	35	87.5	17	23	AAW48645	Anti-inflammatory
37	35	87.5	17	23	AAW48638	Anti-inflammatory
38	35	87.5	17	23	AAW48639	Anti-inflammatory
39	35	87.5	17	23	AAW48643	Anti-inflammatory
40	35	87.5	18	23	AAW48644	Anti-inflammatory
41	35	87.5	18	23	AAW48628	Anti-inflammatory
42	35	87.5	18	23	AAW48629	Anti-inflammatory
43	35	87.5	18	23	AAW48632	Anti-inflammatory
44	35	87.5	22	23	AAW48633	Anti-inflammatory
45	35	87.5	22	23	AAW48630	Anti-inflammatory

ALIGNMENTS

RESULT 1	ABB08731	standard; peptide; 6 AA.
ID	ABB08731	
XX	ABB08731	
AC	ABB08731	
XX	ABB08731	
DT	14-JUN-2002	(first entry)
XX	14-JUN-2002	
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 9.	
XX	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
XX	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KW	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KW	corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;	
KW	osteoarthritis; cytotoxic; neurotrophic; neuroprotective; anti-HIV; human;	
KW	antiartherosclerotic; vitamin; antidiabetic; antiallergic;	
KW	dermatological; antibacterial; antiparasitic; antirheumatic;	
KW	antiarthritic; osteopathic; antitumor; mutant; mucin.	
OS	Human seqs.	
OS	Synthetic.	
XX		
XX		
Key	Location/Qualifiers	
FT	Misc-difference	/note= "Wildtype Asp substituted by Asn"
FT		
PN	WO200183547-A2.	
XX		
XX		
PD	08-NOV-2001.	
XX		

PF	02-MAY-2001; 2001MO-US40654.
XX	
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-064326O.
XX	
PA	(UYVA) UNIV YALE.
XX	
P1	May MJ, Ghosh S;
XX	
DR	WPI; 2002-179350/23.
XX	
PT	Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT	inflammatory disorders, osteoporosis and cancer, comprising contacting a
PT	cell with an anti-inflammatory compound comprising at least one NEMO
PT	binding domain -
XX	
PS	Claim 23; Page 44; 82pp; English.
XX	
CC	The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC	comprising contacting a cell with an anti-inflammatory compound
CC	(ABR08725-ABR08742) comprising at least one NEMO binding domain
CC	(ABR07713). The compound has acts through selective inhibition of
CC	cyclooxygenase-mediated NF-kB activation by blocking the interaction of NEMO
CC	with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC	interaction results in inhibition of IKKbeta kinase activation and
CC	subsequent decreased phosphorylation of Ikbappab. The compound may also
CC	act (directly or indirectly) by blocking the recruitment of leukocytes
CC	into sites of acute and chronic inflammation, by down-regulating the
CC	expression of E-selectin on leukocytes or by blocking osteoclast
CC	differentiation. The compound is useful in treating NF-kB mediated
CC	conditions, where the condition is an inflammatory disorder, an
CC	autoimmune disease, transplant rejection, osteoporosis, cancer,
CC	Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC	telangiectasias. The inflammatory disorder is asthma, allergies,
CC	urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC	rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC	bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC	bursitis. The inflammatory disorder may also be dermatitis, eczema,
CC	psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC	spondyloarthritis. Also for Crohn's disease, ulcerative colitis,
CC	polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC	cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC	caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC	diseases include HIV and influenza. The compound may also be useful for
CC	treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC	sunburn or aging. The compound may be used to replace corticosteroids in
CC	any application in which corticosteroids are used, including
CC	immunosuppression in transplants and cancer therapy. Also for identifying
CC	anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
CC	The compound may be administered alone or in combination with other known
CC	anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC	binding domain of IKKbeta.
XX	
SQ	Sequence 6 AA;
OY	
DB	Query Match 100.0%; Score 40; DB 23; Length 6; Best Local Similarity 100.0%; Pred. NO. 9.3e+05; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0 1 LNMSTL 6 1 LNMSTL 6
RESULT 2	
ID	AAM48514 standard; peptide; 6 AA.
XX	
AC	AAM48514;
XX	
DT	20-MAR-2002 (first entry)
XX	
NBD	mutant peptide SEQ ID NO 9.

XX Antiinflammatory; antiasthmatic; cycostatic; antiapoptotic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiangiogenic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UTYA) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Example 6; Page 47; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAW48645), comprising a membrane translocation domain
CC (AAM48620-AAW48627 or AAM48646-AAW48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAW48619). The antiinflammatory compounds have antiaesthetic,
CC cycostatic, antiapoptotic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antihypertensive, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of Ikappab kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of Ikappab. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursts; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 23; Length 6;
Best Local Similarity 100.0%; Prod. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 LNMSWL 6
DB 1 LNMSWL 6

RESULT 3
ABU08424 standard; peptide; 6 AA.

```

XX AC ABU08424;
XX DT 12-JUN-2003 (first entry)
XX DE Human NEMO binding site (NBD) mutant peptide #7.
XX KM Human; antiinflammatory compound; NEMO binding domain, NBD, IKKbeta,
XX KM IKKappab kinase-beta; Ikappab kinase-alpha; IKKalpha; NF-kappab;
XX KM nuclear factor-kappab induction; inflammatory disorder;
XX KM autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
XX KM atherosclerosis; viral infection; Ataxia telangiectasia;
XX KM transplantation detection; immunosuppressive; osteopathic;
XX KM cytoskeletal; neurotrophic; neuroprotective; antiatherosclerotic; virucide;
XX KM vasotropic; antineumatic; antiarthritic; mutant; muten.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2002156000-A1.
XX PD 24-OCT-2002.
XX PF 02-MAY-2001; 2001US-0847940.
XX PR 02-MAY-2000; 2000US-201261P.
XX PR 22-AUG-2000; 2000US-0643260.
XX PA (MAYM/) MAY M J.
XX PA (GHOS/) GHOSH S.
XX PI May MJ, Ghosh S;
XX DR WPI; 2003-209142/20.
XX PT Novel antiinflammatory peptide compounds comprising NEMO binding
XX PT domain, useful for modulating NF-kappab induction in a cell and for
XX PT creating NF-kappab-mediated inflammation disorders e.g., asthma,
XX PT psoriasis, vasculitis -
XX PS Claim 22; Page 17; 47pp; English.
XX CC The present invention relates to antiinflammatory compounds comprising
XX CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
XX CC found on Ikappab kinase-beta (IKKbeta) and Ikappab kinase-alpha
XX CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
XX CC are useful for modulating nuclear factor-kappab (NF-kappab) induction
XX CC in a cell, where the compounds are capable of blocking the interaction
XX CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
XX CC antiinflammatory compound further comprises at least one membrane
XX CC translocation domain. The compounds are useful for treating
XX CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
XX CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
XX CC telangiectasia, and for transplantation detection. The compounds of
XX CC the invention block NF-kappab induction by IKK but do not inhibit
XX CC the basal activity of NF-kappab. ABU08418-ABU08432 represent human
XX CC NBD mutant peptides.
XX SQ Sequence 6 AA;

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Query Match 100.0%; Score 40; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LNMSWL 6
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DB 1 LNMSWL 6

```

RESULT 4
 ABB62034
 ID ABB62034 standard; Protein; 295 AA.
 XX

```

AC ABB62034;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 12894.
XX KM Drosophila; developmental biology; cell signalling; insecticide;
XX KM pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO20011042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PERK) PB CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX DR N-PSDB; ABL06137.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX PS Disclosure; SEQ ID NO 12894; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
XX CC sequences (AB57737-AB872072).
XX CC (AB57737-AB872072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 295 AA;

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Query Match 100.0%; Score 40; DB 22; Length 295;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LNMSWL 6
   |||||
DB 286 LNMSWL 291

```

RESULT 5
 ABB77304
 ID ABB77304 standard; Protein; 756 AA.
 XX
 XX ABB77304;
 XX DT 14-JUN-2002 (first entry)
 XX DE Human IKKbeta mutant D738N.
 XX KM IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappab; NF-kb;
 XX KM kinase activation; leukocyte; inflammation; B-selectin; osteoclast;
 XX KM autoimmune disease; transplant rejection; osteoporosis; cancer;
 XX KM Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 XX KM rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 XX KM corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 XX KM osteopathic; cytostatic; neurotrophic; neuroprotective; anti-HIV; human;
 XX

OS	Homo sapiens.	
OS	Synthetic.	
XX		Location/Qualifiers
PH	Key	
PT	Misc-difference 738	
XX	/note= "Wildtype Asp substituted by Asn"	
XX	MO200183547-A2.	
PD	08-NOV-2001.	
XX		
PF	02-MAY-2001; 2001MO-US40654.	
XX		
PR	02-MAY-2000; 2000US-201261P.	
XX	22-AUG-2000; 2000US-06433260.	
PA	(UYYA) UNIV YALE.	
PI	May MJ, Ghosh S;	
DR	WPI, 2002-179350/23.	
XX		
PT	Modulating NF-kappaB induction in a cell, useful for treating e.g.	
XX	inflammatory disorders, osteoporosis and cancer, comprises contacting a	
PT	cell with an anti-inflammatory compound comprising at least one NEMO	
XX	binding domain _	
PS	Example 11; Page -; 82pp; English.	
XX		
CC	The invention relates to modulating NF-kappaB (NF-KB) induction in a cell	
CC	comprises contacting a cell with an anti-inflammatory compound	
CC	(ABB08725-ABB08742) comprising at least one NEMO binding domain	
CC	(ABB77313). The compound has acts through selective inhibition of	
CC	cytokine-mediated NF-KB activation by blocking the interaction of NEMO	
CC	with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO	
CC	interaction results in inhibition of IKKbeta kinase activation and	
CC	subsequent decreased phosphorylation of I-kappaB. The compound may also	
CC	act (directly or indirectly) by blocking the recruitment of leukocytes	
CC	into sites of acute and chronic inflammation, by down-regulating the	
CC	expression of B-selectin on leukocytes or by blocking osteoclast	
CC	differentiation. The compound is useful in treating NF-KB mediated	
CC	conditions, where the condition is an inflammatory disorder, an	
CC	autoimmune disease, transplant rejection, osteoporosis, cancer,	
CC	Alzheimer's disease, atherosclerosis, a viral infection or ataxia	
CC	relangiectasia. The inflammatory disorder is asthma, allergies,	
CC	urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,	
CC	rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory	
CC	bowel disease, chronic obstructive pulmonary disease, vasculitis and	
CC	burbitis. The inflammatory disorder may also be dermatitis, eczema,	
CC	psoriasis, osteoarthritis, psoriatic arthritis, lupus and	
CC	spondylarthritis. Also for Crohn's disease, ulcerative colitis,	
CC	polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,	
CC	cryoglobulinemia or multiple sclerosis. For chronic viral infections	
CC	caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral	
CC	diseases include HIV and Influenza. The compound may also be useful for	
CC	treating anaphylaxis, drug and food sensitivity, contact dermatitis,	
CC	sunburn or aging. The compound may be used to replace corticosteroids in	
CC	any application in which corticosteroids are used, including	
CC	immunosuppression in transplants and cancer therapy. Also for identifying	
CC	anti-inflammatory compounds and for diagnosis of an inflammatory disorder.	
CC	The compound may be administered alone or in combination with other known	
CC	anti-inflammatory agents. The present sequence is that of an IKKbeta	
CC	mutant, useful in examples of the invention.	
CC	Note: The present sequence is not given in the specification but is	
CC	derived from GenBank Accession No. 014920 (ABB77294).	
XX		
XX	Sequence 756 AA;	

Query Match
100.0%; Score 40; DB 23; Length 756;

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Qy      1  LNN$WL  6
        |||||
Db      737  LNN$WL 742

Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

	RESULT 6
XX	AA76530
ID	AA76530 standard; Protein; 135 AA.
AC	AA76530;
XX	
DT	10-APR-2000 (first entry)
XX	
DE	Human ovarian tumor EST fragment encoded protein 26.
KW	Expressed sequence tag; EST; human; ovarian tumor; anticancer; gene therapy; treatment.
XX	
OS	Homo sapiens.
XX	
PN	D819817557-A1.
XX	
PD	21-OCT-1999.
XX	
PF	09-APR-1998; 98DE-1017557.
XX	
PR	09-APR-1998; 98DE-1017557.
XX	
PA	(META-) METAGEN GES GENOMFORSCHUNG MEH.

XX
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
DR WPI; 1999-591920/51.
XX
DR N-PSDB; AA277461.
XX
XX
XX New nucleic acid sequences expressed in ovarian, and some other, cancer
PT tissues, and derived polypeptides, for treatment of ovarian cancer and
PT identification of therapeutic agents -
XX
PS Claim 25; Page 254; 310pp; German.

This invention describes novel nucleic acid (cDNA) sequences (A) which have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (1) for recombinant expression of polypeptides (B) and (11) to isolate complete genes. (B) are used (1) to identify agents suitable for treatment of ovarian cancer; (11) directly for treating this form of cancer (including expression from gene therapy vectors) and (111) for generation of specific antibodies. (A) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed. So should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAY75505-Y76638 represent protein fragments encoded by the human ovarian tumor cDNA library derived EST fragments represented in AAY77450-Z77572.

Query Match	95.04%	Score 38	DB 20	Length 135
Best Local Similarity	83.3%	Pred. No.	1.3e+05	
Matches	5	Conservative	0	Indels 0
				Gaps 0
QY	1	LINMSWL	6	
Db	69	LINMSWI	74	

RESULT 7
AA085139
ID AA085139 standard; Protein; 130 AA.
XX
AC AA085139;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:12732.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 02-MAR-2000; 2000US-0184664.
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PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
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PR 14-AUG-2000; 2000US-0225268.
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PR 23-AUG-2000; 2000US-0227009.
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PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
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PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
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PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
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PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241825.
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PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
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PR 08-NOV-2000; 2000US-0246524.
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PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
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PR 17-NOV-2000; 2000US-0249245.
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PR 17-NOV-2000; 2000US-0249265.
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PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.

PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 PT WPI; 2001-483426/52.
 DR N-PSDB; AAK57920.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Claim 11, SEQ ID NO 12732; 3071bp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent
 CC disease and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SO Sequence 130 AA;
 XX
 Query Match 92.5%; Score 37; DB 22; Length 130;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAMSWL 6
 DB 55 LNMWTL 60
 XX
 RESULT 8
 AAB53151
 ID AAB53151 standard; Protein; 464 AA.
 XX
 AC AAB53151;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Macaca mulatta rhadinovirus 17577 RRV ORF32 protein SEQ ID NO:59.
 XX
 KW Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus;
 KW genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6;
 KW IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;
 KW cytotoxic; anti-HIV; gene therapy; infection; Kaposi's sarcoma;
 KW lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
 KW epidermolytic; hypergammaglobulinemia; autoimmune haemolytic anaemia.
 XX
 OS Macaca mulatta rhadinovirus 17577.

PN WO200028040-A2.
 XX
 PD 18-MAY-2000.
 XX
 PF 05-NOV-1999; 99WO-US26260.
 XX
 PR 06-NOV-1998; 98US-0107507.
 PR 20-NOV-1998; 98US-0109409.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 PI Wong SM, Axthelm MK, Searles RP;
 XX
 DR WPI; 2000-376552/32.
 XX
 PT New rhesus rhadino virus for producing non-human primate model useful
 PT for testing potential treatments and efficacy of the candidate vaccine
 PT for conditions associated with RRV infection -
 XX
 PS Claim 5; Page 128-129; 141bp; English.
 XX
 CC The present invention describes a novel rhesus macaque rhadinovirus
 CC called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
 CC RRV genome sequence, and AAB53123 to AAB53204 represent the proteins
 CC encoded by the genome sequence. The present invention also specifically
 CC claims the individual open reading frame (ORF) nucleotide sequences from
 CC the genome which encode the individual proteins, but these sequences are
 CC not given. A non-human animal infected with RRV can be used for testing
 CC the efficacy of drug in the treatment of condition associated with
 CC infection with RRV such as Kaposi's sarcoma, lymphoproliferative
 CC disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly,
 CC hypergammaglobulinemia or autoimmune haemolytic anaemia, by
 CC administering the drug to an immuno-compromised non-human primate
 CC preferably Rhesus macaque monkey obtained by as a result of infection
 CC by Simian Immunodeficiency Virus (SIV). RRV is useful for producing
 CC non-human primate model for testing potential treatments for conditions
 CC associated with RRV infection. It is also useful for testing the
 CC efficacy of the candidate vaccine against RRV infection or conditions
 CC associated with its infection by administering the vaccine to the
 CC subject capable of infection with RRV, inoculating the subject with RRV
 CC and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205
 CC to AAB53213 represent sequence used in the exemplification of the
 CC present invention.
 XX
 SO Sequence 464 AA;
 XX
 Query Match 92.5%; Score 37; DB 21; Length 464;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAMSWL 6
 DB 397 VNMSWL 402
 XX
 RESULT 9
 ABG95220
 ID ABG95220 standard; Protein; 117 AA.
 XX
 AC ABG95220;
 XX
 DT 15-JAN-2003 (first entry)
 XX
 DE Human novel secreted protein #41.
 XX
 KW Human; secreted protein; autoimmune disease; chemotaxis;
 KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
 KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
 KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
 KW nervous system disorders; Alzheimer's disease; infection;
 KW ocular disorder; corneal infection; wound healing; tissue regeneration;
 KW epithelial cell proliferation; organ transplantation; food additive;
 KW preservative; nutritional.

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XX OS Homo sapiens.
XX XX US6420526-B1.
XX PD 16-JUL-2002.
XX PF 08-SEP-1998; 98US-0149476.
XX PR 07-MAR-1997; 97US-038621P.
XX PR 07-MAR-1997; 97US-040161P.
XX PR 07-MAR-1997; 97US-040162P.
XX PR 07-MAR-1997; 97US-040163P.
XX PR 07-MAR-1997; 97US-040333P.
XX PR 07-MAR-1997; 97US-040334P.
XX PR 07-MAR-1997; 97US-040336P.
XX PR 11-APR-1997; 97US-043311P.
XX PR 11-APR-1997; 97US-043312P.
XX PR 11-APR-1997; 97US-043313P.
XX PR 11-APR-1997; 97US-043314P.
XX PR 11-APR-1997; 97US-043315P.
XX PR 11-APR-1997; 97US-043568P.
XX PR 11-APR-1997; 97US-043569P.
XX PR 11-APR-1997; 97US-043576P.
XX PR 11-APR-1997; 97US-043580P.
XX PR 11-APR-1997; 97US-043580P.
XX PR 11-APR-1997; 97US-043669P.
XX PR 11-APR-1997; 97US-043670P.
XX PR 11-APR-1997; 97US-043672P.
XX PR 11-APR-1997; 97US-043674P.
XX PR 23-MAY-1997; 97US-047492P.
XX PR 23-MAY-1997; 97US-047500P.
XX PR 23-MAY-1997; 97US-047502P.
XX PR 23-MAY-1997; 97US-047503P.
XX PR 23-MAY-1997; 97US-047581P.
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XX PR 23-MAY-1997; 97US-047583P.
XX PR 23-MAY-1997; 97US-047584P.
XX PR 23-MAY-1997; 97US-047585P.
XX PR 23-MAY-1997; 97US-047586P.
XX PR 23-MAY-1997; 97US-047587P.
XX PR 23-MAY-1997; 97US-047588P.
XX PR 23-MAY-1997; 97US-047589P.
XX PR 23-MAY-1997; 97US-047590P.
XX PR 23-MAY-1997; 97US-047592P.
XX PR 23-MAY-1997; 97US-047593P.
XX PR 23-MAY-1997; 97US-047594P.
XX PR 23-MAY-1997; 97US-047595P.
XX PR 23-MAY-1997; 97US-047596P.
XX PR 23-MAY-1997; 97US-047597P.
XX PR 23-MAY-1997; 97US-047598P.
XX PR 23-MAY-1997; 97US-047599P.
XX PR 23-MAY-1997; 97US-047600P.
XX PR 23-MAY-1997; 97US-047601P.
XX PR 23-MAY-1997; 97US-047612P.
XX PR 23-MAY-1997; 97US-047613P.
XX PR 23-MAY-1997; 97US-047614P.
XX PR 23-MAY-1997; 97US-047615P.
XX PR 23-MAY-1997; 97US-047617P.
XX PR 23-MAY-1997; 97US-047618P.
XX PR 23-MAY-1997; 97US-047632P.
XX PR 23-MAY-1997; 97US-047633P.
XX PR 06-JUN-1997; 97US-048964P.
XX PR 06-JUN-1997; 97US-048974P.
XX PR 13-JUN-1997; 97US-049610P.
XX PR 08-JUL-1997; 97US-051926P.
XX PR 16-JUL-1997; 97US-052874P.
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XX PR 22-AUG-1997; 97US-056630P.
XX PR 22-AUG-1997; 97US-056631P.

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PR 22-AUG-1997; 97US-056632P.
PR 22-AUG-1997; 97US-056636P.
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PR 22-AUG-1997; 97US-056662P.
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PR 22-AUG-1997; 97US-056665P.
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PR 22-AUG-1997; 97US-056882P.
PR 22-AUG-1997; 97US-056884P.
PR 22-AUG-1997; 97US-056886P.
PR 22-AUG-1997; 97US-056887P.
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PR 22-AUG-1997; 97US-056889P.
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PR 22-AUG-1997; 97US-056894P.
PR 22-AUG-1997; 97US-056903P.
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PR 22-AUG-1997; 97US-056910P.
PR 22-AUG-1997; 97US-056911P.
PR 22-AUG-1997; 97US-057761P.
PR 05-SEP-1997; 97US-057650P.
PR 05-SEP-1997; 97US-057659P.
PR 12-SEP-1997; 97US-058785P.
PR 02-OCT-1997; 97US-061060P.
PR 06-MAR-1998; 98WO-US04493.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX XX Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarek DR;
XX PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Perrie AM;
XX PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
XX PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX DR WPI; 2002-634796/68.
XX DR N-PEDB; ABS73538.
XX PT New isolated human secreted protein for diagnosing, preventing,
XX PT treating or ameliorating medical conditions and used as a food additive
XX PT or preservative -
XX PS
XX XX Example 1; SEQ ID NO 360; 129pp; English.
XX CC The invention relates to an isolated protein that is one of 186 human
XX CC secreted proteins, given in the specification, encoded by one of
XX CC 309 cDNA sequences also given in the specification. The protein is used
XX CC in a pharmaceutical composition used to prevent, treat or ameliorate a
XX CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
XX CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
XX CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
XX CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
XX CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
XX CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
XX CC infections caused by bacteria, viruses and fungi and ocular disorders
XX CC e.g. corneal infection. The polypeptides can also be used to aid wound
XX CC healing and epithelial cell proliferation, to prevent skin aging due to
XX CC sunburn, to maintain organs before transplantation, for supporting cell
XX CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
XX CC polypeptides can also be used as a food additive or preservative to
XX CC increase or decrease storage capabilities, fat content, lipid, protein,
XX CC carbohydrate, vitamins, minerals, cofactors and other nutritional
XX CC components. The present sequence represents one of the novel human

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CC secreted proteins of the invention.
 CC Note: This sequence did not form part of the printed specification,
 CC but was obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=6420526B1.

XX SQ Sequence 117 AA;

Query Match 90.0%; Score 36; DB 23; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSW 5
 |||||
 DB 30 LNMSW 34

RESULT 10
 AAU35054
 ID AAU35054 standard; Protein; 464 AA.

XX AC AAU35054;

XX DT 13-FEB-2002 (first entry)

XX DE Enterococcus faecalis cellular proliferation protein #341.

XX KM Antisense; prokaryotic cellular proliferation protein;
 XX antibiotic; antibacterial; drug design.

XX OS Enterococcus faecalis.

XX PN WO200170955-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US09180.

XX PR 21-MAR-2000; 2000US-191078P.

XX PR 23-MAY-2000; 2000US-206848P.

XX PR 26-MAY-2000; 2000US-207727P.

XX PR 23-OCT-2000; 2000US-242578P.

XX PR 27-NOV-2000; 2000US-253625P.

XX PR 22-DEC-2000; 2000US-257931P.

XX PR 16-FEB-2001; 2001US-269308P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Haselbeck R, Ohlsen KL, Zykkind JW, Wall D, Trawick JD, Carr GJ;
 XX PI Yamamoto RT, Xu HH;

XX DR WPI; 2001-611495/70.

XX DR N-PSDB; AAS52913.

XX PT New polynucleotides for the identification and development of
 XX PT antibiotics, comprise sequences of antisense nucleic acids -

XX PS Example 3; Seq ID No 10647; 511pp; English.

XX CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 464 AA;

Query Match 90.0%; Score 36; DB 22; Length 464;
 Best Local Similarity 100.0%; Pred. No. 8.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMSWL 6
 |||||
 DB 422 NMSWL 426

RESULT 11
 AAU33501
 ID AAU33501 standard; Protein; 467 AA.

XX AC AAU33501;

XX DT 14-FEB-2002 (first entry)

XX DE Enterococcus faecalis cellular proliferation protein #137.

XX KM Antisense; prokaryotic cellular proliferation protein;
 XX antibiotic; antibacterial; drug design.

XX OS Enterococcus faecalis.

XX PN WO200170955-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US09180.

XX PR 21-MAR-2000; 2000US-191078P.

XX PR 23-MAY-2000; 2000US-206848P.

XX PR 26-MAY-2000; 2000US-207727P.

XX PR 23-OCT-2000; 2000US-242578P.

XX PR 27-NOV-2000; 2000US-253625P.

XX PR 22-DEC-2000; 2000US-257931P.

XX PR 16-FEB-2001; 2001US-269308P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Haselbeck R, Ohlsen KL, Zykkind JW, Wall D, Trawick JD, Carr GJ;
 XX PI Yamamoto RT, Xu HH;

XX DR WPI; 2001-611495/70.

XX DR N-PSDB; AAS51360.

XX PT New polynucleotides for the identification and development of
 XX PT antibiotics, comprise sequences of antisense nucleic acids -

XX PS Example 3; Seq ID No 4997; 511pp; English.

XX CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 467 AA;

Query Match 90.0%; Score 36; DB 22; Length 467;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NMSWL 6
 |||||
 Db 425 NMSWL 429

RESULT 12

ABP65725 ID ABP65725 standard; Protein; 767 AA.

XX AC ABP65725;

XX DT 19-NOV-2002 (first entry)

XX DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:469.

XX KW Bifidobacterium longum NCC2705; Bifidobacterium; bacterial;
 KW antiarthritic; antibacterial; inhibitor of Salmonella; detection;
 KW identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;
 KW rotavirus; food composition; pharmaceutical composition.

XX OS Bifidobacterium longum.

XX PN EP1227152-A1.

XX PD 31-JUL-2002.

XX PF 30-JAN-2001; 2001EP-0102050.

XX PR 30-JAN-2001; 2001EP-0102050.

XX PA (NEST) SOC PROD NESTLE SA.

XX DR WPI; 2002-668397/72.

XX PT Novel polynucleotide comprising Bifidobacterium genome sequence useful
 XX as a probe or primer for detecting and/or identifying Bifidobacterium
 XX longum in a biological sample -

XX PS Claim 3; SEQ ID 469; 80pp; English.

XX CC The present invention describes a polynucleotide (I) comprising a
 CC sequence of a Bifidobacterium genome selected from the nucleotide
 CC sequences given in AB081842 and AB081843, or a sequence exhibiting at
 CC least 90% identity or which hybridizes with the sequences given in
 CC AB081842 and AB081843. Also described is a polynucleotide (II) encoding
 CC a fusion protein, comprising a sequence selected from 1097 sequences
 CC given in ABP65258 to ABP6354 ligated in frame to a polynucleotide
 CC encoding a heterologous polypeptide. (I) has antiarthritic and
 CC antibacterial activities, and can be used as an inhibitor of Salmonella.
 CC (I) (which is a probe) is useful for the detection and/or identification
 CC of Bifidobacterium longum in a biological sample. A carrier containing
 CC the lactic acid bacterium Bifidobacterium longum NCC2705 (NCM 1-2618)
 CC can be used for preventing and/or treating diarrhoea brought about by
 CC pathogenic bacteria and/or rotavirus. The carrier is a food composition
 CC selected from milk, yogurt, curd, cheese, fermented milks, milk based
 CC fermented products, ice-creams, fermented cereal based products, milk
 CC based powders, infant formula, pet food or a pharmaceutical composition
 CC selected from tablets, liquid bacterial suspensions, dried oral
 CC supplement, wet oral supplement, dry tube feeding or wet tube feeding.
 CC (I) is useful in DNA arrays or chips to carry out analysis of the
 CC expression of the Bifidobacterium gene. AB081844 to AB081850 represent
 CC Bifidobacterium related nucleotide sequences given in the Sequence

CC Listing from the present invention but not mentioned further within the
 CC specification.
 CC N.B. The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied by the
 CC European Patent Office.

XX SQ Sequence 767 AA;

Query Match 90.0%; Score 36; DB 23; Length 767;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNMSW 5
 |||||
 Db 569 LNMSW 573

RESULT 13

ABB08725 ID ABB08725 standard; peptide; 6 AA.

XX AC ABB08725;

XX DT 14-JUN-2002 (first entry)

XX DE IKKbeta NEMO binding domain peptide SEQ ID NO 2.

XX KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocytes; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cystostatic; nootropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasclerotic; antiallergic;
 KW dermatological; antibacterial; antiparasitic; antineoplastic;
 KW antiarthritic; osteopathic; antitumor.

XX OS Homo sapiens.

XX PN WO200183547-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US40654.

XX PR 02-MAY-2001; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (UYVA) UNIV YALE.

XX PI May MJ, Ghosh S;

XX DR WPI; 2002-179350/23.

XX PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 XX PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 XX PT cell with an anti-inflammatory compound comprising at least one NEMO
 XX binding domain -

XX PS Claim 23; Page 44; 82pp; English.

XX CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB077313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IKKalpha. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast

PA (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX MPI; 2002-121889/16.

DR Novel antiinflammatory compound comprising membrane translocation

XX domain fused to NEMO binding sequence, useful for blocking nuclear

PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis -

XX Example 6; Page 47; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence

CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,

CC cytoprotective, antipsoriatic, antineumatic, antiarthritic, osteopathic,

CC antibacterial, immunosuppressive, dermatological, neuroprotective,

CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFKappaB

CC activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at

CC the NEMO binding domain that results in inhibition of IKKbeta kinase

CC activation and subsequent decreased phosphorylation of IkkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,

CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,

CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia

CC telangiectasia. The compounds are also useful for treating

CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.

XX

XX

XX

XX

XX

XX

XX

SO Sequence 6 AA:

Query Match 87.5%; Score 35; DB 23; Length 6;

Best Local Similarity 83.3%; Pred. No. 9.3e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6

DB 1 LDMWSL 6

Search completed: February 18, 2004, 14:26:21

Job time : 23.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-8

Perfect score: 39
Sequence: 1 LEWSWL 6

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	6	10 US-09-847-940B-8	Sequence 8, Appli
2	39	100.0	6	10 US-09-847-946A-8	Sequence 8, Appli
3	36	92.3	6	10 US-09-847-940B-2	Sequence 2, Appli
4	36	92.3	6	11 US-09-847-946A-2	Sequence 2, Appli
5	36	92.3	6	11 US-09-847-946A-33	Sequence 33, Appli
6	36	92.3	7	11 US-09-847-946A-37	Sequence 37, Appli
7	36	92.3	8	11 US-09-847-946A-30	Sequence 30, Appli
8	36	92.3	8	11 US-09-847-946A-38	Sequence 38, Appli
9	36	92.3	9	11 US-09-847-946A-29	Sequence 29, Appli
10	36	92.3	9	11 US-09-847-946A-32	Sequence 32, Appli
11	36	92.3	9	11 US-09-847-946A-35	Sequence 35, Appli
12	36	92.3	9	11 US-09-847-946A-36	Sequence 36, Appli
13	36	92.3	10	11 US-09-847-946A-31	Sequence 31, Appli
14	36	92.3	10	11 US-09-847-946A-34	Sequence 34, Appli
15	36	92.3	11	11 US-09-847-946A-28	Sequence 28, Appli

16	36	92.3	11	11 US-09-847-946A-132	Sequence 132, App
17	36	92.3	11	11 US-09-847-946A-140	Sequence 140, App
18	36	92.3	13	11 US-09-847-946A-143	Sequence 143, App
19	36	92.3	13	11 US-09-847-946A-144	Sequence 144, App
20	36	92.3	13	11 US-09-847-946A-145	Sequence 145, App
21	36	92.3	13	11 US-09-847-946A-148	Sequence 148, App
22	36	92.3	17	11 US-09-847-946A-141	Sequence 141, App
23	36	92.3	17	11 US-09-847-946A-142	Sequence 142, App
24	36	92.3	17	11 US-09-847-946A-146	Sequence 146, App
25	36	92.3	17	11 US-09-847-946A-147	Sequence 147, App
26	36	92.3	18	11 US-09-847-946A-131	Sequence 131, App
27	36	92.3	18	11 US-09-847-946A-135	Sequence 135, App
28	36	92.3	18	11 US-09-847-946A-136	Sequence 136, App
29	36	92.3	22	11 US-09-847-946A-133	Sequence 133, App
30	36	92.3	22	11 US-09-847-946A-134	Sequence 134, App
31	36	92.3	22	11 US-09-847-946A-137	Sequence 137, App
32	36	92.3	22	11 US-09-847-946A-138	Sequence 138, App
33	36	92.3	22	11 US-09-847-946A-139	Sequence 139, App
34	36	92.3	28	11 US-09-847-940B-18	Sequence 18, Appli
35	36	92.3	28	11 US-09-847-946A-18	Sequence 18, Appli
36	36	92.3	28	11 US-09-771-161A-141	Sequence 141, App
37	36	92.3	745	9 US-09-796-872-2	Sequence 2, Appli
38	36	92.3	745	10 US-09-844-908-10	Sequence 10, Appli
39	36	92.3	745	10 US-09-844-988-10	Sequence 10, Appli
40	36	92.3	745	12 US-10-408-636-3	Sequence 3, Appli
41	36	92.3	745	12 US-10-394-322A-32	Sequence 32, Appli
42	36	92.3	745	15 US-10-243-408-4	Sequence 4, Appli
43	36	92.3	745	15 US-10-059-585-35	Sequence 35, Appli
44	36	92.3	745	15 US-10-338-462-10	Sequence 10, Appli
45	36	92.3	756	9 US-09-796-872-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-09-847-940B-8
; Sequence 8, Application US/09847940B
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-117CP
; CURRENT APPLICATION NUMBER: US/09/847, 940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643, 260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-8

Query Match 100.0%; Score 39; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LEWSWL 6
DB 1 LEWSWL 6
RESULT 2
US-09-847-946A-8
; Sequence 8, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

```

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-8
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Query Match          100.0%; Score 39; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LEWSWL 6
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Db       1 LDMSWL 6
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RESULT 3
US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2
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Query Match          92.3%; Score 36; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LEWSWL 6
        |||||
Db       1 LDMSWL 6
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RESULT 4
US-09-847-946A-2
; Sequence 2, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
```

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; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-2
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Query Match          92.3%; Score 36; DB 11; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LEWSWL 6
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Db       1 LDMSWL 6
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RESULT 5
US-09-847-946A-33
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; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-33
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Query Match          92.3%; Score 36; DB 11; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LEWSWL 6
        |||||
Db       1 LDMSWL 6
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RESULT 6
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; Sequence 37, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
```


APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-37

Query Match 92.3%; Score 36; DB 11; Length 7;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
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DB 1 LDWSWL 6

RESULT 7
US-09-847-946A-30
Sequence 30, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-30

Query Match 92.3%; Score 36; DB 11; Length 8;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
DB 3 LDWSWL 8

RESULT 8
US-09-847-946A-38
Sequence 38, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:

APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 38
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-38

Query Match 92.3%; Score 36; DB 11; Length 8;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
DB 1 LDWSWL 6

RESULT 9
US-09-847-946A-29
Sequence 29, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-29

Query Match 92.3%; Score 36; DB 11; Length 9;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
DB 1 LDWSWL 6

RESULT 10
US-09-847-946A-32

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Sequence 32, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIORITY FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIORITY FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-32
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Query Match          92.3%; Score 36; DB 11; Length 9;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 1 LEWSWL 6
DB 1 LDMSWL 6
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RESULT 11
US-09-847-946A-35
Sequence 35, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIORITY FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIORITY FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-35
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Query Match          92.3%; Score 36; DB 11; Length 9;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 1 LEWSWL 6
DB 3 LDMSWL 8
```

```
RESULT 12
US-09-847-946A-36
Sequence 36, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIORITY FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIORITY FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-36
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Query Match          92.3%; Score 36; DB 11; Length 9;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 1 LEWSWL 6
DB 2 LDMSWL 7
```

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RESULT 13
US-09-847-946A-31
Sequence 31, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIORITY FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIORITY FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-31
```

```
Query Match          92.3%; Score 36; DB 11; Length 10;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 LEWSWL 6
```

DB 2 LDMSWL 7

RESULT 14
US-09-847-946A-34
Sequence 34, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Flindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hamig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NEMO binding
US-09-847-946A-34

Query Match 92.3%; Score 36; DB 11; Length 10;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEMSWL 6
DB 3 LDMSWL 8

RESULT 15
US-09-847-946A-28
Sequence 28, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Flindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hamig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NEMO binding
US-09-847-946A-28

Query Match 92.3%; Score 36; DB 11; Length 11;
Best Local Similarity 83.3%; Pred. No. 73;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEMSWL 6
DB 3 LDMSWL 8

Search completed: February 18, 2004, 15:41:56
Job time : 16.7529 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds

(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-8

Perfect score: 39

Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_19jun03.*

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	6	23	ABB08730
2	39	100.0	6	23	AAW48513
3	39	100.0	6	24	ABU08423
4	39	100.0	756	23	ABU08423
5	36	92.3	6	23	ABU08725
6	36	92.3	6	23	AAW48530
7	36	92.3	6	23	AAW48655
8	36	92.3	6	24	ABU08418
9	36	92.3	7	23	AAW48534

10	36	92.3	8	23	AAW48527	Anti-inflammatory
11	36	92.3	8	23	AAW48535	Anti-inflammatory
12	36	92.3	9	20	AAW485182	IKK-alpha polypeptide
13	36	92.3	9	23	AAW48526	Anti-inflammatory
14	36	92.3	9	23	AAW48529	Anti-inflammatory
15	36	92.3	9	23	AAW48532	Anti-inflammatory
16	36	92.3	10	23	AAW48533	Anti-inflammatory
17	36	92.3	10	23	ABU07313	IKKbeta NEMO bindi
18	36	92.3	10	23	AAW48528	Anti-inflammatory
19	36	92.3	10	23	AAW48531	Anti-inflammatory
20	36	92.3	11	23	ABU07311	Human NBD peptide
21	36	92.3	11	23	AAW48506	Human NBD peptide
22	36	92.3	11	23	AAW48525	Anti-inflammatory
23	36	92.3	11	23	AAW48533	Anti-inflammatory
24	36	92.3	11	23	AAW48533	Anti-inflammatory
25	36	92.3	13	23	AAW48640	NBD peptide, Synt
26	36	92.3	13	23	AAW48641	Anti-inflammatory
27	36	92.3	13	23	AAW48642	Anti-inflammatory
28	36	92.3	13	23	AAW48645	Anti-inflammatory
29	36	92.3	17	23	AAW48638	Anti-inflammatory
30	36	92.3	17	23	AAW48639	Anti-inflammatory
31	36	92.3	17	23	AAW48643	Anti-inflammatory
32	36	92.3	18	23	AAW48628	Anti-inflammatory
33	36	92.3	18	23	AAW48629	Anti-inflammatory
34	36	92.3	18	23	AAW48632	Anti-inflammatory
35	36	92.3	18	23	AAW48633	Anti-inflammatory
36	36	92.3	22	23	AAW48630	Anti-inflammatory
37	36	92.3	22	23	AAW48631	Anti-inflammatory
38	36	92.3	22	23	AAW48634	Anti-inflammatory
39	36	92.3	22	23	AAW48635	Anti-inflammatory
40	36	92.3	22	23	AAW48636	Anti-inflammatory
41	36	92.3	22	23	AAW48637	Anti-inflammatory
42	36	92.3	28	23	ABU08740	IKKbeta NEMO bindi
43	36	92.3	28	23	AAW48523	NBD peptide SEQ ID
44	36	92.3	28	24	ABU08434	wild-type human NE
45	36	92.3	36	23	AAW48652	IKKbeta mutated pe

ALIGNMENTS

RESULT 1	ABB08730	standard; peptide; 6 AA.
AC	ABB08730;	
DT	14-JUN-2002	(first entry)
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 8.	
XX	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
XX	kinase activation; leukocyte; inflammation; B-selectin; osteoclast;	
XX	autoimmune disease; transplant rejection; osteoporosis; cancer;	
XX	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
XX	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
XX	corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;	
XX	osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;	
XX	antiartherosclerotic; vinorelbine; antiaesthatic; antiallergic;	
XX	dermatological; antibacterial; antipruritic; antineumatic;	
XX	antiarthritic; osteopathic; antitumor; mutant; mutein.	
OS	Homo sapiens.	
XX	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference 2	/note="Wildtype Asp substituted by Glu"
PN	WO200183547-A2.	
XX	08-NOV-2001.	
PD		
XX		

PF 02-MAY-2001; 2001WO-US40654.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 binding domain -
 XX
 PS Claim 23; Page 44; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (AAB08725-AAB08742) comprising at least one NEMO binding domain
 CC (AAB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of Ikbppa. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC sporadic arthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 CC
 SQ Sequence 6 AA;
 OY
 DB 1 LEMSWL 6
 1 LEMSWL 6
 Query Match 100.0%; Score 39; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 2
 ID AAM48513 standard; Peptide; 6 AA.
 AC AAM48513;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX NBD mutant peptide SEQ ID NO 8.
 DE

XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutrotic;
 XX antineumatic; antiarthritic; osteopathic; antibacterial; virucide;
 XX immunosuppressive; dermatologic; neuroprotective; antiatherosclerotic;
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 XX rheumatoid arthritis; osteoarthritis; inflammation; bowel disease;
 XX autoimmune disorder; multiple sclerosis; transplant rejection;
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRACIS PHARM INC.
 XX (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Finkel MA, Phillips K;
 XX
 XX WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Example 6; Page 47; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neutrotic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 SQ Sequence 6 AA;
 OY
 DB 1 LEMSWL 6
 1 LEMSWL 6
 Query Match 100.0%; Score 39; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 ID ABU08423 standard; peptide; 6 AA.
 ABU08423

XX AC ABU08423;
 XX XX 12-JUN-2003 (first entry)
 XX DT
 XX DE Human NEMO binding site (NBD) mutant peptide #6.
 XX XX
 XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IKKappab kinase-beta; IKKappab kinase-alpha; IKKalpha; NF-kappab;
 KW nuclear factor-kappab induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplacental detection; immunosuppressive; osteopathic;
 KW cytopathic; noctropic; neuroprotective; antithrombotic; virucide;
 KW vasotropic; antineumatic; antitartaric; mutant; mutain.
 XX XX
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX XX
 XX PN US2002156000-A1.
 XX XX
 XX PD 24-OCT-2002.
 XX XX
 XX PF 02-MAY-2001; 2001US-0847940.
 XX XX
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX XX
 XX PA (MAYM/) MAY M J.
 XX PA (GHOS/) GHOSH S.
 XX XX
 XX PI May MJ, Ghosh S;
 XX XX
 XX DR WPI; 2003-209142/20.
 XX XX
 XX PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappab induction in a cell and for
 PT treating NF-kappab-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX XX
 XX PS Claim 22; Page 17; 47pp; English.
 XX XX
 XX CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on Ikappab kinase-beta (IKKbeta) and Ikappab kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappab (NF-kappab) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappab induction by IKK but do not inhibit
 CC the basal activity of NF-kappab. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 XX CC
 XX SQ Sequence 6 AA;
 XX
 XX Query Match 100.0%; Score 39; DB 24; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 LEWSWL 6
 XX | | | | |
 XX Db 1 LEWSWL 6
 XX
 XX RESULT 4
 XX ABB77305
 XX ID ABB77305 standard; protein; 756 AA.
 XX

AC ABB77305;
 XX XX 14-JUN-2002 (first entry)
 XX DT
 XX XX
 XX DE Human IKKbeta mutant D738E.
 XX XX
 XX KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappab; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; noctropic; neuroprotective; anti-HIV; human;
 KW dermatolosciclerotic; virucide; antiaesthetic; antiallergic;
 KW dermatological; antibacterial; antiparasitic; antineumatic;
 KW antitartaric; osteopathic; antitumor; mutant; mutain.
 XX XX
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX XX
 XX OS
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 738 /note="Wildtype Asp substituted by Glu"
 XX FT
 XX XX
 XX PN WO200183547-A2.
 XX XX
 XX PD 08-NOV-2001.
 XX XX
 XX PF 02-MAY-2001; 2001WO-US40654.
 XX XX
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX XX
 XX PA (UYVA) UNIV YALB.
 XX XX
 XX PI May MJ, Ghosh S;
 XX XX
 XX DR WPI; 2002-179350/23.
 XX XX
 XX PT Modulating NF-kappab induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprising contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX XX
 XX PS Example 11; Page -; 82pp; English.
 XX XX
 XX CC The invention relates to modulating NF-kappab (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of Ikappab. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyomyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,

CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of an IKKbeta
CC mutant, useful in examples of the invention.
CC Note: The present sequence is not given in the specification but is
CC derived from GenBank Accession No. 014920 (ABB77294).

SO Sequence 756 AA;
Query Match 100.0%; Score 39; DB 23; Length 756;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6
Db 737 LEWSWL 742

RESULT 5
ID ABB08725 standard; peptide; 6 AA.
AC ABB08725;
XX
XX 14-JUN-2002 (first entry)
XX
XX IKKbeta NEMO binding domain peptide SEQ ID NO 2.
XX
XX IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
XX kinase activation; leukocyte; inflammation; B-selectin; osteoclast;
XX autoimmunity disease; transplant rejection; osteoporosis; cancer;
XX Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
XX rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
XX corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
XX osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
XX antiatherosclerotic; virucide; antiaesthetic; antiallergic;
XX dermatological; antibacterial; antiparasitic; antineurotic;
XX antirheumatic; osteopathic; antitumor.

OS Homo sapiens.
XX
XX WO200183547-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US40654.
XX
XX 02-MAY-2000; 2000US-201261P.
XX 22-AUG-2000; 2000US-0643260.
XX
XX (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S;
XX
XX WPI; 2002-179350/23.
XX
XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
XX PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
XX PT cell with an anti-inflammatory compound comprising at least one NEMO
XX PT binding domain
XX
XX Claim 23; Page 44; 82pp; English.

CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC comprises contacting a cell with an anti-inflammatory compound
CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
CC (ABB77313). The compound has acts through selective inhibition of
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC interaction results in inhibition of IKKbeta kinase activation and

CC subsequent decreased phosphorylation of Ikbapp. The compound may also
CC act (directly or indirectly) by blocking the recruitment of leukocytes
CC into sites of acute and chronic inflammation. By down-regulating the
CC expression of B-selectin on leukocytes or by blocking osteoclast
CC differentiation. The compound is useful in treating NF-kB mediated
CC conditions, where the condition is an inflammatory disorder, an
CC autoimmune disease, transplant rejection, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC telangiectasia. The inflammatory disorder is asthma, allergies,
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC polyoma, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC diseases include HIV and influenza. The compound may also be useful for
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of the NEMO
CC binding domain of IKKbeta.

SO Sequence 6 AA;
Query Match 92.3%; Score 36; DB 23; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6
Db 1 LEWSWL 6

RESULT 6
ID AAM48530 standard; Peptide; 6 AA.
XX
XX AAM48530;
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 33.
XX
XX Anti-inflammatory; antiaesthetic; cytostatic; antiparasitic; nootropic;
XX anti-inflammatory; antiaesthetic; cytostatic; antiparasitic; nootropic;
XX antirheumatic; antiaesthetic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX allergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX 02-MAY-2000; 2000US-201261P.
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX (UYVA) UNIV YALE.
XX

PI	May MJ, Ghosh S, Findels MA, Phillips K;
XX	WPL; 2002-121889/16.
DR	
XX	
PT	Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
PT	peoriatis -
XX	
PS	Claim 6; Page 61; 88pp; English.
CC	The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic, cyrostatic, antipsoeatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nocotropic, antialtherosclerotic, virocidic and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of Ikappab kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of Ikappab. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.
XX	
SQ	Sequence 6 AA;
Query Match	92.3%; Score 36; DB 23; Length 6;
Bact Local Similarity	83.3%; Pred. NO. 9.3e+05;
Matches	5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY	1 LEMSGL 6 : 1 LDMSWL 6
Dd	
RESULT 7	
AAM48655	ID AAM48655 standard; Peptide; 6 AA.
XX	
AC	AAM48655;
XX	
DT	20-MAR-2002 (first entry)
DE	NBD mutant peptide SEQ ID NO 2.
XX	
KM	Antiinflammatory; antiaesthetic; cyrostatic; antipsoeatic; nocotropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic; immunosuppressive; dermatological; neuroprotective; antialtherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytotoxic; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	
OS	Synthetic.
XX	
PN	WO200183554-A2.
XX	
PD	08-NOV-2001.
XX	
PF	02-MAY-2001; 2001WO-US14346.
XX	

PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-064326C.
XX	
PA	(PRAE-) PRAECTIS PHARM INC.
PA	(UYVA) UNIV YALE.
P1	May MJ, Ghosh S, Findels MA, Phillips K;
XX	
DR	WPI; 2002-112189/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
XX	domain fused to NEMO binding sequence, useful for blocking nuclear
XX	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
PS	
XX	Example 6; Page 47; 88pp; English.
CC	The invention relates to an antiinflammatory compound (especially
CC	AAM48628-AAM48645), comprising a membrane translocation domain
CC	(AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
CC	cytostatic, antipsoriatic, antineumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nootropic, antiatherosclerotic, vitruide and anti-allergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of Ikappab kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of Ikappab. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polyaralgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	dmg or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
SO	Sequence 6 AA;
QY	
Dy	1 LENSML 6 : : : 1 LDMSWL 6
DB	
RESULT 8	
ID	ABU08418 standard; peptide; 6 AA.
AC	ABU08418;
DT	12-JUN-2003 (first entry)
XX	
XX	Human NEMO binding site (NBD) mutant peptide #1.
KM	Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
KM	IkappaB kinase-beta; Ikappab kinase-alpha; IKKalpha; NF-kappaB;
KM	nuclear factor-kappaB induction; inflammatory disorder;
KM	autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
KM	atherosclerosis; viral infection; Ataxia telangiectasia;
KM	transplantation detection; immunosuppressive; osteopathic;
OS	Cytostatic; nootropic; neuroprotective; antiatherosclerotic; vitruide;
OS	vasotropic; antirheumatic; antiarthritic; mutant; mutein.
OS	Homo sapiens.
OS	Synthetic.
XX	

PN US200215600-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 02-MAY-2001; 2001US-0847940.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (MAYM/) MAY M J.
 PA (GHOSH/) GHOSH S.
 PI May MJ, Ghosh S;
 XX
 XX WPI; 2003-209142/20.
 DR N-PSDB; ABX94269, ABX94270.
 XX
 PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 PT
 PS Claim 22; Page 17; 47pp; English.
 XX
 CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infection, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. AB008418-AB008432 represent human
 CC NBD mutant peptides.
 CC
 SQ Sequence 6 AA;
 OY
 Query Match 92.3%; Score 36; DB 24; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 LEMSML 6
 1 LEMSML 6
 ID AAM48534 standard; Peptide; 7 AA.
 XX
 AC AAM48534;
 XX
 DT 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 37.
 XX
 KW Antiinflammatory; antiasthmatic; cytosolic; antipsoriatic; noctropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; vitruide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX

PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 PI May MJ, Ghosh S, Finkels MA, Phillips K;
 XX
 XX WPI; 2002-121889/16.
 DR
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PT
 PS Claim 6; Page 61; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytosolic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC noctropic, antiatherosclerotic, vitruide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 SQ Sequence 7 AA;
 OY
 Query Match 92.3%; Score 36; DB 23; Length 7;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 LEMSML 6
 1 LEMSML 6
 ID AAM48527 standard; Peptide; 8 AA.
 XX
 AC AAM48527;
 XX
 DT 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 30.
 XX
 KW Antiinflammatory; antiasthmatic; cytosolic; antipsoriatic; noctropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; vitruide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW

KM autoimmune disorder; multiple sclerosis; transplant rejection;
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS Synthetic.
XX MO200183554-A2.
PN 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US14346.
PF 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI, 2002-121889/16.
DR Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX Claim 6; Page 61; 88pp; English.
PS The invention relates to an antiinflammatory compound (especially
CC (AAW48628-AAW48645), comprising a membrane translocation domain
CC (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAW48525-AAW48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, vitruclide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
CC Sequence 8 AA;
SQ
XX
XX Query Match 92.3%; Score 36; DB 23; Length 8;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEWSWL 6
|:||||
Db 3 LDMSWL 8
RESULT 11
AAW48535
ID AAW48535 standard; peptide; 8 AA.
XX
XX AAW48535;
AC
XX 20-MAR-2002 (first entry)
DT
XX
XX Anti-inflammatory peptide SEQ ID NO 38.
DE
XX

KM antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KM antirheumatic; antiarthritic; osteopathic; antibacterial; vitruclide;
KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KM anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM autoimmune disorder; multiple sclerosis; transplant rejection;
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS Synthetic.
XX MO200183554-A2.
PN 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US14346.
PF 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI, 2002-121889/16.
DR Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX Claim 6; Page 61; 88pp; English.
PS The invention relates to an antiinflammatory compound (especially
CC (AAW48628-AAW48645), comprising a membrane translocation domain
CC (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAW48525-AAW48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, vitruclide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
CC Sequence 8 AA;
SQ
XX
XX Query Match 92.3%; Score 36; DB 23; Length 8;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEWSWL 6
|:||||
Db 1 LDMSWL 6
RESULT 12
AAW96182
ID AAW96182 standard; peptide; 9 AA.
XX

AC AAW96182;
 XX
 DT 27-APR-1999 (first entry)
 XX
 DE IKK-alpha polypeptide with binding activity.
 XX
 KW I-kappa-B kinase; IKK-alpha; gene expression; modulation;
 KM suppression; activation; tumour necrosis factor; TNF; interleukin-1;
 KM IL-1; TNF receptor associated factor; TRAF.
 XX
 OS Homo sapiens.
 XX
 PN WO9901541-A1.
 XX
 PD 14-JAN-1999.
 XX
 PF 01-JUL-1998; 98WO-US13782.
 XX
 PR 10-JUL-1997; 97US-0890854.
 PR 01-JUL-1997; 97US-0887115.
 XX
 PA (TULSA-) TULARIK INC.
 XX
 PI Cao Z, Regnier C, Roche M,
 DR WPI; 1999-106044/09.
 XX
 PT Newly isolated human kinase Ikappab Kinase (IKK- α) polypeptides -
 PT useful in screening for agents that modulate the interaction of an
 PT IKK polypeptide to a binding target and for modulating signal
 PT transduction involving Ikappab in a cell.
 XX
 PS Disclosure; Page -; 32pp; English.
 XX
 CC I-kappa-B kinase (AAW96182), deletion mutants of it retaining
 CC I-kappa-B kinase activity and I-kappa-B polypeptides (comprising a
 CC six residue domain of I-kappa-B containing one of Ser32 and Ser36,
 CC and a candidate agent) can be used to screen for agents that
 CC modulate the interaction of an IKK polypeptide to a binding target.
 CC The modulation of the kinase activity of IKK-alpha forms a method
 CC for modulating signal transduction involving I-kappa-B in a cell.
 CC The IKK-alpha polypeptides are useful for generating oligonucleotide
 CC primers and probes for use in the isolation of natural
 CC IKK-alpha-encoding nucleic acids. The nucleic acids are useful as
 CC translatable transcripts, hybridization probes, polymerase chain
 CC reaction (PCR) probes and primers. Their diagnostic applications
 CC include IKK-alpha hybridization probes for identifying wild-type and
 CC mutant IKK-alpha alleles in clinical and laboratory samples.
 CC Therapeutic application includes the use of IKK-alpha nucleic acids
 CC for modulating cellular expression or intracellular
 CC concentration/availability of active IKK-alpha.
 CC Catalytically inactive IKK-alpha mutants suppress NF-kappa-B
 CC activation induced by tissue necrosis factor (TNF), interleukin-1
 CC (IL-1) stimulation, TNF receptor-associated factor (TRAF) and
 CC NF-kappa-B-inducing kinase (NIK) overexpression. Polypeptides of
 CC IKK-alpha showing exemplary binding activity are described in
 CC AAW96182. These peptides all comprise one of Cys30, Glu54,
 CC Leu604, Thr679, Ser684, Thr686 or Ser687 of the full length
 CC IKK-alpha described in AAW96157. Deletion mutants of the invention
 CC comprise at least one of these regions.
 CC N.B. The present sequence is not given in the present specification
 CC but is derived from the sequence given in AAW96157 as specified.
 XX
 SQ Sequence 9 AA;
 Query Match 92.3%; Score 36; DB 20; Length 9;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 AAW96526
 ID AAW96526 Brandard; Peptide; 9 AA.
 XX
 AC AAW96526;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 29.
 XX
 KW Anti-inflammatory; antiasthmatic; cytoskeletal; antiproliferative; nocrotic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappa-B; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Rindels MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappab activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 61; 89pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAW96526-AAW9645), comprising a membrane translocation domain
 CC (AAW96520-AAW9627 or AAW9646-AAW9651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAW96525-AAW9619). The antiinflammatory compounds have antiasthmatic,
 CC cytoskeletal, antiproliferative, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nocrotic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappa-B
 CC activation by blocking interaction of Ikappab Kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of Ikappab. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,
 CC granulomatosis, multiple sclerosis, transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 9 AA;
 Query Match 92.3%; Score 36; DB 23; Length 9;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEWSWL 6
|:|||||
Db 1 LDMSWL 6

RESULT 14
ID AAM48529 standard; Peptide; 9 AA.
XX AAM48529;
XX
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 32.
XX
XX
XX Anti-inflammatory; antiaesthetic; cytosolic; antiproliferative; neurotropic;
XX antineuritic; antiproliferative; osteopathic; antibacterial; vitruvian;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.
XX
XX MO200183554-A2.
XX
XX
XX 08-NOV-2001.
XX
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX
XX 02-MAY-2000; 2000US-201261P.
XX
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX (UYVA) UNIV YALE.
XX
XX
XX May MJ, Ghosh S, Finkelstein MA, Phillips K;
XX
XX WPI; 2002-121889/16.
XX
XX
XX Novel anti-inflammatory compound comprising membrane translocation
XX domain fused to NEMO binding sequence, useful for blocking nuclear
XX factor kappaB activation, and for treating asthma, lung inflammation,
XX psoriasis -
XX
XX
XX Claim 6; Page 61; 88pp; English.

PS The invention relates to an anti-inflammatory compound (especially
XX AAM48628-AAM48645), comprising a membrane translocation domain
XX (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
XX amino acid residues, fused to a NEMO binding sequence
XX (AAM48525-AAM48619). The anti-inflammatory compounds have antiaesthetic,
XX cytosolic, antiproliferative, antineuritic, osteopathic,
XX antibacterial, immunosuppressive, dermatological, neuroprotective,
XX neurotropic, antiatherosclerotic, vitruvian, and anti-allergic activity. The
XX compounds act as selective inhibitors of cytokine-mediated NF-kappaB
XX activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
XX the NEMO binding domain that results in inhibition of IKKbeta kinase
XX activation and subsequent decreased phosphorylation of IkappaB. The
XX compounds are useful for treating inflammatory disorders, e.g. asthma,
XX lung inflammation or cancer, psoriasis, rheumatoid arthritis,
XX osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
XX bursitis, autoimmune diseases such as lupus, polyarthritis, scleroderma,
XX granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
XX Alzheimer's disease; atherosclerosis; viral infections; and ataxia
XX telangiectasia. The compounds are also useful for treating
XX pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
XX drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.
XX
XX Sequence 9 AA;
SQ

Query Match 92.3%; Score 36; DB 23; Length 9;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEWSWL 6
|:|||||
Db 1 LDMSWL 6

RESULT 15
ID AAM48532 standard; Peptide; 9 AA.
XX AAM48532;
XX
XX
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 35.
XX
XX
XX Anti-inflammatory; antiaesthetic; cytosolic; antiproliferative; neurotropic;
XX antineuritic; antiproliferative; osteopathic; antibacterial; vitruvian;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.
XX
XX MO200183554-A2.
XX
XX
XX 08-NOV-2001.
XX
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX
XX 02-MAY-2000; 2000US-201261P.
XX
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX (UYVA) UNIV YALE.
XX
XX
XX May MJ, Ghosh S, Finkelstein MA, Phillips K;
XX
XX WPI; 2002-121889/16.
XX
XX
XX Novel anti-inflammatory compound comprising membrane translocation
XX domain fused to NEMO binding sequence, useful for blocking nuclear
XX factor kappaB activation, and for treating asthma, lung inflammation,
XX psoriasis -
XX
XX
XX Claim 6; Page 61; 88pp; English.

PS The invention relates to an anti-inflammatory compound (especially
XX AAM48628-AAM48645), comprising a membrane translocation domain
XX (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
XX amino acid residues, fused to a NEMO binding sequence
XX (AAM48525-AAM48619). The anti-inflammatory compounds have antiaesthetic,
XX cytosolic, antiproliferative, antineuritic, osteopathic,
XX antibacterial, immunosuppressive, dermatological, neuroprotective,
XX neurotropic, antiatherosclerotic, vitruvian, and anti-allergic activity. The
XX compounds act as selective inhibitors of cytokine-mediated NF-kappaB
XX activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
XX the NEMO binding domain that results in inhibition of IKKbeta kinase
XX activation and subsequent decreased phosphorylation of IkappaB. The
XX compounds are useful for treating inflammatory disorders, e.g. asthma,
XX lung inflammation or cancer, psoriasis, rheumatoid arthritis,
XX osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.

XX
SQ Sequence 9 AA;

Query Match 92.3%; Score 36; DB 23; Length 9;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:|:|:|
Db 3 LDWSWL 8

Search completed: February 18, 2004, 14:26:20
Job time : 22.7763 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-7

Perfect score: 38

Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubppa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	6	10	US-09-847-940B-7
2	38	100.0	6	11	US-09-847-946A-7
3	38	100.0	6	12	US-10-369-493-20896
4	38	100.0	1217	12	US-10-104-047-2283
5	35	92.1	196	16	US-10-080-170-120
6	35	92.1	210	16	US-10-080-170-548
7	35	92.1	1055	9	US-09-759-667A-3
8	34	89.5	56	12	US-09-933-767-359
9	34	89.5	56	15	US-10-023-282-359
10	34	89.5	64	9	US-09-864-761-39808
11	34	89.5	170	12	US-10-104-047-2210
12	34	89.5	449	15	US-10-156-761-7842
13	34	89.5	493	12	US-10-147-324-2
14	34	89.5	544	12	US-10-257-378-17
15	34	89.5	544	15	US-10-067-668-8

16	34	89.5	544	15	US-10-175-686-8	Sequence 8, Appl1
17	34	89.5	659	12	US-10-369-493-12634	Sequence 12634, A
18	34	89.5	821	12	US-10-369-493-7850	Sequence 7850, A
19	33	86.8	6	10	US-09-847-940B-8	Sequence 8, Appl1
20	33	86.8	6	11	US-09-847-946A-8	Sequence 8, Appl1
21	33	86.8	186	15	US-10-106-698-8201	Sequence 8201, Ap
22	33	86.8	288	9	US-09-820-893-74	Sequence 74, Appl
23	33	86.8	323	9	US-09-820-893-131	Sequence 131, Appl
24	33	86.8	323	12	US-10-264-237-1765	Sequence 1765, Ap
25	33	86.8	350	9	US-09-820-893-132	Sequence 132, Appl
26	33	86.8	355	10	US-09-712-363-161	Sequence 161, Appl
27	33	86.8	355	12	US-10-084-843-79	Sequence 79, Appl
28	33	86.8	355	12	US-10-193-002-80	Sequence 80, Appl
29	33	86.8	355	12	US-10-098-732A-2	Sequence 2, Appl1
30	33	86.8	433	16	US-10-080-170-547	Sequence 547, Appl
31	33	86.8	440	16	US-10-080-170-164	Sequence 164, Appl
32	33	86.8	828	12	US-10-369-493-20660	Sequence 20660, A
33	33	86.8	1053	12	US-10-369-493-22733	Sequence 22733, A
34	33	86.8	1569	14	US-10-108-605-303	Sequence 303, Appl
35	32	84.2	6	10	US-09-847-940B-2	Sequence 2, Appl1
36	32	84.2	6	10	US-09-847-940B-9	Sequence 9, Appl1
37	32	84.2	6	11	US-09-847-946A-2	Sequence 2, Appl1
38	32	84.2	6	11	US-09-847-946A-9	Sequence 9, Appl1
39	32	84.2	6	11	US-09-847-946A-33	Sequence 33, Appl1
40	32	84.2	7	11	US-09-847-946A-37	Sequence 37, Appl1
41	32	84.2	8	11	US-09-847-946A-30	Sequence 30, Appl1
42	32	84.2	8	11	US-09-847-946A-38	Sequence 38, Appl1
43	32	84.2	9	11	US-09-847-946A-29	Sequence 29, Appl1
44	32	84.2	9	11	US-09-847-946A-32	Sequence 32, Appl1
45	32	84.2	9	11	US-09-847-946A-35	Sequence 35, Appl1

ALIGNMENTS

RESULT 1
US-09-847-940B-7
; Sequence 7, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-7

Query Match 100.0%; Score 38; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 1 LAMSWL 6
DB 1 LAMSWL 6
RESULT 2
US-09-847-946A-7
; Sequence 7, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar
APPLICANT: Firdels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PFI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NBD peptide
US-09-847-946A-7

Query Match 100.0%; Score 38; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6
Db 1 LAMSWL 6

RESULT 3
US-10-369-493-20896
Sequence 20896, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20896
LENGTH: 872
TYPE: PRT
ORGANISM: SYNECHOCOCCUS SP. WH 8102
US-10-369-493-20896

Query Match 100.0%; Score 38; DB 12; Length 872;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6
Db 692 LAMSWL 697

RESULT 4
US-10-104-047-2263
Sequence 2263, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20030236392A1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2263
LENGTH: 1217
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-2263

Query Match 100.0%; Score 38; DB 12; Length 1217;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6
Db 590 LAMSWL 595

RESULT 5
US-10-080-170-120
Sequence 120, Application US/10080170
Publication No. US20030129601A1
GENERAL INFORMATION:
APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 120
LENGTH: 196
TYPE: PRT
ORGANISM: Mycobacterium leprae
US-10-080-170-120

Query Match 92.1%; Score 35; DB 16; Length 196;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6
Db 109 LAMSWL 114

RESULT 6
US-10-080-170-548
Sequence 548, Application US/10080170
Publication No. US20030129601A1
GENERAL INFORMATION:
APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 548
LENGTH: 210
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-10-080-170-548

Query Match 92.1%; Score 35; DB 16; Length 210;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
:|||||
Db 123 VAMSWL 128

RESULT 7
US-09-759-667A-3
; Sequence 3, Application US/09759667A
; Patent No. US20020064777A1
; GENERAL INFORMATION:
; APPLICANT: Mengiste, Teayye
; APPLICANT: Paszkowski, Jerzy
; TITLE OF INVENTION: Recombination Repair Gene, MIM, from Arabidopsis thaliana
; FILE REFERENCE: S-30568A
; CURRENT APPLICATION NUMBER: US/09/759,667A
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 9815485.9
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 9900760.1
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-759-667A-3

Query Match 92.1%; Score 35; DB 9; Length 1055;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
:|||||
Db 248 LAMSWV 253

RESULT 8
US-09-933-767-359
; Sequence 359, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
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; PRIOR APPLICATION NUMBER: 60/048,896
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; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06

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; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
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; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,897
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,898
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165

;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/073,164
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/085,925
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,921
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,923
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,922
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/092,921
;; PRIOR FILING DATE: 1998-07-15
;; PRIOR APPLICATION NUMBER: 60/094,657
;; PRIOR FILING DATE: 1998-07-30
;; NUMBER OF SEQ ID NOS: 1245
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 359
;; LENGTH: 56
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (56)
;; OTHER INFORMATION: Xaa equals stop translation
US-09-933-767-359

Query Match 89.5%; Score 34; DB 12; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSM 5
|||||
Db 9 LAWSM 13

RESULT 9
US-10-023-282-359
;; Sequence 359, Application US/10023282
;; Publication No. US2003002893A1
;; GENERAL INFORMATION:
;; APPLICANT: Young et al.
;; TITLE OF INVENTION: 207 Human Secreted Proteins
;; FILE REFERENCE: P2007P1
;; CURRENT APPLICATION NUMBER: US/10/023,282
;; CURRENT FILING DATE: 2001-12-20
;; EARLIER APPLICATION NUMBER: 09/205,258
;; EARLIER FILING DATE: 1998-12-04
;; EARLIER APPLICATION NUMBER: PCT/US98/11422
;; EARLIER FILING DATE: 1998-06-04
;; EARLIER APPLICATION NUMBER: 60/048,885
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,375
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,881
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,880
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,896
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,020
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,876
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,895
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,884
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,894
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,971
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,964

;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,882
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,899
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,893
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,900
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,901
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,892
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,915
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,019
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,970
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,972
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,916
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,373
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,875
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,374
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,917
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,949
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,974
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,883
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,897
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,898
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,962
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,963
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,877
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,878
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/070,923
;; EARLIER FILING DATE: 1997-12-18
;; EARLIER APPLICATION NUMBER: 60/092,921
;; EARLIER FILING DATE: 1998-07-15
;; EARLIER APPLICATION NUMBER: 60/094,657
;; EARLIER FILING DATE: 1998-07-30
;; NUMBER OF SEQ ID NOS: 1227
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 359
;; LENGTH: 56
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (56)
;; OTHER INFORMATION: Xaa equals stop translation
US-10-023-282-359

Query Match 89.5%; Score 34; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSM 5
|||||

Db 9 LAMSW 13

RESULT 10
US-09-864-761-39808; Sequence 39808, Application US/09864761
; Patent No. US20020046763A1
; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Aeonica-X-1

; CURRENT FILING DATE: 2001-05-23

; PRIOR FILING DATE: 2000-02-04

; PRIOR FILING DATE: 2000-02-04

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-08-03

; PRIOR FILING DATE: 2000-10-04

; PRIOR FILING DATE: 2000-09-27

; PRIOR FILING DATE: 2001-01-30

; PRIOR FILING DATE: 2001-01-30

; PRIOR FILING DATE: 2001-01-30

; PRIOR FILING DATE: 2001-01-30

; PRIOR FILING DATE: 2001-01-30

; PRIOR FILING DATE: 2001-01-30

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; PRIOR FILING DATE: 2001-01-30

; PRIOR FILING DATE: 2001-01-30

Query Match 89.5%; Score 34; DB 9; Length 64;

Best Local Similarity 100.0%; Pred. No. 5.3e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5
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Db 33 LAMSW 37

RESULT 11

US-10-104-047-2210

; Sequence 2210, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA

; FILE REFERENCE: H1-A0105

; CURRENT FILING DATE: US/10/104,047

; PRIOR FILING DATE: 2002-03-25

; PRIOR FILING DATE:

; NUMBER OF SEQ ID NOS: 4096

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2210

; LENGTH: 170

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-104-047-2210

Query Match 89.5%; Score 34; DB 12; Length 170;

Best Local Similarity 83.3%; Pred. No. 1.1e+03; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSW 6
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Db 162 LAMSW 167

RESULT 12

US-10-156-761-7842

; Sequence 7842, Application US/10156761
; Publication No. US20030115018A1
; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT FILING DATE: 2002-05-29

; PRIOR FILING DATE: 2001-05-10

; PRIOR FILING DATE: 2001-05-10

; PRIOR FILING DATE: 2001-05-10

; PRIOR FILING DATE: 2001-05-10

; PRIOR FILING DATE: 2001-05-10

; PRIOR FILING DATE: 2001-05-10

; PRIOR FILING DATE: 2001-05-10

; PRIOR FILING DATE: 2001-05-10

Query Match 89.5%; Score 34; DB 15; Length 449;

Best Local Similarity 83.3%; Pred. No. 2.3e+03; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSW 6
|||
Db 42 LAMSW 47

RESULT 13
US-10-147-324-2
; Sequence 2, Application US/10147224
; Publication No. US20030215812A1
; GENERAL INFORMATION:
; APPLICANT: MA, YAN-HE
; APPLICANT: XUE, YAN-PEN
; TITLE OF INVENTION: GENE ENCODING B-MANNANASE, ENZYME PREPARATION AND USES
; FILE REFERENCE: 0304-0001
; CURRENT APPLICATION NUMBER: US/10/147,324
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-147-324-2

Query Match 89.5%; Score 34; DB 12; Length 493;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 5
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Db 280 LAMSW 284

RESULT 14
US-10-257-378-17
; Sequence 17, Application US/10257378
; Publication No. US20030190642A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Glenville
; APPLICANT: Peckovich, P. Martin
; APPLICANT: White, Jay
; APPLICANT: Ramshaw, Heather A.
; APPLICANT: Stangle, Wayne A.
; TITLE OF INVENTION: A Thymus Expressed Human Cytochrome P450 (P450TEC)
; FILE REFERENCE: 11812-65
; CURRENT APPLICATION NUMBER: US/10/257,378
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/208,785
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/198,617
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-378-17

Query Match 89.5%; Score 34; DB 12; Length 544;
Best Local Similarity 83.3%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LAMSWL 6
| | | | |
Db 46 LAMSWL 51

RESULT 15
US-10-067-668-8
; Sequence 8, Application US/10067668
; Publication No. US20030022334A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN
; TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-136001

; CURRENT APPLICATION NUMBER: US/10/067,668
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-668-8

Query Match 89.5%; Score 34; DB 15; Length 544;
Best Local Similarity 83.3%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LAMSWL 6
| | | | |
Db 46 LAMSWL 51

Search completed: February 18, 2004, 15:41:56
Job time : 17.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-7

Sequence: 1 LAMSWL 6

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38 100.0	6	23	ABB08729	Mutated IKKbeta NE
2	38 100.0	6	23	AA048512	NBD mutant peptide
3	38 100.0	6	24	ABU08422	Human NEMO binding
4	38 100.0	756	23	ABB77303	Human IKKbeta muta
5	35 92.1	196	22	AAU62777	Propionibacterium
6	35 92.1	196	23	ABU05469	M. tuberculosis an
7	35 92.1	210	22	ABU05897	M. tuberculosis an
8	35 92.1	321	23	ABB64219	Drosophila melanog
9	35 92.1	329	22	ABB71850	Drosophila melanog

10	35	92.1	1055	21	AAV44787	Arabidopsis thaliana
11	34	89.5	13	20	AAV78379	Human papillomavir
12	34	89.5	56	20	AAW88644	Secreted protein e
13	34	89.5	56	22	ABG55011	Human secreted pro
14	34	89.5	64	22	ABG55123	Human liver peptid
15	34	89.5	64	22	ABB33983	Peptide #7489 enco
16	34	89.5	64	22	ABB24510	Peptide #6509 enco
17	34	89.5	64	22	AAW60730	Human bone marrow
18	34	89.5	64	22	AAW73401	Human brain exper
19	34	89.5	64	22	AAW33604	Peptide #7641 enco
20	34	89.5	64	23	ABG43260	Human peptide enco
21	34	89.5	93	22	AAO03124	Human polypeptide
22	34	89.5	123	22	AAO08298	Human polypeptide
23	34	89.5	138	20	AAV42442	Novel amino acid s
24	34	89.5	140	20	AAV42443	Novel amino acid s
25	34	89.5	164	22	ABG28076	Novel human diagn
26	34	89.5	170	21	AAV87324	Human signal pepti
27	34	89.5	199	22	ABG07731	Novel human diagn
28	34	89.5	320	21	AAV54132	Amino acid sequenc
29	34	89.5	331	21	AAV54127	Amino acid sequenc
30	34	89.5	369	21	AAV54129	Amino acid sequenc
31	34	89.5	432	22	AAU48985	Propionibacterium
32	34	89.5	468	21	AAV44496	Bacillus agardher
33	34	89.5	468	21	AAV54125	Amino acid sequenc
34	34	89.5	468	23	ABB82020	Bacillus mannanase
35	34	89.5	476	21	AAV54123	A mannanase-linker
36	34	89.5	487	22	ABB60890	Drosophila melanog
37	34	89.5	490	21	AAV54122	Amino acid sequenc
38	34	89.5	493	21	AAV44495	Bacillus agardher
39	34	89.5	493	21	AAV54124	Amino acid sequenc
40	34	89.5	493	23	ABG71218	Bacillus alkaline
41	34	89.5	493	23	ABB82019	B. agardherens ma
42	34	89.5	544	23	AAE21061	Human drug metabo
43	34	89.5	544	23	AAU91320	Human P450TEC prot
44	34	89.5	720	22	ABB66438	Drosophila melanog
45	34	89.5	2311	23	ABG95034	Human translocatio

ALIGNMENTS

RESULT 1
ID ABB08729 standard; peptide; 6 AA.
XX ABB08729;
XX
DT 14-JUN-2002 (first entry)
XX
DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 7.
XX
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
KW osteopathic; cytotoxic; nocitropic; neuroprotective; anti-HIV; human;
KW dermatological; antineoplastic; vitinucide; antineoplastic; antineoplastic;
KW antineoplastic; antineoplastic; antineoplastic; antineoplastic;
XX Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note="Wildtype Asp substituted by Ala"
FT
XX WO200183547-A2.
XX
PD 08-NOV-2001.
XX

No art.

PF 02-MAY-2001; 2001MO-US40654.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYVA) UNITV YALB.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprising contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 PS Claim 23; Page 44; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB07313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkbppaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC polyarthritis. Also for Crohn's disease, ulcerative colitis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections,
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SO Sequence 6 AA;
 QY Query Match 100.0%; Score 38; DB 23; Length 6;
 Db Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAWSWL 6
 Db 1 LAWSWL 6
 XX
 AC AAM48512;
 XX 20-MAR-2002 (first entry)
 DT
 XX NBD mutant peptide SEQ ID NO 7.
 DB

XX
 XX Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; neurotropic;
 XX antirheumatic; antiallergic; osteopathic; antibacterial; virucide;
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 XX autoimmune disorder; multiple sclerosis; transplant rejection;
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX
 PD 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001MO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRACIS PHARM INC.
 PA (UYVA) UNITV YALB.
 XX
 PI May MJ, Ghosh S, Faindeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 DR
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Example 6; Page 47; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cyostatic, antipsoriatic, antirheumatic, antiallergic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer; psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SO Sequence 6 AA;
 QY Query Match 100.0%; Score 38; DB 23; Length 6;
 Db Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAWSWL 6
 Db 1 LAWSWL 6
 XX
 AC AAM48422;
 XX 20-MAR-2002 (first entry)
 DT
 XX AAM48422 standard; peptide; 6 AA.
 DB

XX AC ABU08422;
 XX DT 12-JUN-2003 (first entry)
 XX DE Human NEMO binding site (NBD) mutant peptide #5.
 XX KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IKKappab kinase-beta; IKKappab kinase-alpha; IKKalpha; NF-kappab;
 KW nuclear factor-kappab induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antineumatic; antiarthritic; mutant; mutein.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN US2002156000-A1.
 XX PD 24-OCT-2002.
 XX PF 02-MAY-2001; 2001US-0847940.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (MAYM/) MAY M J.
 XX PA (GHOSH/) GHOSH S.
 XX PI May MJ, Ghosh S;
 XX DR WPI; 2003-209142/20.
 XX PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappab induction in a cell and for
 PT treating NF-kappab-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX PS Claim 22; Page 17; 47pp; English.
 XX CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on Ikappab kinase-beta (IKKbeta) and Ikappab kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappab (NF-kappab) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappab induction by IKK but do not inhibit
 CC the basal activity of NF-kappab. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 XX SO Sequence 6 AA;
 XX Query Match 100.0%; Score 38; DB 24; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 LAMSWL 6
 XX Db 1 LAMSWL 6
 XX RESULT 4
 XX ABB77303
 XX ID ABB77303 standard; protein; 756 AA.
 XX

AC ABB77303;
 XX DT 14-JUN-2002 (first entry)
 XX DE Human IKKbeta mutant D738A.
 XX KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappab; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; neuroprotective; anti-HIV; human;
 KW antiatherosclerotic; virucide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antipsoaratic; antirheumatic;
 KW antiarthritic; osteopathic; antitumor; mutant; mutein.
 XX OS Homo sapiens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT MISC-difference 738 /note= "Wildtype Asp substituted by Ala"
 XX FT
 XX PN WO200183547-A2.
 XX PD 08-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-US40654.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (UYVA) UNIV YALE.
 XX PI May MJ, Ghosh S;
 XX DR WPI; 2002-179350/23.
 XX PT Modulating NF-kappab induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX PS Example 11; Page -; 82pp; English.
 XX CC The invention relates to modulating NF-kappab (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of Ikappab. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC

CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKK β gene
 CC mutant, useful in examples of the invention.
 CC Note: The present sequence is not given in the specification but is
 CC derived from GenBank Accession No. O14920 (ABB71294).

SO Sequence 756 AA;

Query Match 100.0%; Score 38; DB 23; Length 756;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 DB 737 LAWSWL 742

RESULT 5

AAU62777 standard; Protein; 196 AA.

AAU62777;

27-FEB-2002 (first entry)

Propionibacterium acnes immunogenic protein #23673.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 XX uveitis; endophthalmitis; bone; joint; central nervous system; EISA;
 XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 XX dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

PN WO200181581-A2.

01-NOV-2001.

20-APR-2001; 2001WO-US12865.

21-APR-2000; 2000US-199047P.

02-JUN-2000; 2000US-208841P.

07-JUL-2000; 2000US-216747P.

(CORI-) CORIXA CORP.

Skelty YAM, Persing DH, Mitcham JL, Wang SS, Bhactia A;
 PI L.malonneuve J, Zhang Y, Jen S, Carter D;

WPI; 2001-616774/71.

N-PSDB; AAS59629.

Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -

Example 1; SEQ ID No 23972; 10699P; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 196 AA;

Query Match 92.1%; Score 35; DB 22; Length 196;
 Best Local Similarity 83.3%; Pred. No. 4.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 DB 102 VAMSWL 107

RESULT 6

ABU05469 standard; Protein; 196 AA.

ABU05469;

08-APR-2003 (first entry)

M. tuberculosis and M. leprae marker protein #120.

XX Mycobacterioses; survival; virulence; protective antigen; vaccine;
 XX mycobacterial diseases; tuberculosis; leprosy.

OS Mycobacterium tuberculosis.

PN WO200274903-A2.

26-SEP-2002.

22-FEB-2002; 2002WO-IB01973.

22-FEB-2001; 2001US-270123P.

(INSP) INST PASTEUR.

Cole S;

WPI; 2002-759885/82.

Identifying and selecting genes for survival or virulence of
 PT mycobacteria by a comparative genomic analysis of the sequences of
 PT Mycobacterium tuberculosis and M. leprae -

Claim 17; Page 288-289; 8749P; English.

XX This invention relates to a novel method for identifying essential genes
 CC for survival or virulence of mycobacteria species. The method comprises
 CC aligning the genomic sequence of a first mycobacterium species on a
 CC genomic sequence of a second mycobacterium species and selecting a
 CC polynucleotide sequence that is highly conserved in both genomes with no
 CC counterparts in other bacterial genomic sequences and that corresponds
 CC to an essential gene for the survival or virulence of mycobacterium
 CC species. The method of the invention is useful for detecting M.
 CC tuberculosis or M. leprae infection. The method reduces the number of
 CC potential new targets and protective antigens for new drugs and vaccine
 CC compositions to treat and prevent mycobacterial diseases, particularly
 CC tuberculosis and leprosy. The present sequence represents a marker
 CC protein from Mycobacterium tuberculosis and Mycobacterium leprae
 CC identified using the method of the invention.

SO Sequence 196 AA;

Query Match 92.1%; Score 35; DB 23; Length 196;
 Best Local Similarity 83.3%; Pred. No. 4.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
 :|||||
 DB 109 VAMSWL 114

RESULT 7

ABU05897
 ID ABU05897 standard; Protein; 210 AA.

XX AC ABU05897;

DT 08-APR-2003 (first entry)

DE M. tuberculosis and M. leprae marker protein #548.

XX KM Mycobacterioses; survival; virulence; protective antigen; vaccine;
 XX KM Mycobacterial disease; tuberculosis; leprosy.

XX OS Mycobacterium tuberculosis.

XX OS Mycobacterium leprae.

XX PN WO200274903-A2.

XX PD 26-SEP-2002.

XX PF 22-FEB-2002; 2002WO-1B01973.

XX PR 22-FEB-2001; 2001US-270123P.

XX PA (INSP) INST PASTEUR.

XX PI Cole S;

XX DR WPI; 2002-759885/82.

XX PT Identifying and selecting genes for survival or virulence of
 PT Mycobacteria by a comparative genomic analysis of the sequences of
 PT Mycobacterium tuberculosis and M. leprae -

XX PS Claim 17; Page 763-764; 874pp; English.

XX CC This invention relates to a novel method for identifying essential genes
 CC for survival or virulence of mycobacteria species. The method comprises
 CC aligning the genomic sequence of a first mycobacterium species on a
 CC genomic sequence of a second mycobacterium species and selecting a
 CC polynucleotide sequence that is highly conserved in both genomes with no
 CC counterparts in other bacterial genomic sequences and that corresponds
 CC to an essential gene for the survival or virulence of mycobacterium
 CC species. The method of the invention is useful for detecting M.
 CC tuberculosis or M. leprae infection. The method reduces the number of
 CC potential new targets and protective antigens for new drugs and vaccine
 CC compositions to treat and prevent mycobacterial diseases, particularly
 CC tuberculosis and leprosy. The present sequence represents a marker
 CC protein from Mycobacterium tuberculosis and Mycobacterium leprae
 CC identified using the method of the invention.

XX SQ Sequence 210 AA;

Query Match 92.1%; Score 35; DB 23; Length 210;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
 :|||||

DB 123 VAMSWL 128

RESULT 8

ABB64219
 ID ABB64219 standard; Protein; 321 AA.

XX AC ABB64219;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 19449.

XX KM Drosophila; developmental biology; cell signalling; insecticide;
 XX KM pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.

XX PR 23-MAR-2000; 2000US-191637P.

XX PR 11-JUL-2000; 2000US-0614150.

XX PA (PEXE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR N-PSDB; ABL08322.

XX DR WPI; 2001-656860/75.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX PS Disclosure; SEQ ID NO 19449; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutic and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
 CC sequences (ABU1840-ABU16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 321 AA;

Query Match 92.1%; Score 35; DB 22; Length 321;
 Best Local Similarity 83.3%; Pred. No. 7.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
 :|||||

DB 64 LMSWML 69

RESULT 9

ABB71850
 ID ABB71850 standard; Protein; 329 AA.

XX AC ABB71850;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 42342.

XX KM Drosophila; developmental biology; cell signalling; insecticide;
 XX KM pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001, 2001WO-US09231.
 XX PR 23-MAR-2000, 2000US-191637P.
 XX PR 11-JUL-2000, 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI, 2001-656860/75.
 XX DR N-PSDB; ABL15953.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT gene from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX PS Disclosure; SEQ ID NO 42342; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA
 CC sequences (ABL10840-ABL16175) and the encoded proteins
 CC (ABBS7737-ABBS72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 329 AA;
 XX
 XX Query Match 92.1%; Score 35; DB 22; Length 329;
 XX Best Local Similarity 83.3%; Pred. No. 7.8e+02;
 XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 LAWSWL 6
 XX |||||
 XX 17 LAWTWL 22
 XX
 XX RESULT 10
 XX AAY44787
 XX ID AAY44787 standard; Protein; 1055 AA.
 XX AC AAY44787;
 XX XX
 XX DT 04-MAY-2000 (first entry)
 XX XX
 XX DE Arabidopsis thaliana recombination repair protein, MIM.
 XX XX
 XX KM MIM, recombination; plant; DNA repair; hypersensitivity;
 XX KM SMC protein family; Structural Maintenance of Chromosomes; MIM,
 XX KM methyl methanesulphonate; irradiation; mitomycin C.
 XX OS
 XX OS Arabidopsis thaliana.
 XX PH
 XX PH Key Location/Qualifiers
 XX FT Binding-site 49..56
 XX FT /label= NTP_binding_domain
 XX FT Region 184..442
 XX FT /label= Colled_coil_region-I
 XX FT Region 443..627
 XX FT /label= Hinge/spacer
 XX FT Region 628..909
 XX FT /label= Colled_coil_region-II
 XX FT Domain 971..1007
 XX FT /label= DA-box

FT FT /note= "conserved motif which harbours a Walker B type
 FT FT NTP binding domain"
 FT PN WO200004174-A1.
 XX PD 27-JAN-2000.
 XX PF 14-JUL-1999; 99WO-EP04984.
 XX PR 16-JUL-1998; 98GB-0015485.
 XX PR 14-JAN-1999; 99GB-0000760.
 XX PA (NOVS) NOVARTIS AG.
 XX PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX PI Mengler T, Paszkowski J;
 XX DR WPI, 2000-182437/16.
 XX DR N-PSDB; AA250145; AA250146.
 XX PT New Arabidopsis polynucleotide encoding protein useful for assisting
 PT recombinant repair of DNA damage in plants -
 XX PS Claim 1; Pages 22-25; 30pp; English.
 XX CC The present sequence is a MIM protein from Arabidopsis thaliana, which
 CC contributes to recombination repair of DNA damage in plant cells.
 CC The protein was tracked down with the help of a T-DNA tagged Arabidopsis
 CC mutant showing hypersensitivity to methyl methanesulphonate (MMS). It
 CC shows homology to a member of SMC (Structural Maintenance of Chromosomes)
 CC protein family and confers hypersensitivity to treatment with MMS,
 CC X-rays, UV light or mitomycin C. The present sequence is useful for DNA
 CC repair in plant cells.
 XX SQ Sequence 1055 AA;
 XX
 XX Query Match 92.1%; Score 35; DB 21; Length 1055;
 XX Best Local Similarity 83.3%; Pred. No. 2.6e+03;
 XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 LAWSWL 6
 XX |||||
 XX 248 LAWSWV 253
 XX
 XX RESULT 11
 XX AAY78379
 XX ID AAY78379 standard; peptide; 13 AA.
 XX AC AAY78379;
 XX XX
 XX DT 08-MAY-2000 (first entry)
 XX XX
 XX DE Human papillomavirus E7 protein inhibiting peptide SEQ ID NO.5.
 XX XX
 XX KM HPV; E7 protein; inhibition; virucide; carcinoma.
 XX OS
 XX OS Human papillomavirus.
 XX OS Synthetic.
 XX PN EP969013-A1.
 XX PD 05-JAN-2000.
 XX PF 30-JUN-1998; 98EP-0112047.
 XX PR 30-JUN-1998; 98EP-0112047.
 XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX PA Jansen-Duerr P, Zwerschke W;
 XX PI WPI, 2000-149116/14.
 XX DR

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XX  New peptides used for the prevention and treatment of human papilloma
PT  virus associated disease .
XX
XX  Claim 1, Page 22, 26pp; English.
XX
CC  AAY78375 to AAY78415 represent peptides capable of inhibiting the human
CC  papillomavirus (HPV) E7 protein. The peptides have virucide activity.
CC  The peptides can be used in pharmaceutical compositions to inhibit
CC  HPV E7 protein, which allows the prevention and/or treatment of HPV
CC  associated diseases, which may comprise carcinomas.
XX
SQ  Sequence 13 AA;

Query Match      89.5%; Score 34; DB 21; Length 13;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 LAMSW 5
    |||||
    3 LAMSW 7

Db

RESULT 12
AAW8644
ID  AAW8644 standard; Protein; 56 AA.
XX
AC  AAW8644;
XX
DT  01-MAR-1999 (first entry)
XX
DE  Secreted protein encoded by gene 111 clone HTMBY29.
XX
XX  Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW  diagnosis; cisase; cancer; tumour; neurodegenerative disorder; leukaemia;
KW  developmental abnormality; foetal deficiency; blood; allergy; renal;
KW  immune system; aschaemia; lymphocytic disease; brain; hepatic; lymphoma;
KW  inflammation; ischaemic shock; Alzheimer's disease; reostoclast; AIDS;
KW  cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW  osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW  endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS  Homo sapiens.
XX
XX  WO9854963-A2.
XX
PD  10-DEC-1998.
XX
XX  04-JUN-1998; 98WC-US11422.
XX
PR  18-DEC-1997; 97US-0070923.
PR  06-JUN-1997; 97US-0048877.
PR  06-JUN-1997; 97US-0048881.
PR  06-JUN-1997; 97US-0048884.
PR  06-JUN-1997; 97US-0048893.
PR  06-JUN-1997; 97US-0048896.
PR  06-JUN-1997; 97US-0048899.
PR  06-JUN-1997; 97US-0048915.
PR  06-JUN-1997; 97US-0048949.
PR  06-JUN-1997; 97US-0048964.
PR  06-JUN-1997; 97US-0048972.
PR  06-JUN-1997; 97US-0049020.
PR  06-JUN-1997; 97US-0049375.
PR  05-SEP-1997; 97US-0057628.
PR  05-SEP-1997; 97US-0057635.
PR  05-SEP-1997; 97US-0057644.
PR  05-SEP-1997; 97US-0057647.
PR  05-SEP-1997; 97US-0057650.
PR  05-SEP-1997; 97US-0057661.
PR  05-SEP-1997; 97US-0057667.
PR  05-SEP-1997; 97US-0057761.
PR  05-SEP-1997; 97US-0057764.
PR  05-SEP-1997; 97US-0057770.

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PR  05-SEP-1997; 97US-0057775.
PR  05-SEP-1997; 97US-0057778.
PR  06-JUN-1997; 97US-0048875.
PR  06-JUN-1997; 97US-0048878.
PR  06-JUN-1997; 97US-0048882.
PR  06-JUN-1997; 97US-0048885.
PR  06-JUN-1997; 97US-0048894.
PR  06-JUN-1997; 97US-0048897.
PR  06-JUN-1997; 97US-0048900.
PR  06-JUN-1997; 97US-0048916.
PR  06-JUN-1997; 97US-0048962.
PR  06-JUN-1997; 97US-0048970.
PR  06-JUN-1997; 97US-0048974.
PR  06-JUN-1997; 97US-0049373.
PR  05-SEP-1997; 97US-0057584.
PR  05-SEP-1997; 97US-0057629.
PR  05-SEP-1997; 97US-0057642.
PR  05-SEP-1997; 97US-0057645.
PR  05-SEP-1997; 97US-0057648.
PR  05-SEP-1997; 97US-0057651.
PR  05-SEP-1997; 97US-0057662.
PR  05-SEP-1997; 97US-0057668.
PR  05-SEP-1997; 97US-0057762.
PR  05-SEP-1997; 97US-0057765.
PR  05-SEP-1997; 97US-0057771.
PR  05-SEP-1997; 97US-0057776.
PR  06-JUN-1997; 97US-0048876.
PR  06-JUN-1997; 97US-0048880.
PR  06-JUN-1997; 97US-0048883.
PR  06-JUN-1997; 97US-0048892.
PR  06-JUN-1997; 97US-0048895.
PR  06-JUN-1997; 97US-0048898.
PR  06-JUN-1997; 97US-0048901.
PR  06-JUN-1997; 97US-0048917.
PR  06-JUN-1997; 97US-0048963.
PR  06-JUN-1997; 97US-0048971.
PR  06-JUN-1997; 97US-0049019.
PR  06-JUN-1997; 97US-0049374.
PR  05-SEP-1997; 97US-0057627.
PR  05-SEP-1997; 97US-0057634.
PR  05-SEP-1997; 97US-0057643.
PR  05-SEP-1997; 97US-0057646.
PR  05-SEP-1997; 97US-0057649.
PR  05-SEP-1997; 97US-0057654.
PR  05-SEP-1997; 97US-0057660.
PR  05-SEP-1997; 97US-0057760.
PR  05-SEP-1997; 97US-0057763.
PR  05-SEP-1997; 97US-0057769.
PR  05-SEP-1997; 97US-0057774.
PR  05-SEP-1997; 97US-0057777.

XX  (HUMA-) HUMAN GENOME SCI INC.
XX
XX  Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA;
PI  Pan P, Feng P, Ferric AM, Fischer CL, Florence C;
PI  Florence K, Greene JM, Hu J, Kyaw H, Latleut DW;
PI  Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM;
PI  Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
XX  MPI; 1999-059665/05.
XX  N-PSDB; AAW84521.
XX
XX  New isolated human genes and the secreted polypeptides they encode -
PT  useful for diagnosis and treatment of e.g. cancer, neurological
PT  disorders, immune diseases, inflammation or blood disorders
XX
XX  Claim 11, Page 542; 772pp; English.
XX
XX  The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
CC  encoding human secreted proteins (AAW88534 to AAW88756). The secreted
CC  protein gene sequences are deposited with the ATCC under deposit numbers
CC  ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
CC  209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host

```

CC cells comprising recombinant vectors containing the nucleic acid
CC sequences are used for the recombinant production of the secreted
CC proteins. The polynucleotide and amino acid sequences are useful for are
CC useful for preventing, treating or ameliorating medical conditions e.g.
CC by protein or gene therapy. Pathological conditions can be also
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the polynucleotides, based on
CC which tissues they are most highly expressed in, and include developing
CC products for the diagnosis or treatment of cancer, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC retinosis, prostate diseases, obesity, disorders involving osteoclasts
CC such as osteoporosis, arthritis or malignancies, diseases of testes,
CC lung or thymus, digestive/endocrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners.
CC The present sequence represents human secreted protein (see descriptor
CC line for gene number and clone identification).

SQ **Sequence** **56 AA;**

Query Match	89.5%	Score 34	DB 20	Length 56
PostgreSQL	100.0%	34	20	56

```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1	LAWSW	5
Db	9	LAWSW	13

RESULT 13

ID ABB50411 standard; Protein; 56 AA.

AC ABB50411

DT 07-FEB-2002 (first entry)

DE Human secreted protein encoded by gene 111 SEQ ID NO:359.

KM Human, secreted protein; immunomodulatory; anti-sclerotic; anti-HIV;
KM dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
KM cytostatic; cardiac; vascular; anti-angiogenic; ophthalmological;
KM neuroprotective; neurotropic; anticonvulsant; antiallers; vulnerable;
KM antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
KM multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
KM human immunodeficiency virus; hyperproliferative disorder; wound healing
KM Gaucher's disease; cardiovascular diseases; Schmitz syndrome; chemotaxis
KM Chagas's cardiomyopathy; coronary arteriosclerosis; angogenic disorder;
KM corneal graft neurovascularization; diabetic retinopathy; regeneration;
KM neurological disorder; Huntington's chorea; Alzheimer's disease;
KM Parkinson's disease; infectious disease; chromosome 10.

Homo sapiens

PN WO200162891-A2.

PD 30-AUG-2001

PF 21-FEB-2001; 2001WO-US05614.

PR 24-FEB-2000; 2000US-184836P.

XX
XX
/TTTTT) TTTTTT CTTTTT TTTT

PA (HUMA-) HUMAN GENOME SCI INC.

PI N1 J, Ehnert R, Lafleur DM, Moore PA, Olsen HS, Rosen CA,
PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y,
PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P
PI Peng P, Andrews GR, Dillon PJ, Carter KC, Brewer LA, Yu G,
PI Zeng Z, Greene JM;

XX WPI; 2001-625724/72.
DR N-PSDB; ABA83304.
DR

PT Nucleic acids enc

PT disease and diabetic retinopathy -

PS Claim 11; Page 1140; 1533pp; English
v

CC ABB50300 to ABB51287 and ABA83194 to ABA83441 represent human secreted
CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
CC activities based on the tissues and cells the genes are expressed in.
CC Example of these activities include: immunomodulatory; antileukrotic;
CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
CC anti-HIV; cytotoxic; cardiant; anti-angiogenic; ophthalmological;
CC neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
CC antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used
CC in gene therapy and vaccine production. (I) and (II) can be used in the
CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
CC Gaucher's disease), cardiovascular diseases (e.g. Schmittar syndrome,
CC Chagas's cardiomyopathy and coronary arteriosclerosis), angiogenic
CC disorders (e.g. corneal graft neovascularization and diabetic
CC retinopathy), neurological disorders (e.g. Huntington's chorea,
CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to
CC ABA83193 and ABB50300 represent sequences used in the exemplification of
CC the present invention.

SQ Sequence 56 AA;

Query Match	Score 34;	DB 22;	Length 56;
89.54;			

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
---------	----	--------------	----	------------	----	--------	----	------	---

QY	1	LAWSW	5
Db	9	LAWSW	13

RESULT 14

ID ABG55123 standard; Peptide; 64 AA

AC ABG55123 ;

DT 25-FEB-2003 (first entry)

DE Human liver peptide, SEQ ID No 33771.

KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia
KW hypercholesterolaemia; coronary heart disease.

OS Homo sapiens.

PN WO200157273-A2

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00664

PR 04-FEB-2000; 2000US-0180312

PR 30-JUN-2000; 2000US-0608408

PR 03-AUG-2000; 2000US-0632366

PR 27-SEP-2000; 2000US-0236359

XX

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488898/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human adult liver -
 XX
 PS Claim 27; SEQ ID No 33771; 658bp; English.
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridizes at high
 CC stringency to a nucleic acid molecule expressed in the human adult
 CC liver. (I) may be used for predicting, measuring and displaying gene
 CC expression in samples derived from human adult liver. The genes
 CC identified may be involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
 CC is associated with coronary heart disease. ABG47348-ABG5930 represent
 CC human liver single exon encoded peptides of the invention.
 CC Note: The sequence information for this patent does not appear in the
 CC printed specification but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX

SO Sequence 64 AA;

Query Match 89.5%; Score 34; DB 22; Length 64;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5
 |||||

DB 33 LAMSW 37

RESULT 15

ABB39983
 ID ABB39983 standard; Peptide; 64 AA.

XX ABB39983;

DT 04-FEB-2002 (first entry)

DE Peptide #7489 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00669.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.

PS Claim 27; SEQ ID NO 32618; 639pp + sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC foetal liver. The present sequence is a peptide encoded by a single exon
 CC nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX

SO Sequence 64 AA;

Query Match 89.5%; Score 34; DB 22; Length 64;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5
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DB 33 LAMSW 37

Search completed: February 18, 2004, 14:26:20
 Job time : 23.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-6
Perfect score: 40
Sequence: 1 ADMSWA 6

Scoring table: BL0SUM62
Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCF_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	11	US-09-847-946A-41
2	40	100.0	6	11	US-09-847-946A-73
3	40	100.0	7	11	US-09-847-946A-77
4	40	100.0	8	11	US-09-847-946A-70
5	40	100.0	8	11	US-09-847-946A-78
6	40	100.0	9	11	US-09-847-946A-69
7	40	100.0	9	11	US-09-847-946A-72
8	40	100.0	9	11	US-09-847-946A-75
9	40	100.0	9	11	US-09-847-946A-76
10	40	100.0	10	11	US-09-847-946A-71
11	40	100.0	10	11	US-09-847-946A-74
12	40	100.0	11	11	US-09-847-946A-68
13	37	92.5	12	12	US-10-441-625-17
14	37	92.5	885	9	US-09-815-242-5090
15	36	90.0	6	10	US-09-847-940B-4

16	36	90.0	6	10	US-09-847-940B-5	Sequence 5, Appl1
17	36	90.0	6	11	US-09-847-946A-4	Sequence 4, Appl1
18	36	90.0	6	11	US-09-847-946A-5	Sequence 5, Appl1
19	36	90.0	6	11	US-09-847-946A-39	Sequence 39, Appl1
20	36	90.0	6	11	US-09-847-946A-40	Sequence 40, Appl1
21	36	90.0	6	11	US-09-847-946A-51	Sequence 51, Appl1
22	36	90.0	6	11	US-09-847-946A-52	Sequence 52, Appl1
23	36	90.0	7	11	US-09-847-946A-62	Sequence 62, Appl1
24	36	90.0	7	11	US-09-847-946A-55	Sequence 55, Appl1
25	36	90.0	8	11	US-09-847-946A-66	Sequence 66, Appl1
26	36	90.0	8	11	US-09-847-946A-56	Sequence 56, Appl1
27	36	90.0	8	11	US-09-847-946A-59	Sequence 59, Appl1
28	36	90.0	8	11	US-09-847-946A-67	Sequence 67, Appl1
29	36	90.0	9	11	US-09-847-946A-47	Sequence 47, Appl1
30	36	90.0	9	11	US-09-847-946A-50	Sequence 50, Appl1
31	36	90.0	9	11	US-09-847-946A-53	Sequence 53, Appl1
32	36	90.0	9	11	US-09-847-946A-54	Sequence 54, Appl1
33	36	90.0	9	11	US-09-847-946A-58	Sequence 58, Appl1
34	36	90.0	9	11	US-09-847-946A-61	Sequence 61, Appl1
35	36	90.0	9	11	US-09-847-946A-64	Sequence 64, Appl1
36	36	90.0	9	11	US-09-847-946A-65	Sequence 65, Appl1
37	36	90.0	10	11	US-09-847-946A-49	Sequence 49, Appl1
38	36	90.0	10	11	US-09-847-946A-52	Sequence 52, Appl1
39	36	90.0	10	11	US-09-847-946A-57	Sequence 57, Appl1
40	36	90.0	10	11	US-09-847-946A-60	Sequence 60, Appl1
41	36	90.0	10	11	US-09-847-946A-63	Sequence 63, Appl1
42	36	90.0	11	11	US-09-847-946A-66	Sequence 66, Appl1
43	36	90.0	173	15	US-10-156-761-15045	Sequence 15045, A
44	36	90.0	174	15	US-10-219-220-163	Sequence 163, App
45	36	90.0	225	15	US-10-219-220-162	Sequence 162, App

ALIGNMENTS

RESULT 1
US-09-847-946A-41
; Sequence 41, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Fingels, Mark A
; APPLICANT: Phillips, Kathryn
; TITLE OF INVENTION: Anti-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NEMO binding
; OTHER INFORMATION: Sequence
US-09-847-946A-41

Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADMSWA 6
Db 1 ADMSWA 6

No 4-7

RESULT 2
US-09-847-946A-73
Sequence 73, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Flindeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-73

Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
|||||
Db 1 ADMSWA 6

RESULT 3
US-09-847-946A-77
Sequence 77, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Flindeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 77
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-77

Query Match 100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
|||||

Db 1 ADMSWA 6
RESULT 4
US-09-847-946A-70
Sequence 70, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Flindeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 70
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-70

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
|||||
Db 3 ADMSWA 8

RESULT 5
US-09-847-946A-78
Sequence 78, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Flindeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 78
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-78

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
Db 1 ADMSWA 6

RESULT 6

US-09-847-946A-69
; Sequence 69, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 69
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
US-09-847-946A-69

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
Db 1 ADMSWA 6

RESULT 7

US-09-847-946A-72
; Sequence 72, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
US-09-847-946A-72

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADMSWA 6
Db 1 ADMSWA 6

RESULT 8

US-09-847-946A-75
; Sequence 75, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 75
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
US-09-847-946A-75

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
Db 3 ADMSWA 8

RESULT 9

US-09-847-946A-76
; Sequence 76, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 76
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding

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OTHER INFORMATION: sequence
US-09-847-946A-76

Query Match          100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
   |||||
Db 2 ADMSWA 7

RESULT 10
US-09-847-946A-71
; Sequence 71, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-71

Query Match          100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
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Db 2 ADMSWA 7

RESULT 11
US-09-847-946A-74
; Sequence 74, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
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ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-74

Query Match          100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
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Db 3 ADMSWA 8

RESULT 12
US-09-847-946A-68
; Sequence 68, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-68

Query Match          100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
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Db 3 ADMSWA 8

RESULT 13
US-10-441-626-17
; Sequence 17, Application US/10441626
; Publication No. US20030186418A1
; GENERAL INFORMATION:
; APPLICANT: Qualiceti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. US20030186418A1e1 Variant EGIII-Like Cellulase
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441,626
; PRIOR FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Glisocladium roseum (3)
US-10-441-626-17
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Query Match 92.5%; Score 37; DB 12; Length 236;
 Best Local Similarity 83.3%; Pred. No. 3.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6
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 DB 63 ADWSMS 68

RESULT 14
 US-09-815-242-5090
 ; Sequence 5090, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; FILE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: PastSeq for Windows Version 4.0
 ; SEQ ID NO 5090
 ; LENGTH: 885
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-815-242-5090

Query Match 92.5%; Score 37; DB 9; Length 885;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6
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 DB 563 ADWSMA 568

RESULT 15
 US-09-847-940B-4
 ; Sequence 4, Application US/09847940B
 ; Patent No. US2002015600A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J.
 ; APPLICANT: Ghosh, Sankar
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-117CP
 ; CURRENT APPLICATION NUMBER: US/09/847,940B
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
 ; US-09-847-940B-4

Query Match 90.0%; Score 36; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSM 5
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 DB 1 ADWSM 5

Search completed: February 18, 2004, 15:41:55
 Job time: 16.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-6
Perfect score: 40
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 1_A_Geneseq_19Jun03:*

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4: /SIDSI/gcgcdata/geneseq/geneseq-emb1/AA1983.DAT:*
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24: /SIDSI/gcgcdata/geneseq/geneseq-emb1/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	AAW48538	Anti-Inflammatory
2	40	100.0	6	AAW48570	Anti-Inflammatory
3	40	100.0	7	AAW48574	Anti-Inflammatory
4	40	100.0	8	AAW48567	Anti-Inflammatory
5	40	100.0	8	AAW48575	Anti-Inflammatory
6	40	100.0	9	AAW48566	Anti-Inflammatory
7	40	100.0	9	AAW48569	Anti-Inflammatory
8	40	100.0	9	AAW48572	Anti-Inflammatory
9	40	100.0	9	AAW48573	Anti-Inflammatory

10	40	100.0	10	23	AAW48568
11	40	100.0	10	23	AAW48571
12	40	100.0	11	23	AAW48565
13	37	92.5	33	22	AAU21305
14	37	92.5	103	20	AAV06332
15	37	92.5	236	20	AAV06363
16	37	92.5	236	21	AAV14876
17	37	92.5	236	21	AAV148341
18	37	92.5	236	23	AAU77428
19	37	92.5	236	23	AAU77584
20	37	92.5	274	23	ABP65718
21	37	92.5	597	22	ABP65635
22	37	92.5	885	22	AAU3594
23	36	90.0	6	23	ABB08727
24	36	90.0	6	23	ABB08728
25	36	90.0	6	23	AAW48509
26	36	90.0	6	23	AAW48510
27	36	90.0	6	23	AAW48536
28	36	90.0	6	23	AAW48537
29	36	90.0	6	23	AAW48548
30	36	90.0	6	23	AAW48559
31	36	90.0	6	24	ABU08420
32	36	90.0	7	23	AAW48552
33	36	90.0	7	23	AAW48563
34	36	90.0	8	23	AAW48545
35	36	90.0	8	23	AAW48553
36	36	90.0	8	23	AAW48556
37	36	90.0	8	23	AAW48564
38	36	90.0	9	23	AAW48544
39	36	90.0	9	23	AAW48547
40	36	90.0	9	23	AAW48550
41	36	90.0	9	23	AAW48551
42	36	90.0	9	23	AAW48555
43	36	90.0	9	23	AAW48558
44	36	90.0	9	23	AAW48561
45	36	90.0	9	23	AAW48561

ALIGNMENTS

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RESULT 1
ID AAW48538 standard; Peptide; 6 AA.
AC AAW48538;
XX
DT 20-MAR-2002 (first entry)
XX
DB Anti-inflammatory peptide SEQ ID NO 41.
XX
XX Anti-inflammatory; antiasthmatic; osteostatic; antipeptidic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; vitruclide;
XX immunosuppressive; dermatological; neuroprotective; antihemostatic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX 02-MAY-2000; 2000US-201261P.
XX
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECS PHARM INC.
```

No cut

PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findels MA, Phillips K;
 XX
 XX WPI, 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6, Page 61, 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiallergic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC borreliis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSWA 6
 DB 1 ADMSWA 6
 AC
 XX AAM48570;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 73.
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KM antirheumatic; antiallergic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN W0200183554-A2.
 XX
 PD 08-NOV-2001.
 XX

PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECTIS PHARM INC.
 PA (UYVA) UNIV YALE.
 PI May MJ, Ghosh S, Findels MA, Phillips K;
 XX
 XX WPI, 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6, Page 62, 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiallergic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC borreliis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSWA 6
 DB 1 ADMSWA 6
 AC
 XX AAM48574;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 77.
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KM antirheumatic; antiallergic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX

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OS Synthetic.
PN WO200183554-A2.
XX
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14346.
PF
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA ) UNIV YALE.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
PI WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PS psoriasis -
XX
XX Claim 6; Page 62; 88pp; English.
PS
XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48625-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cycostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antihypertensive, virocidic and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of Ikappa kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of Ikbappas. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis/ autoimmune diseases such as lupus, polyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 40; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 ADMSWA 6
| | | | |
DB 1 ADMSWA 6
RESULT 4
ID AAM48567 standard; Peptide; 8 AA.
XX
XX AAM48567;
AC
XX 20-MAR-2002 (first entry)
DE
XX Anti-inflammatory peptide SEQ ID NO 70.
XX
XX Antinflammatory; antiasthmatic; cycostatic; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;
XX immunosuppressive; dermatological; neuroprotective; antihypertensive;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;

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KM		cytokine NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
KM		rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM		autoimmune disorder; multiple sclerosis; transplant rejection;
KM		osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM		ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS		Synthetic.
XX		
PN		WO200183554-A2.
XX		
PD		08-NOV-2001.
XX		
PF		02-MAY-2001; 2001WO-US14346.
XX		
PR		02-MAY-2000; 2000US-201261P.
XX		22-AUG-2000; 2000US-0643260.
PA		(PRAE-) PRAECIS PHARM INC.
XX		(UYVA) UNIV YALE.
PI		May MJ, Ghosh S, Findele MA, Phillips K,
DR		WPI; 2002-121889/16.
XX		
PT		Novel antiinflammatory compound comprising membrane translocation
PT		domain fused to NEMO binding sequence, useful for blocking nuclear
PT		factor kappaB activation, and for treating asthma, lung inflammation,
PT		psoriasis -
PS		Claim 6; Page 62; 88pp; English.
XX		
CC		The invention relates to an antiinflammatory compound (especially
CC		AAW48628-AAW48645), comprising a membrane translocation domain
CC		(AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
CC		amino acid residues, fused to a NEMO binding sequence
CC		(AAW48525-AAW48619). The antiinflammatory compounds have antiaesthetic,
CC		cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC		antibacterial, immunosuppressive, dermatological, neuroprotective,
CC		nootropic, antithrombotic, virucide and anti-allergic activity. The
CC		compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC		activation by blocking interaction of Ikappab kinase beta (IKKbeta) at
CC		the NEMO binding domain that results in inhibition of IKKbeta kinase
CC		activation and subsequent decreased phosphorylation of Ikappab. The
CC		compound are useful for treating inflammatory disorders, e.g. asthma,
CC		lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC		osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC		burstils; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC		gastroenteritis, multiple sclerosis; transplant rejection; osteoporosis;
CC		Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC		telangiectasia. The compounds are also useful for treating
CC		pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC		drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC		arthritis.
XX		
SQ		Sequence 8 AA;
QY		
DB		
Query Match		100.0%; Score 40; DB 23; Length 8;
Best Local Similarity		100.0%; Pred. No. 9.3e+5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
ADMSWA 6		1
ADMSWA 8		
RESULT 5		
AAW48575		
ID AAW48575 standard; Peptide; 8 AA.		
AAW48575;		
AC		
DT		20-MAR-2002 (first entry)

DE Anti-Inflammatory peptide SEQ ID NO 78.
 XX
 XX Antinflammatory; antiaesthetic; cyostatic; antiporiatic; nootropic;
 KW antineumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001MO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYTA) UNITV YALE.
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 PT Novel antinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PS
 PS Claim 6; Page 62; 88pp; English.
 XX
 XX The invention relates to an antinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiaesthetic,
 CC cyostatic, antiporiatic, antineumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 CC Sequence 8 AA;
 SO
 Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSWA 6
 DB 1 ADMSWA 6
 RESULT 6
 AAM48566

ID AAM48566 standard; Peptide; 9 AA.
 XX
 XX AAM48566;
 AC
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-Inflammatory peptide SEQ ID NO 69.
 XX
 XX Antinflammatory; antiaesthetic; cyostatic; antiporiatic; nootropic;
 KW antineumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 KW
 OS Synthetic.
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001MO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYTA) UNITV YALE.
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI; 2002-121889/16.
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 PT Novel antinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
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 PS Claim 6; Page 62; 88pp; English.
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 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiaesthetic,
 CC cyostatic, antiporiatic, antineumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 CC Sequence 9 AA;
 SO
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSWA 6

CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADMSWA 6
DB 3 ADMSWA 8
RESULT 9
ID AAM48573 standard; Peptide; 9 AA.
XX AAM48573;
AC
XX
DT 20-MAR-2002 (first entry)
XX
DB Anti-inflammatory peptide SEQ ID NO 76.
XX
XX Anti-inflammatory; antiasthmatic; cytoskeletal; antiporiatic; nootropic;
XX anti-rheumatic; antiarthritic; osteopathic; antibacterial; virocidic;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K,
PI WPI; 2002-121889/16.
DR
XX
XX Novel anti-inflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX Claim 6; Page 62; 88pp; English.
PS
XX The invention relates to an anti-inflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
CC cytoskeletal, antiporiatic, anti-rheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiecholesteric, virocidic and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC burns; autoimmune diseases such as lupus, polyarthritis, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADMSWA 6
DB 2 ADMSWA 7
RESULT 10
ID AAM48568 standard; Peptide; 10 AA.
XX
XX AAM48568;
AC
XX
DT 20-MAR-2002 (first entry)
XX
DB Anti-inflammatory peptide SEQ ID NO 71.
XX
XX Anti-inflammatory; antiasthmatic; cytoskeletal; antiporiatic; nootropic;
XX anti-rheumatic; antiarthritic; osteopathic; antibacterial; virocidic;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K,
PI WPI; 2002-121889/16.
DR
XX
XX Novel anti-inflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX Claim 6; Page 62; 88pp; English.
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CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
CC cytoskeletal, antiporiatic, anti-rheumatic, antiarthritic, osteopathic,

CC antibacterial, immunosuppressive, dermatological, neuroprotective, CC
 CC nootropic, antithrombotic, vitruclide and antiallergic activity. The CC
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB CC
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at CC
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase CC
 CC activation and subsequent decreased phosphorylation of IkappaB. The CC
 CC compounds are useful for treating inflammatory disorders, e.g. asthma, CC
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis, CC
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, CC
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, CC
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; CC
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia CC
 CC telangiectasia. The compounds are also useful for treating CC
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis, CC
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and CC
 CC arthritis.

SO Sequence 10 AA;

Query Match 100.0%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
 |||||
 Db 2 ADMSWA 7

RESULT 11
 AAM48571
 ID AAM48571 standard; Peptide; 10 AA.
 AC AAM48571;

DT 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 74.

KW Antiinflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; vitruclide;
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

XX (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findele MA, Phillips K;

XX WPI; 2002-121889/16.

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 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 PS Claim 6; Page 62; 88pp; English.

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 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
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 CC nootropic, antithrombotic, vitruclide and antiallergic activity. The CC
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, CC
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, CC
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; CC
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia CC
 CC telangiectasia. The compounds are also useful for treating CC
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis, CC
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and CC
 CC arthritis.

SO Sequence 10 AA;

Query Match 100.0%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
 |||||
 Db 3 ADMSWA 8

RESULT 12
 AAM48565
 ID AAM48565 standard; Peptide; 11 AA.

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 68.

KW Antiinflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; vitruclide;
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

XX (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findele MA, Phillips K;

XX WPI; 2002-121889/16.

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PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
PS Claim 6; Page 62; 88pp; English.
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XX
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CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
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CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antiproliferative, antineoplastic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neurotropic, antitumorocytotoxic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
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CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of Ikbppa. The
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CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX
SQ Sequence 11 AA:
Query Match 100.0%; Score 40; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSMA 6
| | | | |
Db 3 ADWSMA 8
RESULT 13
AAU21305
ID AAU21305 standard; Protein: 33 AA.
XX
XX AAU21305;
AC
XX
XX 18-DEC-2001 (first entry)
DT
XX
XX Human novel foetal antigen, SEQ ID NO 1549.
DE
XX
XX Human; foetal tissue antigen; antiinflammatory; neuroprotective;
XX immunomodulator; cardiovascular; cytostatic; nephroprotective;
XX cardiovascular; autoimmune disease; rheumatoid arthritis;
XX hyperproliferative disorder; breast neoplasm; cancer;
XX cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
XX cerebral ischaemia; angiogenesis; nervous system disorder;
XX Alzheimer's disease; infection; ocular disorder; corneal infection;
XX wound healing; epithelial cell proliferation; food additive.
OS Homo sapiens.
XX
XX W0200155312-A2.
FN
XX
XX 02-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-0601331.
PF
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR

PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225477.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226682.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228824.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235634.
PR 27-SEP-2000; 2000US-0235636.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR

20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-024617.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0256719.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251889.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-488782/53.
 XX
 DR N-PSDB; AAS34125.
 XX
 XX New polynucleotides and polypeptides for diagnosing, treating,
 PT preventing or prognosing e.g. diseases or disorders of the nervous,
 PT musculoskeletal, excretory, gastrointestinal, reproductive, and
 PT respiratory systems -
 XX
 XX Claim 11; SEQ ID No 1549; 642bp; English.
 XX
 CC The invention relates to novel nucleic acids encoding novel human foetal

CC antigen. The nucleic acids and proteins are used to prevent, treat (e.g.
 CC by gene therapy) or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
 CC are also used in diagnosing a pathological condition or susceptibility
 CC to a pathological condition. The antibodies to the antigens can also
 CC be used in alleviating symptoms associated with the disorders and in
 CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
 CC immunosorbent assays (ELISA). Disorders which are diagnosed or treated
 CC include autoimmune diseases e.g. rheumatoid arthritis,
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
 CC and ocular disorders e.g. corneal infection. The polypeptides can also
 CC be used to aid wound healing and epithelial cell proliferation, to
 CC prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, for supporting cell culture of primary tissues, to
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used
 CC as a food additive or preservative to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, cofactors and other nutritional components. Numerous
 CC examples of diseases and disorders treated by the nucleic acids and
 CC proteins are given in the specification. The present sequence

Query Match 92.5%; Score 37; DB 22; Length 33;
 Best Local Similarity 83.3%; Pred. No. 19;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
 |||:
 Db 9 ADMTWA 14

RESULT 14
 ID AAY06332 standard; Protein; 103 AA.
 XX AAY06332
 AC AAY06332;
 DT 06-SEP-1999 (first entry)
 XX
 DB Gliocladium roseum EGII-1-like cellulase (partial sequence).
 XX
 KM Cellulase; endoglucanase; EGII; textile; feed additive; baking;
 KM food processing; grain wet milling; pulp; paper.
 OS Gliocladium roseum.
 XX
 PN MO9931255-A2.
 PD 24-JUN-1999.
 XX
 PF 14-DEC-1998; 98WO-US26552.
 XX
 PR 16-DEC-1997; 97US-0991720.
 XX
 PA (GENV) GENENCOR INT INC.
 XX
 PI Bower BS, Fowler T, Phillips JI;
 XX
 DR WPI; 1999-395187/33.
 XX
 PT EGII 1-like cellulase
 XX
 PS Example; Fig 3; 47bp; English.
 CC The present polypeptide represents a partial sequence of a novel
 CC EGII-1-like cellulase of Gliocladium roseum. It was deduced from
 CC a partial gene sequence isolated from genomic DNA using PCR
 CC primers (see AAY59180-91) based on conserved motifs (see AAY06335-29)
 CC of Trichoderma reesei EGII cellulase and related enzymes. PCR
 CC has been used to identify novel EGII-1-like enzymes, including the
 CC present polypeptide, from bacterial and fungal sources (see

CC AAY06331-70). Also provided by the invention are vectors, host
 CC cells and methods for the recombinant production of such enzymes,
 CC which can be used in the treatment of cellulose-containing textiles,
 CC as feed additives, in the treatment of wood pulp, in the reduction
 CC of biomass to glucose, in the stone washing of indigo dyed denim,
 CC or as laundry detergent components (all claimed).

XX Sequence 103 AA;

Query Match 92.5%; Score 37; DB 20; Length 103;

Best Local Similarity 83.3%; Pred. No. 63;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6

DB 29 ADMSWS 34

RESULT 15

AAY06363 ID AAY06363 standard; Protein; 236 AA.

XX AC AAY06363;

XX DT 06-SEP-1999 (first entry)

XX DE Glucocladium roseum EGI11-like cellulase.

XX KM Cellulase; endoglucanase; EGI11; textile; feed additive; baking;

XX KM food processing; grain wet milling; pulp; paper.

XX OS Glucocladium roseum.

XX PN WO931255-A2.

XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98MO-US26552.

XX PR 16-DEC-1997; 97US-0991720.

XX PA (GBMV) GENENCOR INT INC.

XX PI Bower BS, Fowler T, Phillips JT;

XX DR WPI; 1999-395187/33.

XX PT EGI11 like cellulase

XX PS Example; Fig 6; 47pp; English.

XX CC The present polypeptide represents a full-length sequence of a
 CC novel EGI11-like cellulase of Glucocladium roseum. It was deduced
 CC from a gene sequence isolated from genomic DNA using PCR
 CC primers (see AAY59180-91) based on conserved motifs (see AAY06325-29)
 CC of Trichoderma reesei EGI11 cellulase and related enzymes. PCR
 CC has been used to identify novel EGI11-like enzymes, including the
 CC present protein, from bacterial and fungal sources (see AAY06331-70).
 CC The sequence shows homology to T. reesei EGI11 (see AAY06330). Also
 CC provided by the invention are vectors, host cells and methods
 CC for the recombinant production of such enzymes, which can be used
 CC in the treatment of cellulose-containing textiles, as feed
 CC additives, in the treatment of wood pulp, in the reduction of
 CC biomass to glucose, in the stone washing of indigo dyed denim, or
 CC as laundry detergent components (all claimed).

XX SQ Sequence 236 AA;

Query Match 92.5%; Score 37; DB 20; Length 236;

Best Local Similarity 83.3%; Pred. No. 1.5e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6

DB 63 ADMSWS 68

Search completed: February 18, 2004, 14:26:19
 Job time : 22.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-5
Perfect score: 40
Sequence: 1 LDM5MA 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCPUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	242	US-09-345-236B-3	Sequence 3, App1
2	38	95.0	245	US-09-252-991A-22368	Sequence 22368, A
3	37	92.5	316	US-09-252-991A-17312	Sequence 17312, A
4	36	90.0	68	US-09-252-991A-18367	Sequence 18367, A
5	36	90.0	100	US-08-241-853-28	Sequence 28, App1
6	36	90.0	100	US-08-241-853-29	Sequence 29, App1
7	36	90.0	100	US-08-850-917-28	Sequence 28, App1
8	36	90.0	100	US-08-850-917-29	Sequence 29, App1
9	36	90.0	452	US-09-252-991A-21704	Sequence 21704, A
10	36	90.0	745	US-08-887-518-3	Sequence 3, App1
11	36	90.0	745	US-09-023-321-3	Sequence 3, App1
12	36	90.0	745	US-08-890-853-4	Sequence 4, App1
13	36	90.0	745	US-09-032-475-3	Sequence 3, App1
14	36	90.0	745	US-09-032-475-4	Sequence 4, App1
15	36	90.0	745	US-09-032-476-4	Sequence 4, App1
16	36	90.0	745	US-09-032-476-4	Sequence 4, App1
17	36	90.0	745	US-08-890-854-4	Sequence 4, App1
18	36	90.0	745	US-09-023-324-4	Sequence 4, App1
19	36	90.0	745	US-09-168-629-2	Sequence 2, App1
20	36	90.0	745	US-08-910-820-10	Sequence 10, App1
21	36	90.0	745	US-08-910-820-10	Sequence 10, App1
22	36	90.0	745	US-09-109-886-4	Sequence 2, App1
23	36	90.0	745	US-09-844-908-10	Sequence 10, App1
24	36	90.0	745	US-09-868-758-3	Sequence 3, App1
25	36	90.0	756	US-08-887-518-4	Sequence 4, App1
26	36	90.0	756	US-09-023-321-4	Sequence 4, App1
27	36	90.0	756	US-08-890-853-2	Sequence 2, App1

28	36	90.0	756	2	US-09-032-475-4	Sequence 4, App1
29	36	90.0	756	2	US-09-099-125A-2	Sequence 2, App1
30	36	90.0	756	2	US-09-099-125A-2	Sequence 2, App1
31	36	90.0	756	3	US-09-032-476-2	Sequence 2, App1
32	36	90.0	756	3	US-08-890-854-2	Sequence 2, App1
33	36	90.0	756	3	US-09-023-324-2	Sequence 2, App1
34	36	90.0	756	3	US-09-168-629-15	Sequence 15, App1
35	36	90.0	756	3	US-08-910-820-9	Sequence 9, App1
36	36	90.0	756	4	US-09-109-986-2	Sequence 2, App1
37	36	90.0	756	4	US-09-844-908-9	Sequence 9, App1
38	36	90.0	756	4	US-09-868-758-4	Sequence 4, App1
39	36	90.0	982	2	US-08-673-789-4	Sequence 4, App1
40	36	90.0	983	1	US-08-162-809-16	Sequence 16, App1
41	36	90.0	983	1	US-08-167-919A-10	Sequence 10, App1
42	36	90.0	983	2	US-08-449-645A-21	Sequence 21, App1
43	36	90.0	983	3	US-08-702-367A-21	Sequence 21, App1
44	36	90.0	983	3	US-08-715-106-10	Sequence 10, App1
45	36	90.0	983	5	PCT-US95-04681-21	Sequence 21, App1

ALIGNMENTS

RESULT 1
US-09-345-236B-3
Sequence 3, Application US/09345236B
Patent No. 6521454
GENERAL INFORMATION:
APPLICANT: Becnel, James J.
APPLICANT: Tukuo, Fukuda
APPLICANT: Moser, Bettina
APPLICANT: Cockburn, Andrew
APPLICANT: White, Susan B.
APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
FILE REFERENCE: 21042.0004
CURRENT APPLICATION NUMBER: US/09/345,236B
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 242
TYPE: PRT
ORGANISM: mosquito baculovirus
US-09-345-236B-3

Query Match
Best Local Similarity 100.0%; Score 40; DB 4; Length 242;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDM5MA 6
Db 79 LDM5MA 84

RESULT 2
US-09-252-991A-22368
Sequence 22368, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ASERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22368

LENGTH: 445
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22368

Query Match 95.0%; Score 38; DB 4; Length 445;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 LDMSWA 6
303 MDMSWA 308

RESULT 3
US-09-252-991A-17312
Sequence 17312, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17312
LENGTH: 316
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17312

Query Match 92.5%; Score 37; DB 4; Length 316;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 LDMSWA 6
271 LDMSWA 276

RESULT 4
US-09-252-991A-18367
Sequence 18367, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18367
LENGTH: 68
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18367

Query Match 90.0%; Score 36; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 DMSWA 6
|||||

Db 2 DMSWA 6

RESULT 5
US-08-241-853-28
Sequence 28, Application US/08241853
Patent No. 563468
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,853
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-241-853-28

Query Match 90.0%; Score 36; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LDMSW 5
19 LDMSW 23

RESULT 6
US-08-241-853-29
Sequence 29, Application US/08241853
Patent No. 563468
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA

ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,853
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-241-853-29

Query Match 90.0%; Score 36; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
|||||
DB 19 LDMSW 23

RESULT 7
US-08-850-917-28
Sequence 28, Application US/08850917
Patent No. 5854045
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hideaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,917
FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,853
FILING DATE: 12-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-850-917-28

Query Match 90.0%; Score 36; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
|||||
DB 19 LDMSW 23

RESULT 8
US-08-850-917-29
Sequence 29, Application US/08850917
Patent No. 5854045
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hideaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,917
FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,853
FILING DATE: 12-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-850-917-29

Query Match 90.0%; Score 36; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
| | | |
Db 19 LDMSW 23

RESULT 9
US-09-252-991A-21704
Sequence 21704, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21704
LENGTH: 462
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21704

Query Match 90.0%; Score 36; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
| | | |
Db 169 DMSWA 173

RESULT 10
US-08-887-518-3
Sequence 3, Application US/0887518
Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
| | | |
Db 738 LDMSW 742

RESULT 11
US-09-023-321-3
Sequence 3, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
| | | |
Db 738 LDMSW 742

RESULT 12
US-08-890-853-4
Sequence 4, Application US/08890853
Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.

APPLICANT: Moronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
|||||
DB 738 LDMSW 742

RESULT 13
US-09-032-475-3
Sequence 3, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
FILING DATE:
CLASSIFICATION: 435
Prior Application Data:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
|||||
DB 738 LDMSW 742

RESULT 14
US-09-099-125A-4
Sequence 4, Application US/09099125A
Patent No. 5916760
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Moronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
FILING DATE:
CLASSIFICATION:
Prior Application Data:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5

Db 738 LDMSW 742

RESULT 15
US-09-099-124A-4
Sequence 4, Application US/09099124A
Patent No. 5939302
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Moronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,124A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-124A-4

Query Match 90.0%; Score 36; DB 2; Length 745;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
Db 738 LDMSW 742

Search completed: February 18, 2004, 14:41:46
Job time: 7.06579 secs

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OM protein - protein search, using SW model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40
Sequence: 1 LDWSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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12: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT.*
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23: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	ABB08728	Mutated IKKbeta NE
2	40	100.0	6	AA048510	NBD mutant peptide
3	40	100.0	6	AA048537	Anti-inflammatory
4	40	100.0	6	AA048559	Anti-inflammatory
5	40	100.0	6	ABU08421	Human NEMO binding
6	40	100.0	7	AA048563	Anti-inflammatory
7	40	100.0	8	AA048556	Anti-inflammatory
8	40	100.0	8	AA048564	Anti-inflammatory
9	40	100.0	9	AA048555	Anti-inflammatory

10	40	100.0	9	AA048558	Anti-inflammatory
11	40	100.0	9	AA048561	Anti-inflammatory
12	40	100.0	9	AA048562	Anti-inflammatory
13	40	100.0	10	AA048554	Anti-inflammatory
14	40	100.0	10	AA048557	Anti-inflammatory
15	40	100.0	10	AA048560	Anti-inflammatory
16	40	100.0	745	AB077292	Human IKKalpha mut
17	40	100.0	756	AB077309	IKKbeta NEMO bindi
18	36	90.0	6	AB080725	Anti-inflammatory
19	36	90.0	6	AA048530	Anti-inflammatory
20	36	90.0	6	AA048538	Anti-inflammatory
21	36	90.0	6	AA048570	Anti-inflammatory
22	36	90.0	6	AA048555	NBD mutant peptide
23	36	90.0	6	ABU08418	Human NEMO binding
24	36	90.0	7	AA048534	Anti-inflammatory
25	36	90.0	7	AA048574	Anti-inflammatory
26	36	90.0	8	AA048527	Anti-inflammatory
27	36	90.0	8	AA048535	Anti-inflammatory
28	36	90.0	8	AA048567	Anti-inflammatory
29	36	90.0	8	AA048575	Anti-inflammatory
30	36	90.0	9	AA048518	IKK-alpha polypept
31	36	90.0	9	AA048526	Anti-inflammatory
32	36	90.0	9	AA048529	Anti-inflammatory
33	36	90.0	9	AA048532	Anti-inflammatory
34	36	90.0	9	AA048533	Anti-inflammatory
35	36	90.0	9	AA048566	Anti-inflammatory
36	36	90.0	9	AA048569	Anti-inflammatory
37	36	90.0	9	AA048572	Anti-inflammatory
38	36	90.0	9	AA048573	Anti-inflammatory
39	36	90.0	10	AB077313	IKKbeta NEMO bindi
40	36	90.0	10	AA048528	Anti-inflammatory
41	36	90.0	10	AA048531	Anti-inflammatory
42	36	90.0	10	AA048568	Anti-inflammatory
43	36	90.0	10	AA048571	Anti-inflammatory
44	36	90.0	11	AB077311	Human NBD peptide
45	36	90.0	11	AA048506	Human IKKbeta pept

ALIGNMENTS

RESULT 1	AB08728	standard; peptide; 6 AA.
ID	AB08728	
AC	AB08728	
XX	14-JUN-2002	(first entry)
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 5.	
KW	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
KW	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KW	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KW	corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;	
KW	osteopathic; cyclostatic; neotropic; neuroprotective; anti-HIV; human;	
KW	antiarteriosclerotic; vincristine; antiasthmatic; antiallergic;	
KW	dermatological; antibacterial; antipruritic; antirheumatic;	
KW	antiarthritic; osteopathic; anticancer; mutanc; muteln.	
OS	Homo sapiens.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
FT	Misc-difference	/note= "Wildtype Leu substituted by Ala"
FT	WT	
PN	MO200183547-A2.	
PD	08-NOV-2001.	

PF	02-MAY-2001; 2001MO-US40654.
XX	
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-064326O.
XX	
PA	(UYUA) UNIV YALE.
XX	
P1	May MD, Ghosh S;
XX	
DR	WPI; 2002-179350/23.
XX	
PT	Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT	inflammatory disorders, osteoporosis and cancer, comprising contacting a
PT	cell with an anti-inflammatory compound comprising at least one NEMO
PT	binding domain -
PS	Claim 23; Page 44; 82pp; English.
XX	
CC	The invention relates to modulating NF-kappaB (NF-KB) induction in a cell
CC	comprising contacting a cell with an anti-inflammatory compound
CC	(ABB087125-ABB08742) comprising at least one NEMO binding domain
CC	(ABB77313). The compound has acts through selective inhibition of
CC	cyclo-oxygen-mediated NF-kB activation by blocking the interaction of NEMO
CC	with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC	interaction results in inhibition of IKKbeta kinase activation and
CC	subsequent decreased phosphorylation of Ikbappab. The compound may also
CC	act (directly or indirectly) by blocking the recruitment of leukocytes
CC	into sites of acute and chronic inflammation, by down-regulating the
CC	expression of E-selectin on leukocytes or by blocking osteoclast
CC	differentiation. The compound is useful in treating NF-kB mediated
CC	conditions, where the condition is an inflammatory disorder, an
CC	autoimmune disease, transplant rejection, osteoporosis, cancer,
CC	Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC	telangiectasia. The inflammatory disorder is asthma, allergies,
CC	urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC	rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC	bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC	bursitis. The inflammatory disorder may also be dermatitis, eczema,
CC	psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC	spondyloarthritis. Also for Crohn's disease, ulcerative colitis,
CC	polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC	cryoglobulinemia or multiple sclerosis. For chronic viral infections
CC	caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC	diseases include HIV and influenza. The compound may also be useful for
CC	treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC	sunburn or aging. The compound may be used to replace corticosteroids in
CC	any application in which corticosteroids are used, including
CC	immunosuppression in transplants and cancer therapy. Also for identifying
CC	antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC	The compound may be administered alone or in combination with other known
CC	anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC	binding domain of IKKbeta.
XX	
SQ	Sequence 6 AA;
Query Match	100.0%; Score 40; DB 23; Length 6;
Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 LDMSWA 6
Db	1 LDMSWA 6
RESULT 2	
AAM48510	
ID	AAM48510 standard; Peptide; 6 AA.
AC	
XX	AAM48510;
XX	
DT	20-MAR-2002 (first entry)
XX	
NBD	mutant peptide SEQ ID NO 5.

XX Antinflammatory; antiaesthetic; cyrostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-alleergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anophylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001, 2001WO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYTA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K,
 PI WPI, 2002-121889/16.
 DR
 XX
 XX Novel antinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Example 6; Page 47; 88pp; English.
 XX
 XX The invention relates to an antinflammatory compound (especially
 CC AAM48628-AAM48651), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiaesthetic,
 CC cyrostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 93e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSWA 6
 |||||
 Db 1 LDMSWA 6
 |||||

XX	AC	AA049537;
XX	DT	20-MAR-2002 (first entry)
XX	DE	Anti-inflammatory peptide SEQ ID NO 40.
XX	KM	Antiinflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;
KM	KM	antirheumatic; antiauricular; osteopathic; antibacterial; viricide;
KM	KM	immunopreservative; dermatological; neuroprotective; antithrombotic;
KM	KM	antiallergic; membrane translocation domain, NEMO binding domain; eczema;
KM	KM	cytokine; NRKappab; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
KM	KM	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM	KM	autoimmune disorder; multiple sclerosis; transplant rejection;
KM	KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM	KM	ataxia telangiectasia; allergy; anaphylaxis; arthritis.

PE	02-MAY-2001; 2001IMO-US14346
XX	
PR	02-MAY-2000; 2000OUS-201261P
PR	22-AUG-2000; 2000OUS-0643360
XX	
PA	(PRAE-) PRAECTIS PHARM INC.
XX	(UYTA) UNIV YALE.
PA	
XX	
PI	May MJ, Ghosh S, Finkelstein S
DR	WPI; 2002-121889/16.

PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation
PT psoriasis -
XX
PS Claim 6, Page 61; 86pp; English.

PS Claim 6; Page 61; 88pp; English.

XX

CC The invention relates to an antiinflammatory compound (especially
CC AA448628-AA448645), comprising a membrane translocation domain
CC (AA448620-AA448645) or AA448646-AA448651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AA448652-AA446619). The antiinflammatory compounds have antiaesthetic,
CC cytostatic, antiproliferic, antihemmatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatologicall, neuroprotective,
CC neurotropic, antitumorocytotoxic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NF-kappa
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of I-kappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis, autoimmune diseases such as lupus, polyarthritis, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis
CC Alzheimer's disease, atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.

Query Match	100.0%	Score 40	DB 23	length 6
Similarity	100.0%	Pred. No.	9.3e+05	
Beet Local	0	Conservative	0	Indels 0
Matches	6	Mismatches	0	Gaps 0

QY 1 LDWSWA 6
|||||

Db	1	LDMSWA	6
RESULT 4			
AA#48559			
ID	AA#48559	standard; Peptide; 6 AA.	
EV			

DT	20-MAR-2002	(first entry)
XX		
DE	Anti-inflammatory peptide SEQ ID NO 62	

[illegible]

OS	Synthetic.
XX	
PN	WO200183554-A2.
XX	
PD	08-NOV-2001.
XX	
PF	02-MAY-2001; 2001WO-US14346

PR 02-MAY-2000; 2000US-201261P
PR 22-AUG-2000; 2000US-0643260

PA (PRAE-) PRAECIS PHARM INC.
PA (UYTA) UNIV YALE.

PI May MJ, Ghosh S, Findels MA, Phillips K,
XX
DR WPI; 2002-121889/16.

PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Claim 6, Page 62, 88pp; English

CC The invention relates to an anti-inflammatory compound (especially
CC **AMM46528-AMM46645**), comprising a membrane translocation domain
CC (**AMM48620-AMM48627** or **AMM48646-AMM48651**) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (**AMM48525-AMM48619**). The anti-inflammatory compounds have antiasthmatic,
CC cytostatic, antiproliferative, antineoplastic, antirheumatic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neurotropic, antihypertensive, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NF κ B activation
CC by blocking interaction of I κ B kinase beta (IKK β) at
CC the NEMO binding domain that results in inhibition of IKK β kinase
CC activation and subsequent decreased phosphorylation of I κ Bp32. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis, autoimmune diseases such as lupus, polyarthritis, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.

Sequence 6 AA,

Query Match 100.0%; Score 40; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
DB 1 LDMSWA 6

RESULT 5

ABU08421
ID ABU08421 standard; peptide; 6 AA.

AC ABU08421;

DT 12-JUN-2003 (first entry)

XX Human NEMO binding site (NBD) mutant peptide #4.

XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
XX IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
XX nuclear factor-kappaB induction; inflammatory disorder;
XX autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
XX atherosclerosis; viral infection; Ataxia telangiectasia;
XX transglutaminase detection; immunosuppressive; osteopathic;
XX cytoskeletal; neurotrophic; neuroprotective; antiatherosclerotic; virucide;
XX vasostrictive; antirheumatic; antiarthritic; mutant; mutcin.

XX Homo sapiens.
XX Synthetic.

XX US2002156000-A1.

XX 24-OCT-2002.

XX 02-MAY-2001; 2001US-0847940.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (MAYM/) MAY M J.

XX (GHOSH/) GHOSH S.

XX May MJ, Ghosh S;

XX WPI; 2003-209142/20.

XX Novel antiinflammatory peptide compound comprising NEMO binding
XX domain, useful for modulating NF-kappaB induction in a cell and for
XX treating NF-kappaB-mediated inflammation disorders e.g., asthma,
XX psoriasis, vasculitis -

XX Claim 22; Page 17; 47pp; English.

XX The present invention relates to antiinflammatory compounds comprising
XX NEMO binding domain (NBD) peptides. The NEMO binding domains are
XX found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
XX (IKKalpha) proteins. The antiinflammatory compounds of the invention
XX are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
XX in a cell, where the compounds are capable of blocking the interaction
XX between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
XX antiinflammatory compound further comprises at least one membrane
XX translocation domain. The compounds are useful for treating
XX inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
XX Alzheimer's disease, atherosclerosis, viral infections, Ataxia
XX telangiectasia, and for transplant rejection. The compounds of
XX the invention block NF-kappaB induction by IKK but do not inhibit
XX the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
XX NBD mutant peptides.

XX Sequence 6 AA;

XX Query Match 100.0%; Score 40; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
DB 1 LDMSWA 6

RESULT 6

AAM48563
ID AAM48563 standard; Peptide; 7 AA.

AC AAM48563;

DT 20-MAR-2002 (first entry)

XX Anti-inflammatory peptide SEQ ID NO 66.

XX Antiinflammatory; antiaesthetic; cytotoxic; antiproliferative; neurotrophic;
XX antirheumatic; antiaesthetic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NF-kappaB; IkappaB kinase-beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAEIS PHARM INC.

XX (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Pindels MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation
XX domain fused to NEMO binding sequence, useful for blocking nuclear
XX factor kappaB activation, and for treating asthma, lung inflammation,
XX psoriasis -

XX Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
XX AAM48628-AAM48645), comprising a membrane translocation domain
XX (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
XX amino acid residues, fused to a NEMO binding sequence
XX (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
XX cytotoxic, antiproliferative, antirheumatic, antiarthritic, osteopathic,
XX antibacterial, immunosuppressive, dermatological, neuroprotective,
XX neurotrophic, antiatherosclerotic, virucide and antiallergic activity. The
XX compounds act as selective inhibitors of cytokine-mediated NF-kappaB
XX activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
XX the NEMO binding domain that results in inhibition of IKKbeta kinase
XX activation and subsequent decreased phosphorylation of IkappaB. The
XX compounds are useful for treating inflammatory disorders, e.g., asthma,
XX lung inflammation or cancer, psoriasis, rheumatoid arthritis,
XX osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
XX bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,
XX granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
XX Alzheimer's disease; atherosclerosis; viral infections; and ataxia
XX telangiectasia. The compounds are also useful for treating
XX pro-inflammatory responses such as allergies, uterine, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 40; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
 |||||
 Db 1 LDMSWA 6

RESULT 7
 AAM48556
 ID AAM48556 standard; Peptide; 8 AA.
 XX
 AC AAM48556;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 59.
 XX
 KM Antiinflammatory; antiaesthetic; cytostatic; antiporiatic; nootropic;
 KM antineumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antiporiatic, antineumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
 |||||
 Db 3 LDMSWA 8

RESULT 8
 AAM48564
 ID AAM48564 standard; Peptide; 8 AA.
 XX
 AC AAM48564;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 67.
 XX
 KM Antiinflammatory; antiaesthetic; cytostatic; antiporiatic; nootropic;
 KM antineumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antiporiatic, antineumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
SQ Sequence 8 AA;
Query Match 100.0%; Score 40; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSWA 6
DB 1 LDMSWA 6
RESULT 9
ID AAM48555 standard; Peptide; 9 AA.
XX
AC AAM48555;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 58.
XX
KW Anti-inflammatory; antiasthmatic; cytosolic; antipsoriatic; neutrotic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiangiogenic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
XX
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI, 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Claim 6; Page 62; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytosolic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neutrotic, antiatherosclerotic, virucide and antiangiogenic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
SQ Sequence 9 AA;
Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSWA 6
DB 1 LDMSWA 6
RESULT 10
ID AAM48558 standard; Peptide; 9 AA.
XX
AC AAM48558;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 61.
XX
KW Anti-inflammatory; antiasthmatic; cytosolic; antipsoriatic; neutrotic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiangiogenic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
XX
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI, 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT

PR	22-AUG-2000; 2000US-0643260.
XX	(PRAE-) PRAECTIS PHARM INC.
PA	(UYTA) UNIV YALE.
XX	
P1	May MJ, Ghosh S, Findeis MA, Phillips K;
XX	WPI; 2002-121889/16.
DR	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Claim 6, Page 62; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAM48620-AAM48645), comprising a membrane translocation domain
CC	(AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAM48625-AAM48619). The antiinflammatory compounds have antiaesthetic,
CC	cytostatic, antiproliferative, antirheumatic, antiarthritic, osteoprotic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective, The
CC	neotropic, antihypertensive, virucide and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	during or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
SQ	Sequence 9 AA;
	Query Match 100.0%; Score 40; DB 23; Length 9;
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 LDWSWA 6
Dd	2 LDWSWA 7
	RESULT 13
	AAM48554
ID	AAM48554 standard; Peptide; 10 AA.
XX	
XX	AAM48554;
XX	
DT	20-MAR-2002 (first entry)
XX	
XX	Anti-inflammatory peptide SEQ ID NO 57.
KM	Antiinflammatory; antiaesthetic; cytostatic; antiproliferative; neotropic;
KM	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KM	immunosuppressive; dermatologic; neuroprotective; antihypertensive;
KM	antiallergic; moderate translocation domain; NEMO binding domain; eczema;
KM	cyclokin; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KM	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM	autoimmune disorder; multiple sclerosis; transplant rejection;
KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS	Synthetic.
PN	WO200103554-A2.

XX	08-NOV-2001.
PD	
XX	
PF	02-MAY-2001, 2001MO-US14346.
XX	
PR	02-MAY-2000, 2000US-201261P.
PR	22-AUG-2000, 2000US-0643260.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
PA	(UTYA) UNIV YALE.
PI	
PI	May MJ, Ghosh S, Findeis MA, Phillips K,
XX	
XX	WPI, 2002-121889/16.
DR	
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Claim 6; Page 62; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAW48628-AAW48645), comprising a membrane translocation domain
CC	(AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAW48525-AAW48619). The antiinflammatory compounds have antiasthmatic,
CC	cytostatic, antiproliferative, antirheumatic, antiarthritic, osteoprotective,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	neurotropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	burialitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	relangulocastasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
CC	
XX	
XX	
SQ	Sequence 10 AA;
	Query Match 100.0%; Score 40; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 2,6; Mismatches 0; Gaps 0;
	Matches 6; Conservative 0; Indels 0; Gaps 0;
QY	1 LDMSWA 6
DB	2 LDMSWA 7
RESULT 14	
AAW48557	
ID	AAW48557 standard; Peptide; 10 AA.
XX	
AC	AAW48557;
XX	
XX	
DT	20-MAR-2002 (first entry)
XX	
DS	Anti-inflammatory peptide SEQ ID NO 60.
XX	
KW	Antiinflammatory; antiasthmatic; cytostatic; antiproliferative; neurotropic;
KW	antiinflammatory; antiarthritic; osteoprotective; antibacterial; virucide;
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW	anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;

KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYUA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI; 2002-121889/16.
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
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 CC (AAW48620-AAW48645), comprising a membrane translocation domain
 CC (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAW48525-AAW48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 CC
 SQ Sequence 10 AA;
 QY
 DB Query Match 100.0%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSWA 6
 |||||
 DB 2 LDMSWA 7
 |||||
 RESULT 15
 AAW48560
 ID AAW48560 standard; Peptide; 10 AA.
 XX
 AC AAW48560;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 63.
 DE
 XX Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;
 KM

KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYUA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI; 2002-121889/16.
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC (AAW48620-AAW48645), comprising a membrane translocation domain
 CC (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAW48525-AAW48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 CC
 SQ Sequence 10 AA;
 QY
 DB Query Match 100.0%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSWA 6
 |||||
 DB 3 LDMSWA 8
 |||||
 Search completed: February 18, 2004, 14:26:19
 Job time : 23.7763 secs

PF 02-MAY-2001; 2001MO-US40654.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (UYVA) UNIV YALE.
 PA
 PI May MJ, Ghosh S;
 DR WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 PS
 PS Claim 23; Page 44; 82pp; English.
 XX
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (AB808725-AB808742) comprising at least one NEMO binding domain
 CC (AB877313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkbppaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC sporadic lactitis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 QY
 Db 1 ADMSWL 6
 1
 |||||
 1 ADMSWL 6
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 KW Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antihypertensive;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkbppaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 EN
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001MO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Rindeis MA, Phillips K;
 PT WPI; 2002-121889/16.
 DR
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PT
 PS Example 6; Page 47; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48630-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antihypertensive, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkbppaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkbppaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer; psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 XX
 SQ Sequence 6 AA;
 QY
 Db 1 ADMSWL 6
 1
 |||||
 1 ADMSWL 6
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
AC AAM48536;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 39.
XX
KW Anti-inflammatory; antiasthmatic; cytosolic; antiproliferative; neurotrophic;
KW antithrombotic; antidiabetic; osteoporosis; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
XX
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Finkelstein MA, Phillips K,
XX
PI WPI; 2002-121889/16.
XX
DR Novel anti-inflammatory compound comprising membrane translocation
XX
PT domain fused to NEMO binding sequence, useful for blocking nuclear
XX
PT factor kappaB activation, and for treating asthma, lung inflammation,
XX
PT psoriasis -
XX
PS Claim 6; Page 61; 88pp; English.
XX
XX
CC The invention relates to an anti-inflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
CC cytosolic, antiproliferative, antineoplastic, antidiabetic, osteoporotic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neurotrophic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX
SQ Sequence 6 AA;
XX
Query Match 100.0%; Score 40; DB 23; Length 6;
Best Local Similarity 100.0%; P-adj. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 ADMSWL 6
RESULT 4
AAM48548
ID AAM48548 standard; Peptide; 6 AA.
XX
AC AAM48548;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 51.
XX
KW Anti-inflammatory; antiasthmatic; cytosolic; antiproliferative; neurotrophic;
KW antithrombotic; antidiabetic; osteoporotic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
XX
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Finkelstein MA, Phillips K,
XX
PI WPI; 2002-121889/16.
XX
DR Novel anti-inflammatory compound comprising membrane translocation
XX
PT domain fused to NEMO binding sequence, useful for blocking nuclear
XX
PT factor kappaB activation, and for treating asthma, lung inflammation,
XX
PT psoriasis -
XX
PS Claim 6; Page 62; 88pp; English.
XX
XX
CC The invention relates to an anti-inflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
CC cytosolic, antiproliferative, antineoplastic, antidiabetic, osteoporotic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neurotrophic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ADMSWL 6
 |||||
 Db 1 ADMSWL 6

RESULT 5
 ABU08420
 ID ABU08420 standard; peptide: 6 AA.

XX AC ABU08420;
 XX 12-JUN-2003 (first entry)
 XX

DE Human NEMO binding site (NBD) mutant peptide #3.

XX Human, antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cyostatic; neutrotropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasostrictic; antirheumatic; antiarthritic; mutant; muteln.

XX Homo sapiens.
 OS Synthetic.

XX US2002156000-A1.

XX 24-OCT-2002.

XX 02-MAY-2001; 2001US-0847940.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (MAYM/) MAY M J.

XX (GHOSH/) GHOSH S.

XX May MJ, Ghosh S;

XX WPI; 2003-209142/20.

XX Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -

XX Claim 22; Page 17; 47pp; English.

XX The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplant rejection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.

XX Sequence 6 AA;

Query Match 100.0%; Score 40; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ADMSWL 6
 |||||
 Db 1 ADMSWL 6

RESULT 6
 AAM48552
 ID AAM48552 standard; peptide: 7 AA.

XX AC AAM48552;

XX 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 55.

XX Antiinflammatory; antiaesthetic; cyostatic; antiprotic; neutrotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

XX (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Finkel MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -

XX Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAM48528-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cyostatic, antiprotic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neutrotropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 40; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWL 6
 Db 1 ADMSWL 6

RESULT 7
 AAM48545 standard; Peptide; 8 AA.
 XX
 AC AAM48545;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 48.
 XX
 KW Anti-inflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PP 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis.

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWL 6
 Db 3 ADMSWL 8

RESULT 8
 AAM48553 standard; Peptide; 8 AA.
 XX
 AC AAM48553;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 56.
 XX
 KW Anti-inflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PP 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
SQ Sequence 8 AA;
Query Match 100.0%; Score 40; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ADMSWL 6
DB 1 ADMSWL 6
RESULT 9
ID AAM48544 standard; Peptide; 9 AA.
XX AAM48544;
AC
XX
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 47.
XX
XX Antinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS Synthetic.
XX
XX WO200183554-A2.
XX
XX PD 08-NOV-2001.
XX
XX PF 02-MAY-2001; 2001WO-US14346.
XX
XX PR 02-MAY-2000; 2000US-201261P.
XX PR 22-AUG-2000; 2000US-0643260.
XX
XX PA (PRAE-) PRAECIS PHARM INC.
XX PA (UYVA) UNIV YALE.
XX
XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX DR Novel antinflammatory compound comprising membrane translocation
XX PT domain fused to NEMO binding sequence, useful for blocking nuclear
XX PT factor kappaB activation, and for treating asthma, lung inflammation,
XX PT psoriasis -
XX
XX PS Claim 6; Page 62; 88pp; English.
XX
XX The invention relates to an antinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antinflammatory compounds have antiaesthetic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
SQ Sequence 9 AA;
Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ADMSWL 6
DB 1 ADMSWL 6
RESULT 10
ID AAM48547
XX AAM48547 standard; Peptide; 9 AA.
XX
XX AC AAM48547;
XX
XX DT 20-MAR-2002 (first entry)
XX
XX DE Anti-inflammatory peptide SEQ ID NO 50.
XX
XX Antinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS Synthetic.
XX
XX XX WO200183554-A2.
XX
XX PN 08-NOV-2001.
XX
XX PD 02-MAY-2001; 2001WO-US14346.
XX
XX PF 02-MAY-2000; 2000US-201261P.
XX PR 22-AUG-2000; 2000US-0643260.
XX
XX PA (PRAE-) PRAECIS PHARM INC.
XX PA (UYVA) UNIV YALE.
XX
XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX DR Novel antinflammatory compound comprising membrane translocation
XX PT domain fused to NEMO binding sequence, useful for blocking nuclear
XX PT factor kappaB activation, and for treating asthma, lung inflammation,
XX PT psoriasis -
XX
XX PS Claim 6; Page 62; 88pp; English.
XX
XX The invention relates to an antinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain

PT proctiasis -
 XX Claim 6, Page 62; 88pp; English.
 PS
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipneumatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFKappaB
 CC activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSWL 6
 DB 1 ADMSWL 6
 RESULT 11
 AAM48550 standard; Peptide; 9 AA.
 XX
 AC AAM48550;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 53.
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipneumatic; nootropic;
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFKappaB; IkkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 PD 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECTIS PHARM INC.
 PA (UYA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findels MA, Phillips K;

XX
 DR WPI, 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT proctiasis -
 XX
 PS Claim 6, Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipneumatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFKappaB
 CC activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSWL 6
 DB 3 ADMSWL 8
 RESULT 12
 AAM48551 standard; Peptide; 9 AA.
 XX
 ID AAM48551
 XX
 AC AAM48551;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 54.
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipneumatic; nootropic;
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NFKappaB; IkkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 PD 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR

PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
PA	(UYTA) UNIV YALE.
XX	
PI	May MU, Ghosh S, Findels MA, Phillips K;
XX	
DR	WPI; 2002-121889/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Claim 6; Page 62; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AA48628-AA48643), comprising a membrane translocation domain
CC	(AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AA48525-AA48619). The antiinflammatory compounds have antiaesthetic,
CC	cytostatic, antiproliferative, antiinflammatory, antiallergic, osteoprotic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	neurotropic, antihypertensive, vasculic and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	dermatitis, autoimmune diseases such as lupus, polyarthritis, scleroderma,
CC	granulomatosis, multiple sclerosis, transplant rejection; osteoporosis,
CC	Alzheimer's disease, atherosclerosis; viral infections; and ataxia
CC	relanguectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
XX	Sequence 9 AA;
SO	
Query Match	100.0%; Score 40; DB 23; Length 9;
Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
QY	1 ADMSWL 6
Db	2 ADMSWL 7
RESULT 13	
AA48546	
ID	AA48546 standard; Peptide; 10 AA.
XX	
XX	AA48546;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 49.
XX	
KW	Antiinflammatory; antiaesthetic; cytostatic; antiproliferative; neurotropic;
KW	antiinflammatory; antiallergic; osteoprotic; antibacterial; antiviral;
KW	immunosuppressive; dermatological; neuroprotective; antihypertensive;
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema,
KW	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangectasia; allergy; anaphylaxis; arthritis.
XX	
OS	Synthetic.
XX	
PN	WO200183554-A2.

XX	06-NOV-2001.
PD	
XX	
PF	02-MAY-2001; 2001MO-US14346.
XX	
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRAEIS PHARM INC.
PA	(UYTA) UNIV YALE.
PI	
PI	May MJ, Ghosh S, Findeis MA, Phillips K;
XX	
DR	WPI; 2002-121869/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
XX	psoriasis
XX	
PS	Claim 6; Page 62; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAW48628-AAW48651), comprising a membrane translocation domain
CC	(AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAW48525-AAW48619). The antiinflammatory compounds have antiasthmatic,
CC	cytostatic, antiproliferative, antirheumatic, antiarthritic, osteoprotective,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	neurotropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	relangictasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
XX	
SQ	Sequence 10 AA;
	Query Match 100.0%; Score 40; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 2.5;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ADMSWL 6
DB	2 ADMSWL 7
RESULT 14	
AAW48549	
ID	AAW48549 standard; Peptide; 10 AA.
XX	
XX	AAW48549;
XX	
XX	
DT	20-MAR-2002 (first entry)
DE	
XX	Anti-inflammatory peptide SEQ ID NO 52.
XX	
XX	Antiinflammatory; antiasthmatic; cytostatic; antiproliferative; neurotropic;
XX	antiinflammatory; antiarthritic; osteoprotective; antibacterial; virucide;
XX	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX	anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
XX	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX	autoimmune disorder; multiple sclerosis; transplant rejection;

KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	Synthetic.
OS	
PN	WO200183554-A2.
PP	
PD	08-NOV-2001.
XX	
PF	02-MAY-2001; 2001WO-US14346.
XX	
PR	02-MAY-2000; 2000US-201261P.
XX	22-AUG-2000; 2000US-0643260.
PA	(PRAE-) PRAECTIS PHARM INC.
FP	(UYTA) UNIV YALE.
XX	
P1	May MJ, Ghosh S, Findels MA, Phillips K;
DR	WPI: 2002-121889/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PS	psoriasis _
XX	
PS	Claim 6; Page 62; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAM48628-AAM48645), comprising a membrane translocation domain
CC	(AAM48620-AAM48637 or AAM48646-AAM48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAM48625-AAM48619). The antiinflammatory compounds have antiaesthetic,
CC	cycostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nootropic, antischistosomic, virucide and anti-allergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappa B
CC	activation by blocking interaction of Ikappab kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of Ikappab. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polyaralgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
CC	
CC	Sequence 10 AA;
QQ	
Query March	100.0%; Score 40; DB 23; Length 10;
Best Local Similarity	100.0%; Pred. NO. 2.5;
Matches 6; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ADMGWL 6
Db	3 ADMGWL 8
RESULT 15	
ID	AAM48543 standard; Peptide; 11 AA.
AC	AAM48543;
XX	
XX	20-MAR-2002 (first entry)
DT	
XX	
DE	Anti-inflammatory peptide SEQ ID NO 46.
XX	
KM	Antiinflammatory; antiaesthetic; cycostatic; antipsoriatic; nootropic;

KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KM anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KM autoimmune disorder; multiple sclerosis; transplant rejection;
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYTA) UNIV YALE.
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI, 2002-121889/16.
 XX
 PT Novel anti-inflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an anti-inflammatory compound (especially
 CC AA048628-AA048645) comprising a membrane translocation domain
 CC (AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AA048523-AA048619). The anti-inflammatory compounds have antiasthmatic,
 CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC burns; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 CC
 SO Sequence 11 AA;
 XX

QY	1	ADMSWL	6	100.0%	Score	40;	DB	23;	Length	11;
Best Local	Similarity	100.0%	Pred.	No.	2.7;	0;	Indels	0;	Gaps	0;
Matches	6;	Conservative	0;	Mismatches	0;					
Db	3	ADMSWL	8							

Search completed: February 18, 2004, 14:26:18
 Job time : 22.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 / Search time 16.5769 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-19
Perfect score: 148
Sequence: 1 DRQIKWPNRMKMKKTALDASALQTE 28

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	69.6	224	1 HXB6_HUMAN	P17509 homo sapien
2	103	69.6	224	1 HXB6_MOUSE	P09033 mus musculu
3	100	67.6	105	1 HXA7_RAT	P09604 rattus norv
4	100	67.6	229	1 HXA7_MOUSE	P02830 mus musculu
5	99	66.9	75	1 HXSA_SALSA	P09636 salmo salar
6	98	66.2	84	1 HXB6_CHICK	P14839 gallus gall
7	96.5	65.2	96	1 HXC6_BRARE	P15862 brachydanio
8	96	64.9	208	1 HXA7_HERF	Q91425 heterodontu
9	96	64.9	234	1 HXC6_XENTLA	P09925 xenopus lae
10	95	64.2	153	1 HXC6_SHEEP	P12688 homo sapien
11	95	64.2	230	1 HXA7_HUMAN	P09019 xenopus lae
12	95	64.2	230	1 HXB5_XENTLA	P14858 notophthalm
13	95	64.2	234	1 HXC6_NOTVI	P14858 notophthalm
14	95	64.2	235	1 HXC6_HUMAN	P09630 homo sapien
15	95	64.2	235	1 HXC6_MOUSE	P10629 mus musculu
16	95	64.2	242	1 HXA7_COTJA	P24061 coturnix co
17	94.5	63.9	81	1 HXB5_BRARE	P09067 homo sapien
18	94.5	63.9	269	1 HXB5_HUMAN	P09079 mus musculu
19	94.5	63.9	269	1 HXB5_MOUSE	P09079 mus musculu
20	94.5	63.9	275	1 HXB5_BRARE	P09079 mus musculu
21	94	63.5	48	1 HXB6_XENTLA	P09079 mus musculu
22	94	63.5	49	1 HXA7_SHEEP	P12688 homo sapien
23	94	63.5	71	1 HXA7_SHEEP	Q28600 ovis aries
24	94	63.5	71	1 HXC5_NOTVI	P12688 homo sapien
25	94	63.5	74	1 HXB5_MOUSE	P09079 mus musculu
26	94	63.5	76	1 HXC4_RAT	P18865 rattus norv
27	94	63.5	78	1 HXA5_SALSA	P09637 salmo salar
28	94	63.5	80	1 HXA4_LINSA	P09637 salmo salar
29	94	63.5	82	1 HXB5_CHICK	P14838 gallus gall
30	94	63.5	86	1 SCR_APIME	P15859 apis mellif
31	94	63.5	87	1 HXC5_XENTLA	P09079 mus musculu
32	94	63.5	93	1 HXB6_PIG	P09079 mus musculu
33	94	63.5	105	1 HXB4_BRARE	P22574 brachydanio

34	94	63.5	112	1 HXB7_RAT	P18664 rattus norv
35	94	63.5	148	1 HXA5_AMBME	P50208 ambystoma m
36	94	63.5	209	1 HXA7_XENTLA	P09071 xenopus lae
37	94	63.5	217	1 HXB7_BOVIN	Q91689 bos taurus
38	94	63.5	217	1 HXB7_HUMAN	P09629 homo sapien
39	94	63.5	217	1 HXB7_MOUSE	P09024 mus musculu
40	94	63.5	220	1 HXB7_XENTLA	Q91771 xenopus lae
41	94	63.5	220	1 HXB7_XENTLA	P04476 xenopus lae
42	94	63.5	222	1 HXC5_HUMAN	Q00444 homo sapien
43	94	63.5	222	1 HXC5_MOUSE	P32043 mus musculu
44	94	63.5	225	1 HXA7_MORSA	Q9pw44 morone saxa
45	94	63.5	228	1 HXB6_BRARE	P15861 brachydanio

ALIGNMENTS

RESULT 1
ID HXB6_HUMAN STANDARD; PRT; 224 AA.
AC P17509; P09068; Q9HB11; Q9UGH2;
DT 01-NOV-1988 (Rel. 09, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Homeobox protein Hox-B6 (Hox-2b) (Hox-2.2) (HU-2).
GN HOXB6 OR Hox2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RX MEDLINE=91187672; PubMed=1672751;
RA Shen W.-F., Delmer K., Simonitch-Eason T.A., Lawrence H.J.,
RA Laryman C.;
RT "Alternative splicing of the HOX 2.2 homeobox gene in human
RT hematopoietic cells and murine embryonic and adult tissues.";
RL Nucleic Acids Res. 19:539-545(1991).
RN (2)
RP SEQUENCE FROM N.A.
RA Frezza D., D'Esposito M., Migliaccio E., Santini S.M., Fruscalzo A.,
RT "Expression of HOX genes in T lymphocytes and hairy leukemia cell
RT lines.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Kidd K.R., Bueyria V., Demille M.M.C., Speed W.C., Ruggieri V.,
RA "Overall linkage disequilibrium in 33 populations for highly
RT informative multistate haplotypes spanning the HOXB gene cluster.";
RL Am. J. Hum. Genet. 67:235-235(2000).
RN (4)
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Gronow L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenn C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helen F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Donald M.F., Casavant T.P., Schetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshynski S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

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RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP SEQUENCE OF 135-224 FROM N.A.
RX MEDLINE=90046832; PubMed=2573064;
RA Shen W.-F., Largman C., Lowrey P., Corral J.C., Detmer K.,
RA Hauser C.A., Simionitch T.A., Hack P.M., Lawrence H.J.;
RT "Lineage-restricted expression of homeobox-containing genes in human
RT hematopoietic cell lines."
RL Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540 (1989).
RN [6]
RP PRELIMINARY SEQUENCE OF 136-240 FROM N.A.
RX MEDLINE=85024858; PubMed=6091895;
RA Levine M., Rubin G.M., Tjian R.;
RT "Human DNA sequences homologous to a protein coding region conserved
RT between homeotic genes of Drosophila."
RL Cell 38:667-673 (1984).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL, REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=p17509-1; Sequence=Displayed;
CC Name=2; Synonyms=Homeobox-less;
CC IsoId=p17509-2; Sequence=VSP_002388, VSP_002389;
CC -1- SIMILARITY: BELONGS TO THE ANTF HOMEOBOX FAMILY.
CC -----
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CC -----
DR EMBL, X58431; CAA41335.1; -.
DR EMBL, X58431; CAA41336.1; -.
DR EMBL, AJ270993; CAB65909.1; -.
DR EMBL, AF287967; AAG31552.1; -.
DR EMBL, BC014651; AAH14651.1; -.
DR EMBL, M30597; AAB36004.1; -.
DR EMBL, K02571; -. NOT_ANNOTATED_CDS.
DR PIR, S26400; S26400.
DR HSSP, P02833; IHOM.
DR TRANSFAC, T01732; -.
DR Genew; HGNC:5117; HOXB6.
DR MIM, 142961; -.
DR GO, GO:0005634; C:nucleus; NAS.
DR GO, GO:0003700; F:transcription factor activity; NAS.
DR GO, GO:0008595; P:regulation of anterior/posterior axis, e...; NAS.
DR GO, GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
DR InterPro, IPR001827; Antennapedia.
DR InterPro, IPR001356; Homeobox.
DR Pfam, PF00046; homeobox.1.
DR PRINTS, PR00025; ANTENNAPEDIA.
DR PRINTS, PR00024; HOMEOBOX.
DR ProDom, PDO00010; Homeobox.1.
DR SMART, SMO0389; HOX.1.
DR PROSITE, PS00032; ANTENNAPEDIA.1.
DR PROSITE, PS00027; HOMEOBOX.1; 1.
DR PROSITE, PS50071; HOMEOBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation; Alternative splicing.
KW Transcription regulation; Alternative splicing.
FT SITE 127 132
FT DNA_BIND 146 205 HOMEOBOX.
FT DOMAIN 216 220 POLY_GLU.
FT VARSPLIC 140 140 S -> E (in isoform 2).
FT VARSPLIC 141 224 /FTId=VSP_002388.
FT VARSPLIC 141 224 Missing (in isoform 2).
FT /FTId=VSP_002389.

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FT CONFLICT 24 25 HV -> OL (IN REF. 3 AND 4).
FT CONFLICT 33 33 A -> R (IN REF. 1).
FT CONFLICT 60 60 P -> R (IN REF. 1).
FT CONFLICT 73 73 D -> A (IN REF. 1).
FT CONFLICT 149 150 GR -> A (IN REF. 5).
SQ SEQUENCE 224 AA; 25427 MW; D8F96AFAC893D878 CRC64;

Query Match 69.6%; Score 103; DB 1; Length 224;
Best Local Similarity 70.0%; Pred. No. 1, 2e-08;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

OY 1 DROIKWPNRRMKKXTA--LDASALQTE 28
DB 187 EROIKWPNRRMKKESKLLSASQLSAR 216
:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:

RESULT 2
HXB_MOUSE STANDARD; PRT; 224 AA.
ID HXB_MOUSE
AC P09023;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B6 (Hox-2.2) (MH-22A).
GN HOXB6 OR HOXB-6 OR HOX-2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86289762; PubMed=2899893;
RA Schughart K., Uset M.F., Awgulewitsch A., Ruddle F.H.;
RT "Structure and expression of Hox-2.2, a murine homeobox-containing
gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5582-5586(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91187672; PubMed=1672751;
RA Shen W.F., Detmer K., Simonitch-Bason T.A., Lawrence H.J.,
RA Laryman C.;
RT "Alternative splicing of the HOX 2.2 homeobox gene in human
hematopoietic cells and murine embryonic and adult tissues.";
RL Nucleic Acids Res. 19:539-545(1991).
RN [3]
RP SEQUENCE OF 144-224 FROM N.A.
RX MEDLINE=86054465; PubMed=2890503;
RA Lonai P., Arman B., Czornick H., Ruddle F.H., Blatt C.;
RT "New murine homeoboxes: structure, chromosomal assignment, and
differential expression in adult erythropoiesis.";
RL DNA 6:409-416(1987).
RN [4]
RP SEQUENCE OF 140-224 FROM N.A.
RX MEDLINE=86085193; PubMed=2891608;
RA Hart C.P., Painmed A., Ruddle F.H.;
RT "Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeoboxes:
evolutionary and structural comparisons.";
RL Genomics 1:182-195(1987).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC -----
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CC -----
DR EMBL; M18166; AAA37644.1; -.

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DR EMBL; X56459; CAA39834.1; ALT-SEQ.
 DR EMBL; M18401; AAC27130.1; ALT-SEQ.
 DR EMBL; J03782; AAA37843.1; ALT-SEQ.
 DR PIR; A31324; A31324.
 DR HSSP; P02833; IHOM.
 DR TRANSFAC; T01733; ANT.
 DR MGD; MGI; 96187; Hoxb6.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; Homeobox.1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD00010; Homeobox.1.
 DR SMART; SM00389; HOX.1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA.1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT SITE 127 132 ANT-PTYPE HEXAPEPTIDE.
 FT DNA_BIND 146 205 HOMEBOX.
 FT DOMAIN 216 220 POLY-GLU.
 FT CONFLICT 186 186 T -> P (IN REF. 3).
 SQ SEQUENCE 224 AA; 25310 MW; B8FC0BDEB57F5C3D CRC64;

Query Match 69.6%; Score 103; DB 1; Length 224;
 Best Local Similarity 70.0%; Pred. No. 1.2e-08;
 Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

OY 1 DROIKIFQNRMMKKKTA-LDASALQTE 28
 DB 187 EROIKIFQNRMMKKKSKLSASQLSAE 216

RESULT 3
 HXAT RAT STANDARD; PRT; 105 AA.
 ID HXAT RAT STANDARD; PRT; 105 AA.
 AC P09634.
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-A7 (Hox-1.1) (R5) (Fragment).
 GN HOXA7 OR HOXA-7.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=87277429; PubMed=2886401;
 RA Falzon M., Sanderson N., Chung S.Y.;
 RT "Cloning and expression of rat homeo-box-containing sequences";
 RL Gene 54:23-32(1987).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ANT-PTYPE HEXAPEPTIDE.
 CC -----
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 CC -----
 CC EMBL; M16807; NOT_ANNOTATED_CDS.
 DR PIR; A27471; A27471.
 DR HSSP; P02833; NANT.
 DR TRANSFAC; T01707; ANT.
 DR InterPro; IPR001827; Antennapedia.

DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; Homeobox.1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD00010; Homeobox.1.
 DR SMART; SM00389; HOX.1.
 DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT NON_TER 1 1 HOMEBOX.
 FT DNA_BIND 5 64 GLU-RICH (ACIDIC).
 FT DOMAIN 91 105
 SQ SEQUENCE 105 AA; 12552 MW; 106C1DF93BF2864B CRC64;

Query Match 67.6%; Score 100; DB 1; Length 105;
 Best Local Similarity 70.4%; Pred. No. 1.5e-08;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 DROIKIFQNRMMKKKTA-LDASALQTE 27
 DB 46 EROIKIFQNRMMKKKHDEBSQAPT 72

RESULT 4
 HXAT MOUSE STANDARD; PRT; 229 AA.
 ID HXAT MOUSE STANDARD; PRT; 229 AA.
 AC P02830;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-A7 (Hox-1.1) (M6-12) (M6).
 GN HOXA7 OR HOXA-7 OR HOX-1.1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=87260976; PubMed=2885847;
 RA Kessel M., Schulze F., Fiddi M., Gruss P.;
 RT "Primary structure and nuclear localization of a murine homeodomain
 RT protein";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5306-5310(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=95197009; PubMed=7890170;
 RA Parikh H., Shah S., Hilt D., Peterkofsky A.;
 RT "Organization, sequence and regulation of expression of the murine
 RT Hoxa-7 gene";
 RL Gene 154:237-242(1995).
 RN [3]
 RP SEQUENCE OF 126-229 FROM N.A.
 RC MEDLINE=85188311; PubMed=2986010;
 RA Colberg-Poley A.M., Voss S.D., Chowdhury K., Gruss P.;
 RT "Structural analysis of murine genes containing homoeo box sequences
 RT and their expression in embryonal carcinoma cells";
 RL Nature 314:713-718(1985).
 RN [4]
 RP SEQUENCE OF 129-197 FROM N.A.
 RC MEDLINE=87053860; PubMed=2877873;
 RX Breier G., Bucan M., Francke U., Colberg-Poley A.M., Gruss P.;
 RT "Sequential expression of murine homeo box genes during F9 EC cell
 RT differentiation";
 RL EMBO J. 5:2209-2215(1986).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ANT-PTYPE HEXAPEPTIDE.
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CC -----
 DR EMBL; M17192; AAA37833.1; -
 DR PIR; A03314; AAC52160.1; -
 DR PIR; A28329; A28329.
 DR HSSP; P02833; 9ANT.
 DR TRANSFAC; T01278; -
 DR MGD; MGI:96179; Hoxa7.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT SITE 118 123 ANTP-TYPE HEXAPEPTIDE.
 FT DNA BIND 129 188 HOMEBOX.
 FT DOMAIN 156 159 POLY-ARG.
 FT DOMAIN 211 229 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 215 229 POLY-GLU.
 FT CONFLIT 43 45 GAG -> APA (IN REF. 1).
 SQ SEQUENCE 229 AA; 25682 MW; D36E6BD61D8D5C6F CRC64;
 Query Match 67.6%; Score 100; DB 1; Length 229;
 Best Local Similarity 70.4%; Pred. No. 3.5e-08;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 DROIKIWPQNRKMKKTALDASALQT 27
 DB 170 EROIKIWPQNRKMKKTALDASALQT 196
 RESULT 5
 HNSA_SALSA STANDARD; PRT; 75 AA.
 AC P03636;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein S12-A (Fragment).
 OS Salmo salar (Atlantic salmon).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostomi;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OC NCBI_TaxID=8030;
 RX MEDLINE=88226009; PubMed=2897318;
 RA Pfoser A., Mølven A., Eiken H.G.;
 RT "Molecular cloning and characterization of homeo-box-containing genes
 RT from Atlantic salmon.";
 RL Gene 62:141-152(1988).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
 CC -----
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CC -----
 DR EMBL; M18903; AAA49559.1; -
 DR PIR; I51341; I51341.
 DR HSSP; P02833; 9ANT.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR ProDom; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein.
 FT NON_TER 1 1
 FT DNA BIND 1 60 HOMEBOX.
 FT NON_TER 75 75
 SQ SEQUENCE 75 AA; 9330 MW; FC02C3672F35475D CRC64;
 Query Match 66.9%; Score 99; DB 1; Length 75;
 Best Local Similarity 75.0%; Pred. No. 1.5e-08;
 Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 DROIKIWPQNRKMKKTALDASALQT 24
 DB 42 EROIKIWPQNRKMKKTALDASALQT 65
 RESULT 6
 HXB6 CHICK STANDARD; PRT; 84 AA.
 ID HXB6 CHICK
 AC P14839;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-B6 (HOX-2.2) (Fragment).
 GN HOXB6 OR HOXB6-2.2.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 CC Gallus.
 OC NCBI_TaxID=9031;
 RX MEDLINE=90126373; PubMed=2575515;
 RA Wedden S.E., Pang K., Sichele G.;
 RT "Expression pattern of homeobox-containing genes during chick
 RT embryogenesis.";
 RL Development 105:639-650(1989).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
 CC -----
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KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KM Transcription regulation.
 FT NON TER 1
 FT DNA_BIND 7 66 HOMEBOX.
 SQ SEQUENCE 84 AA; 10279 MW; BC06B10165B19E71 CRC64;

Query Match 66.2%; Score 96; DB 1; Length 84;
 Best Local Similarity 66.7%; Pred. No. 2.4e-08;
 Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
 Oy 1 DROIKIFQNRBMKMKK--TALDASALQTE 28
 ID :|||||
 Db 48 EROIKIFQNRBMKMKKENTLSTVPQTE 77

RESULT 7
 HXC6_BRARE STANDARD; PRT; 96 AA.
 AC P15862;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-C6 (ZF-61) (Fragment).
 GN HOXC6 OR HOXC6A OR Hox-C6 OR ZF-61.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 OC Cyprinidae; Danio.
 ON NCBI_Taxid=7955;
 RX MEDLINE=90151628; PubMed=1968004;
 RA Mollerad P.R., Molyen A., Apold J., Fjose A.;
 RT "The zebrafish homeobox gene hoxd-2.2: transcription unit, potential
 regulatory regions and in situ localization of transcripts.";
 RL EMO J. 9:515-524 (1990).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
 CC
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 CC
 DR EMBL; X17266; CAJ35170.1; -.
 DR PIR; S08639; S08639.
 DR HSSP; P02833; 9ANT.
 DR ZFIN; ZDB-GENE-990415-113; hoxc6a.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KM Transcription regulation.
 FT NON TER 1
 FT DNA_BIND 7 66 HOMEBOX.
 SQ SEQUENCE 96 AA; 11638 MW; F1ED7AF3A3B640C CRC64;
 Query Match 65.2%; Score 96.5; DB 1; Length 96;
 Best Local Similarity 69.0%; Pred. No. 4.7e-08;
 Matches 20; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Oy 1 DROIKIFQNRBMKMKK--TALDASALQTE 28
 ID :|||||
 Db 48 EROIKIFQNRBMKMKKENTLSTVPQTE 76

RESULT 8
 HXA7_HETFR STANDARD; PRT; 208 AA.
 AC O91A25;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-A7.
 GN HoxA7.
 OS Heterodontus francisci (Horn shark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Heterodontidae; Heterodontiformes;
 OC Heterodontidae; Heterodontus.
 ON NCBI_Taxid=7792;
 RX MEDLINE=20144096; PubMed=10677514;
 RA Kim C.B., Anemiyi C., Bailey W., Kawasaki K., Mezey J., Miller W.,
 RA Minoshima S., Shimizu N., Wagner G., Ruddle F.;
 RT "Hox cluster genomics in the horn shark, Heterodontus francisci.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1655-1660 (2000).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
 CC
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 CC
 DR EMBL; AF224262; AAF44645.1; -.
 DR HSSP; P02833; 9ANT.
 DR TRANSFAC; T04478; -.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KM Transcription regulation.
 FT SITE 124 129 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 135 194 HOMEBOX.
 SQ SEQUENCE 208 AA; 23786 MW; 71B61AB78E064D0 CRC64;
 Query Match 64.9%; Score 96; DB 1; Length 208;
 Best Local Similarity 66.7%; Pred. No. 1.3e-07;
 Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 Oy 1 DROIKIFQNRBMKMKK--TALDASALQTE 27
 ID :|||||
 Db 176 EROIKIFQNRBMKMKKTKAGSSSTT 202

RESULT 9
 HXC6_XENLA STANDARD; PRT; 234 AA.
 ID HXC6_XENLA

AC P02832;
 DT 21-JUN-1996 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-C6 (XlHbox-1) (AC1).
 GN HOXC6 OR XlHBOX1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RX MEDLINE=88157707; PubMed=2901347;
 RA Cho K.W.Y., Goetz J., Wright C.V.E., Fritz A., Hardwicke J.,
 RA de Robertis E.M.;
 RT "Differential utilization of the same reading frame in a Xenopus
 RT homeobox gene encodes two related proteins sharing the same
 RT DNA-binding specificity.";
 RL EMBO J. 7:2139-2149(1988).
 RN [2]
 RP SEQUENCE OF 121-234 FROM N.A.
 RX MEDLINE=88157707; PubMed=2894634;
 RA Fritz A., de Robertis E.M.;
 RT "Xenopus homeobox-containing cDNAs expressed in early development.";
 RL Nucleic Acids Res. 16:1453-1469(1988).
 RN [3]
 RP SEQUENCE OF 134-200 FROM N.A.
 RX MEDLINE=84205675; PubMed=6327066;
 RA Carrasco A.E., McGinnis W., Gehring W.J., de Robertis E.M.;
 RT "Cloning of an X. laevis gene expressed during early embryogenesis
 RT coding for a peptide region homologous to Drosophila homeotic
 RT genes.";
 RL Cell 37:409-414(1984).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY IN EARLY XENOPUS
 CC EMBRYOS.
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC -----
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 CC -----
 DR EMBL; X12499; CAA31020.1; ALT_INIT.
 DR EMBL; X12500; CAA31021.1; -.
 DR EMBL; K01943; AAA49743.1; -.
 DR EMBL; X07101; CAA30122.1; -.
 DR PIR; S00992; S00992.
 DR HSSP; P02833; 9ANT.
 DR TRANSFAC; T01745; -.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox.1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox.1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 DR Transcription regulation.
 KW Homeobox protein Hox-C6 PRII.
 FT CHAIN 83 234 HOMEBOX PROTEIN HOX-C6 PRII.
 FT SITE 122 127 ANTP-TYPE HEXAPEPTIDE.

FT DNA_BIND 141 200 HOMEBOX.
 FT VARIANT 139 139 T -> S.
 SQ SEQUENCE 234 AA; 26689 MW; 4C371CC5252D2C58 CRC64;
 Query Match 64.9%; Score 96; DB 1; Length 234;
 Best Local Similarity 72.0%; Pred. No. 1.5e-07;
 Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 DRQIKWFONRNMRKKTALDASAL 25
 Db 182 ERQIKWFONRNMRKKTESNLSTL 206
 RESULT 10
 HXCG SHEEP STANDARD; PRT; 153 AA.
 ID HXCG SHEEP
 AC P49925;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-C6.
 GN HOXC6.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cebay N.C., Hernandez-Ledezma J., Mathialagan N., Roberts R.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC -----
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 CC -----
 DR EMBL; U33049; AAA75473.1; -.
 DR HSSP; P02833; 9ANT.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox.1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox.1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT SITE 40 45 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 59 118 HOMEBOX.
 FT DOMAIN 86 89 POLY-ARG.
 FT DOMAIN 126 130 POLY-GLY.
 FT DOMAIN 139 153 GLU/LYS-RICH.
 SQ SEQUENCE 153 AA; 17804 MW; 291E24399159621E CRC64;
 Query Match 64.2%; Score 95; DB 1; Length 153;
 Best Local Similarity 72.0%; Pred. No. 1.3e-07;
 Matches 16; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 DRQIKWFONRNMRKKTALDASAL 25
 Db 100 ERQIKWFONRNMRKKTESNLSTL 124

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DR EMBL: X84804; CA59270.1; JOINED.
DR EML: S15536; S15536.
DR HSSP: P02833; 9ANT.
DR TRANSFAC: T01705; --
DR Genew; HGNC:5108; H0XA7.
DR MIM; 142950; --
DR GO; GO:0003700; F:transcription factor activity; TAS.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW transcription regulation.
FT SITE 119 124 ANT-P-TYPE HEXAPEPTIDE.
FT DNA BIND 130 189 HOMEBOX.
FT DOMAIN 157 160 POLY-ARG.
FT DOMAIN 196 199 POLY-ALA.
FT DOMAIN 214 230 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 223 230 POLY-GLU.
FT CONFLICT 18 18 T -> A (IN REF. 3).
FT CONFLICT 75 76 DA -> RR (IN REF. 6).
FT CONFLICT 78 78 MISSING (IN REF. 5).
FT CONFLICT 174 174 I -> V (IN REF. 4).
FT CONFLICT 194 195 PT -> RL (IN REF. 5).
FT CONFLICT 195 195 T -> I (IN REF. 7).
FT CONFLICT 222 222 D -> Y (IN REF. 5).
SQ SEQUENCE 230 AA; 25385 MW; 6E2F1991F1BBED21 CRC64;

Query March 64.2%; Score 95; DB 1; Length 230;
Best Local Similarity 81.0%; Prod. No. 2.1e-07;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMRMKKTALD 21
Db 171 EROIKIWFQNRMRMKKEKHD 191

RESULT 12
HXBS_XENLA
ID HXBS_XENLA STANDARD; PRT; 230 AA.
AC P09019;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 26-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B5 (X1Hbox-4) (Xbox-1B) (Fragment).
GN H0XB5 OR X1HBOX4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88157707; PubMed=2894634;
RA Fritz A., de Robertis E.M.;
RT "Xenopus homeobox-containing cDNAs expressed in early development.";
RL Nucleic Acids Res. 16:1453-1469(1988).
RN [2]
RP SEQUENCE OF 155-214 FROM N.A.
RX MEDLINE=86274626; PubMed=3015593;
RA Harvey R.P., Tabin C.J., Melton D.A.;
RT "Embryonic expression and nuclear localization of Xenopus homeobox
RT (Xbox) gene products."
RL EMBO J. 5:1237-1244(1986).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

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CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
-----
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CC or send an email to license@1sb-sib.ch).
-----
DR EMBL; X07104; CA30125.1; -.
DR EMBL; M26883; AAA49755.1; -.
DR PIR; S00592; S00592.
DR HSSP; P02833; 1SAN.
DR TRASPAC; T03764; -.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEOBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00071; HOMEOBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON TER 1 1 ANTP-TYPE HEXAPEPTIDE.
FT SITE 137 142 HOMEOBOX.
FT DNA_BIND 155 214
SQ SEQUENCE 230 AA; 25276 MW; AD040C030F85532B CRC64;

Query Match 64.2%; Score 95; DB 1; Length 230;
Best Local Similarity 58.8%; Pred. No. 2.1e-07;
Matches 20; Conservative 2; Mismatches 4; Indels 8; Gaps 1;

Qy 1 DROIKTFQNRMRMKWKK-----TALDASALQ 26
Db 196 ERQIKTFQNRMRMKWKKDKNKLKSMELATGSSAFQ 229

RESULT 13
HXCG NOTVI STANDARD; PRT; 234 AA.
ID HXCG NOTVI
AC P14858; P14857;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C6 (NvHox-1) (FH-2).
GN HOKX6 OR NVHOKX1.
OS Nematostella viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroides; Salamandridae;
OC Nothophthalmus.
OC NCBI_TaxID=8316;
OX NCBI_TaxID=8316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89210814; PubMed=2907476;
RA Savard P., Gates P.B., Brookes J.P.;
RT "Position dependent expression of a homeobox gene transcript in
RT relation to amphibian limb regeneration.";
RL EMBO J. 7:4275-4282(1988).
RN [2]
RP SEQUENCE OF 131-234 FROM N.A.
RX MEDLINE=90091821; PubMed=2574663;
RA Tabin C.J.;
RT "Isolation of potential vertebrate limb-identity genes.";
RT Development 105:813-820(1989).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

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CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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CC or send an email to license@1sb-sib.ch).
-----
DR EMBL; X13957; CA32139.1; -.
DR EMBL; X16848; CA34745.1; -.
DR PIR; S02014; S02014.
DR HSSP; P02833; 9ANT.
DR TRASPAC; T01747; -.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEOBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00071; HOMEOBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT SITE 122 127 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 141 200 HOMEOBOX.
SQ SEQUENCE 234 AA; 26901 MW; EA15BED91ED294B0 CRC64;

Query Match 64.2%; Score 95; DB 1; Length 234;
Best Local Similarity 72.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DROIKTFQNRMRMKWKKTALDASAL 25
Db 182 ERQIKTFQNRMRMKWKKSNTLSTL 206

RESULT 14
HXCG HUMAN STANDARD; PRT; 235 AA.
ID HXCG HUMAN
AC P09630;
DT 01-MAR-1989 (Rel. 10, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C6 (Hox-3C) (HHO.C8) (CP25).
GN HOKX6 OR HOKX3C.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=87260899; PubMed=2885844;
RA Simeone A., Mavilio F., Acampora D., Giampaolo A., Faiella A.;
RA Zappavigna V., D'Esposito M., Panese M., Russo G., Boncinelli E.,
RA Paschle C.;
RT "Two human homeobox genes, c1 and c8: structure analysis and
RT expression in embryonic development.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4914-4918(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=88262550; PubMed=2898768;
RA Simeone A., Panese M., Acampora D., D'Esposito M., Boncinelli E.;
RT "At least three human homeoboxes on chromosome 12 belong to the same
RT transcription unit.";
RL Nucleic Acids Res. 16:5379-5390(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=97024425; PubMed=8870653;

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RA Charlot A., Castronovo V., Le P., Gillet C., Sobel M.E., Gielen J.;
 RT "Cloning and expression of a new HoxC6 transcript encoding a
 RT repressing protein."; www.ncbi.nlm.nih.gov/pubmed/11939197.
 RL Biochem. J. 319:91-97 (1996).
 RN (4)
 RN SEQUENCE OF 141-206 FROM N.A.
 RX MEDLINE=9021556; PubMed=2576652;
 RA Boccia E., Acampora D., Pannese M., D'Esposito M., Somma R.,
 RA Gaetano G., Stornaiuolo A., Cafiero M., Falella A., Simone A.;
 RT "Organization of human class I homeobox genes.";
 RL Genome 31:745-756 (1989).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P09630-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P09630-2; Sequence=VSP_002392;
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC -----
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 CC -----
 DR EMBL; S82986; AAB46892.1; -;
 DR EMBL; M16938; AAA36007.1; -;
 DR PIR; B28030; WHH3C.
 DR HSSP; P02833; 9ANT.
 DR TRANSPAC; T01742; -;
 DR Genew; HGNC:5128; HoxC6.
 DR MIM; 142972; -;
 DR GO; GO:0003714; P:transcription co-repressor activity; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0006357; P:regulation of transcription from Pol II pro. .; TAS.
 DR InterPro; IPR001827; Antennapedia.
 DR Pfam; PF00046; homeobox.1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEOBOX.
 DR PRODOM; PD000010; Homeobox.1.
 DR SMART; SM00389; Hox.1.
 DR PROSITE; PS00027; HOMEOBOX_1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00071; HOMEOBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation; Alternative splicing;
 KW SITE 122 127 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 141 200 HOMEOBOX.
 FT DOMAIN 168 171 POLY-ARG.
 FT DOMAIN 208 212 POLY-GLY.
 FT DOMAIN 221 235 GLU/LYS-RICH.
 FT VASAPLIC 1 82 Missing (in isoform 2).
 FT FT
 FT CONFLICT 218 218 M -> L (in REF. 3).
 SQ SEQUENCE 235 AA; 26933 MW; BD68870347CB71C0 CRC64;
 Query Match 64.2%; Score 95; DB 1; Length 235;
 Best Local Similarity 72.0%; Pred. NO. 2.1e-07;
 Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

HXC6 MOUSE
 ID HXC6_MOUSE STANDARD; PRT; 235 AA.
 AC P10629; 061683;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-C6 (Hox-3.3) (Hox-6.1).
 GN HXC6 OR HXC6-6 OR HXC-3.3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94131843; PubMed=7905473;
 RA Shmied S.M., Gaunt S.J., Coletta P.L., Gada A.M., Sharpe P.T.;
 RT "Spatial localisation of transcripts of the Hox-C6 gene.";
 RL J. Anat. 183:515-523 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92102952; PubMed=1684715;
 RA Coletta P.L., Shmied S.M., Chaudhuri C., Mueller U., Clarke J.P.,
 RA Sharpe P.T.;
 RT "Characterisation of the murine Hox-3.3 gene and its promoter.";
 RL Mech. Dev. 35:129-142 (1991).
 RN [3]
 RP SEQUENCE OF 15-235 FROM N.A.
 RC TISSUE=Bone marrow, and Spleen;
 RX MEDLINE=88329001; PubMed=2901346;
 RA Kongswan K., Webb E., Houstaux P., Adams J.M.;
 RT "Expression of multiple homeobox genes within diverse mammalian
 RT hemopoietic lineages.";
 RL EMBO J. 7:2131-2138 (1988).
 RN [4]
 RP SEQUENCE OF 131-235 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=88328811; PubMed=2458223;
 RA Sharpe P.T., Miller J.R., Evans E.P., Burenshaw M.D., Gaunt S.J.;
 RT "Isolation and expression of a new mouse homeobox gene.";
 RL Development 102:397-407 (1988).
 RN [5]
 RP SEQUENCE OF 133-235 FROM N.A.
 RX MEDLINE=89357988; PubMed=2570032;
 RA Schupfart K., Pravecheva D., Newman M.S., Hunnhan L.W., Jiang Z.,
 RA Ruddle P.H.;
 RT "Isolation and regional localization of the murine
 RT homeobox-containing gene Hox-3.3 to mouse chromosome region 15B.";
 RL Genomics 5:76-83 (1989).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=PR1;
 CC Name=PR1;
 CC IsoId=P10629-1; Sequence=Displayed;
 CC Name=PR1;
 CC IsoId=P10629-2; Sequence=VSP_002393;
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC -----
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 CC -----
 DR EMBL; J03074; AAA37832.1; -;
 DR EMBL; M35986; AAA37854.1; -;
 DR EMBL; X16511; CAA34518.1; -;
 DR EMBL; X16510; CAA34517.1; -;
 DR EMBL; S74185; AAB30717.1; -;

DR EMBL: X12504; CAA31022.1; -;
 DR EMBL: X12504; CAA31023.1; -;
 DR EMBL: X16838; CAA34737.1; -;
 DR PIR: A32167; A32167.
 DR PIR: A56568; A56568.
 DR PIR: S00987; WJMSX6.
 DR HSSP: P02833; 9ANT.
 DR TRANSPAC: T01743; -.
 DR TRANSPAC: T01744; -.
 DR MGD; MGI:96197; Hoxc6.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS50071; HOMEBOX 2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation; Alternative splicing.
 FT SITE 122 127 HOMEBOX.
 FT DNA BIND 141 200 GLU/LYS-RICH.
 FT DOMAIN 221 235 ANTP-TYPE HEXAPEPTIDE.
 FT VARSPLIC 1 82 Missing (in isoform PRI).
 FT CONFLICT 15 18 AGGQ -> QGRP (IN REF. 3).
 FT CONFLICT 131 131 S -> N (IN REF. 4).
 FT CONFLICT 192 192 R -> A (IN REF. 4).
 FT CONFLICT 228 229 TE -> OK (IN REF. 1 AND 2).
 SQ SEQUENCE 235 AA; 26915 MW; BD695C7347CB71C0 CRC64;

Query Match 64.2%; Score 95; DB 1; Length 235;
 Best local similarity 72.0%; Pred. No. 2.1e-07;
 Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DROIKWPNRRMKKTALDASL 25
 DB 182 ERQIKWPNRRMKKESNLTSTL 206

Search completed: February 18, 2004, 14:28:15
 Job time : 17.5789 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 81.0526 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKWFRNRKMKKTALDASALQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110.5	74.7	274	5	Q9XYT7
2	101.5	68.6	627	5	Q95YH8
3	100	67.6	108	11	Q8JZM2
4	98	66.2	93	5	Q9U9Z5
5	97	65.5	60	5	Q26375
6	97	65.5	90	5	Q817C9
7	97	65.5	181	5	Q26611
8	97	65.5	194	5	Q26478
9	97	65.5	435	5	Q817C8
10	96.5	65.2	231	13	Q9PMM4
11	96	64.9	101	13	Q9PMD5
12	95.5	64.5	82	13	Q9PVS0
13	95	64.2	219	13	Q9VWZ9
14	94.5	63.9	43	13	Q57359
15	94.5	63.9	80	5	Q05008
16	94.5	63.9	230	11	Q9CZV0

17	94.5	63.9	275	13	Q8AWY7	Q8AWY7 brachydanio
18	94.5	63.9	276	13	Q8JH53	Q8JH53 brachydanio
19	94.5	63.9	276	13	Q9PMM0	Q9PMM0 brachydanio
20	94.5	63.9	348	5	Q8WRG6	Q8WRG6 artemia san
21	94	63.5	39	13	Q57368	Q57368 brachydanio
22	94	63.5	46	13	Q9PVR9	Q9PVR9 oryzias lat
23	94	63.5	51	5	Q27413	Q27413 ctenodrilus
24	94	63.5	51	5	Q23743	Q23743 ctenodrilus
25	94	63.5	51	5	Q26407	Q26407 ctenodrilus
26	94	63.5	57	13	Q9PVR8	Q9PVR8 oryzias lat
27	94	63.5	58	5	Q9Y188	Q9Y188 pitapulus c
28	94	63.5	58	5	Q25208	Q25208 junonia coe
29	94	63.5	58	13	Q57362	Q57362 brachydanio
30	94	63.5	59	5	Q8WRM9	Q8WRM9 lithobius a
31	94	63.5	59	5	Q9NB42	Q9NB42 anopheles g
32	94	63.5	59	13	Q9PVR5	Q9PVR5 oryzias lat
33	94	63.5	60	5	Q77143	Q77143 archeogozete
34	94	63.5	60	5	Q77139	Q77139 archeogozete
35	94	63.5	60	13	Q8QGL5	Q8QGL5 petromyzon
36	94	63.5	60	13	Q8QGL3	Q8QGL3 petromyzon
37	94	63.5	60	13	Q8QGL6	Q8QGL6 petromyzon
38	94	63.5	60	13	Q8QGL2	Q8QGL2 petromyzon
39	94	63.5	60	13	Q8QGL7	Q8QGL7 petromyzon
40	94	63.5	61	5	Q27910	Q27910 polyandroca
41	94	63.5	61	5	Q77138	Q77138 archeogozete
42	94	63.5	63	5	Q8WXB2	Q8WXB2 holopneuste
43	94	63.5	66	13	Q57356	Q57356 brachydanio
44	94	63.5	69	5	Q9U9T4	Q9U9T4 nectris vire
45	94	63.5	69	5	Q9U9T4	Q9U9T4 nectris vire

ALIGNMENTS

RESULT 1

Q9XYT7 PRELIMINARY: PRT; 274 AA.

AC Q9XYT7; 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Scx-3 homeodomain protein (Fragment).

GN SCOX-3.

OS Caasiopsea xamachana.

OC Eukaryota; Metazoa; Chordata; Scyphozoa; Rhizostomaeae; Caasiopseidae;

OC Caasiopsea.

OX NCBI_Taxid=12993;

RN [1]

RP SEQUENCE FROM N.A.

RA Kuhn K., Streit B., Schlerwater B.;

RT "Isolation of Hox genes from the scyphozoan *Caasiopsea xamachana*;

RT Implications for the early evolution of Hox genes.";

RT J. Exp. Zool. 0-0-0(1999)

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

DR EMBL; AF124593; A032577.1; -.

DR HSSP; P02833; GANT.

DR InterPro; IPR001356; Homeobox.

DR InterPro; IPR000047; HTH_LambdaRepress.

DR Pfam; PF000046; homeobox; 1.

DR PRINTS; PR000024; HOMEBOX.

DR PRINTS; PR000031; HTHREPRESSR.

DR ProDom; PD000010; Homeobox; 1.

DR SMART; SM00389; Hox; 1.

DR PROSITE; PS00027; HOMEBOX 1; 1.

DR PROSITE; PS00071; HOMEBOX 2; 1.

KW DNA-binding; Homeobox; Nuclear protein.

FT NON_TER

SQ

SEQUENCE 274 AA; 31041 MW; 588E91F6E540C3A9 CRC64;

Query Match 74.7%; Score 110.5; DB 5; Length 274;

Best local similarity 67.7%; Pred. No. 1.7e-08;

Matches 21; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

QY 1 DROIKIWFQNRKMKK---TALDASALQTE 28
 DB 182 EROIKIWFQNRKMKKGGTTSIDANLEERE 212

RESULT 2

ID Q95YH8 PRELIMINARY; PRT; 627 AA.
 AC Q95YH8; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Homeotic protein.
 OS Daphnia magna.
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Diplostetraca;
 OC Cladocera; Anomopoda; Daphniidae; Daphnia.
 NCBI_TaxId=35525;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shiga Y., Yasumoto R., Hayaashi S., Yamagata H.;
 RT "Functional diversification of homeotic protein Antennapedia in
 RT arthropod evolution."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AB069680; BAB64346.1; -
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00071; HOMEBOX 2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 627 AA; 69425 MW; A5A7962761C85D10 CRC64;

Query Match 68.6%; Score 101.5; DB 5; Length 627;
 Best Local Similarity 69.0%; Pred. No. 9.2e-07;
 Matches 20; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 1 DROIKIWFQNRKMKK---KTDASALQ 26
 DB 587 EROIKIWFQNRKMKKKNKADGCLB 615

RESULT 3

ID Q8UZW2 PRELIMINARY; PRT; 108 AA.
 AC Q8UZW2; 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE:Colon;
 RA Straubberg R.;
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC036986; AAH36986.1; -
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_Lamdbrepressr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX 1; 1.

DR PROSITE; PS00071; HOMEBOX 2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 108 AA; 13070 MW; 123A78CDD0E7D90 CRC64;

Query Match 67.6%; Score 100; DB 11; Length 108;
 Best Local Similarity 70.4%; Pred. No. 2.5e-07;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRKMKKKTALDASALQ 27
 DB 49 EROIKIWFQNRKMKKKEKHDSQAFT 75

RESULT 4

ID Q9U9Z5 PRELIMINARY; PRT; 93 AA.
 AC Q9U9Z5; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Sex comb reduced homeodomain protein (Fragment).
 OS Lingula unguis.
 OC Eukaryota; Metazoa; Brachiopoda; Linguliformes; Lingulata; Lingulidae;
 OC Lingulidae; Lingulidae; Lingula.
 NCBI_TaxId=7574;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 99318125; PubMed; 10391241;
 RA de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adourte A., Akam M.,
 RA Carroll S.B., Balavoine G.;
 RT "Hox genes in brachiopods and priapulids and protostome evolution."
 RL Nature 399:772-776(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AF144674; MAD45589.1; -
 DR HSSP; P02833; ISAN.
 DR TRANSFAC; T03872; -
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR00047; HTH_Lamdbrepressr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00071; HOMEBOX 2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON TER 1
 SQ SEQUENCE 93 AA; 11224 MW; 5DC0379A30DF0137 CRC64;

Query Match 66.2%; Score 98; DB 5; Length 93;
 Best Local Similarity 67.9%; Pred. No. 4.3e-07;
 Matches 19; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRKMKKKTALDASALQ 28
 DB 48 EROIKIWFQNRKMKKKEQKALHTKTE 75

RESULT 5

ID Q26375 PRELIMINARY; PRT; 60 AA.
 AC Q26375; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE DNA binding protein Ahox2 (Fragment).
 GN AHOX2.
 OS Styela clava (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Styelidae; Styela.
 NCBI_TaxId=7725;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=95011617; PubMed=7926803;
RA Ge T., Lee H., Tomlinson C.R.;
RT "identification of an antenapedia-like homeobox gene in the ascidians
Styela clava and S. plicata.";
RL Gene 147:219-222 (1994).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: S73920; AAB33061.2; -.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000047; HTH_lambdarepressr.
DR Pfam: PF00046; homeobox_1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 7630 MW; F506301E9679BA25 CRC64;
Query Match 65.5%; Score 97; DB 5; Length 60;
Best Local Similarity 94.1%; Pred. No. 3.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRQIKWIFQNRMKMKK 17
DB 42 DRQYKIFQNRMKMKK 58
RESULT 6
ID Q817C9 PRELIMINARY; PRT; 90 AA.
AC Q817C9;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative homeobox protein Hox6/7 (Fragment).
GN Hox6/7.
OS Clona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cloniidae; Clona.
OX NCBI_Taxid=7719;
RN [1]
RP SEQUENCE FROM N.A.
RA Spagnuolo A., Ristoreatore F., Di Gregorio A., Antello F., Branno M.,
RT "unusual number and genomic organization of Hox genes in the tunicate
Clona intestinalis.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ535674; CAD59670.1; -.
KW Homeobox; DNA-binding; Nuclear protein.
FT NON_TER 1
FT NON_TER 11352 MW; CAAADGB261FE908E CRC64;
SQ SEQUENCE 90 AA; 11352 MW; CAAADGB261FE908E CRC64;
Query Match 65.5%; Score 97; DB 5; Length 90;
Best Local Similarity 64.3%; Pred. No. 5.9e-07;
Matches 18; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 DRQIKWIFQNRMKMKK 28
DB 57 EROIKWIFQNRMKMKK 84
RESULT 7
ID Q26611 PRELIMINARY; PRT; 181 AA.
AC Q26611;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Homeobox protein (Fragment).
Query Match 65.5%; Score 97; DB 5; Length 194;
Best Local Similarity 94.1%; Pred. No. 1.2e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRQIKWIFQNRMKMKK 17
DB 80 DRQYKIFQNRMKMKK 96
RESULT 8
ID Q26478 PRELIMINARY; PRT; 194 AA.
AC Q26478;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Homeobox protein (Fragment).
GN Styela clava (Sea squirt).
OS Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Scolidobranchia; Styelidae; Styela.
OX NCBI_Taxid=7725;
RN [1]
RP SEQUENCE FROM N.A.
RA Ge T., Lee H., Tomlinson C.R.;
RT "identification of an Antenapedia-like Homeobox Gene in the Ascidians
Styela clava and Plicata.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: U05571; AAL16226.1; -.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000047; HTH_lambdarepressr.
DR Pfam: PF00046; homeobox_1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 20873 MW; AF39911408F06672 CRC64;
Query Match 65.5%; Score 97; DB 5; Length 181;
Best Local Similarity 94.1%; Pred. No. 1.2e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRQIKWIFQNRMKMKK 17
DB 80 DRQYKIFQNRMKMKK 96
RESULT 8
ID Q26478 PRELIMINARY; PRT; 194 AA.
AC Q26478;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Homeobox protein (Fragment).
GN Styela clava (Sea squirt).
OS Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Scolidobranchia; Styelidae; Styela.
OX NCBI_Taxid=7725;
RN [1]
RP SEQUENCE FROM N.A.
RA Ge T., Lee H., Tomlinson C.R.;
RT "identification of an Antenapedia-like Homeobox Gene in the Ascidians
Styela clava and Plicata.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: U05571; AAL16226.1; -.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000047; HTH_lambdarepressr.
DR Pfam: PF00046; homeobox_1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 21866 MW; 8AD1B15B3R4800BC CRC64;
Query Match 65.5%; Score 97; DB 5; Length 194;

OS Styela plicata (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Scolidobranchia; Styelidae; Styela.
OX NCBI_Taxid=7725;
RN [1]
RP SEQUENCE FROM N.A.
RA Ge T., Lee H., Tomlinson C.R.;
RT "identification of an Antenapedia-like Homeobox Gene in the Ascidians
Styela clava and Plicata.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: U05600; AAL16288.1; -.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000047; HTH_lambdarepressr.
DR Pfam: PF00046; homeobox_1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 20873 MW; AF39911408F06672 CRC64;
Query Match 65.5%; Score 97; DB 5; Length 181;
Best Local Similarity 94.1%; Pred. No. 1.2e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRQIKWIFQNRMKMKK 17
DB 80 DRQYKIFQNRMKMKK 96
RESULT 8
ID Q26478 PRELIMINARY; PRT; 194 AA.
AC Q26478;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Homeobox protein (Fragment).
GN Styela clava (Sea squirt).
OS Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Scolidobranchia; Styelidae; Styela.
OX NCBI_Taxid=7725;
RN [1]
RP SEQUENCE FROM N.A.
RA Ge T., Lee H., Tomlinson C.R.;
RT "identification of an Antenapedia-like Homeobox Gene in the Ascidians
Styela clava and Plicata.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: U05571; AAL16226.1; -.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000047; HTH_lambdarepressr.
DR Pfam: PF00046; homeobox_1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 21866 MW; 8AD1B15B3R4800BC CRC64;
Query Match 65.5%; Score 97; DB 5; Length 194;

Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DROIKIFQNRMRKWK 17
|||:|||||
DB 52 DROIKIFQNRMRKWK 68

RESULT 9

0817C8 PRELIMINARY; PRT; 435 AA.
ID 0817C8
AC 0817C8
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Putative homeobox protein Hox10.
GN Hox10.
OS Clona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Clona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RA Spagnuolo A., Ristocratore F., Di Gregorio A., Aniello F., Branno M.,
Di Lauro R.;
RT "Unusual number and genomic organization of Hox genes in the tunicate
Clona intestinalis."
RL Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ535675; CAD59671.1; -.
KW Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 435 AA; 48739 MW; D8D0F579C02BC9E2 CRC64;

Query Match 65.5%; Score 97; DB 5; Length 435;
Best Local Similarity 94.1%; Pred. No. 3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DROIKIFQNRMRKWK 17
|||:|||||
DB 295 DROIKIFQNRMRKWK 311

RESULT 10

09PMM4 PRELIMINARY; PRT; 231 AA.
ID 09PMM4
AC 09PMM4
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
GN Homeobox protein.
OS Brachydonto rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99051425; PubMed=9831563;
RA Amores A., Force A., Yan Y.-L., Wang Y.-L., Fritz A., Prince V.,
Ho R., Amemiya C., Langeland J., Westerfield M., Ekker M.,
Postlethwait J.;
RT "Zebrafish hox clusters and vertebrate genome evolution."
RL Science 282:1711-1714 (1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF071265; AAD15958.1; -.
DR HSSP; P02833; 9ANT.
DR TRANSFAC; T03667;
DR ZFIN; ZDB-GENE-990415-113; hox6a.
DR InterPro; IPR001827; Antennapedia.
DR Pfam; PF00046; homeobox.1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEOBOX.

DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 231 AA; 26733 MW; 65164A13541D78BA CRC64;

Query Match 65.2%; Score 96.5; DB 13; Length 231;
Best Local Similarity 69.0%; Pred. No. 1.8e-06;
Matches 20; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

OY 1 DROIKIFQNRMRKWK-TLDSALQTE 28
:|||||:|||||:|:|
DB 183 EROIKIFQNRMRKWKETLSTVPGTE 211

RESULT 11

09PSDS PRELIMINARY; PRT; 101 AA.
ID 09PSDS
AC 09PSDS
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE HOXC-6 product (HOXC-6 protein).
GN HOXC-6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RC MEDLINE=95151548; PubMed=7848839;
RA Gaunt S.J.;
RT "Conservation in the Hox code during morphological evolution."
RL In: J. Dev. Biol. 38:549-552 (1994).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; X80114; CAB94151.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox.1.
DR PRINTS; PR00024; HOMEOBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 101 AA; 11592 MW; 9637DB0AAB85546D CRC64;

Query Match 64.9%; Score 96; DB 13; Length 101;
Best Local Similarity 72.0%; Pred. No. 9.4e-07;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 DROIKIFQNRMRKKTALDASAL 25
:|||||:|||||:|:|
DB 49 EROIKIFQNRMRKKSINLSTYL 73

RESULT 12

09PVS0 PRELIMINARY; PRT; 82 AA.
ID 09PVS0
AC 09PVS0
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE HOXB5A (Fragment).
GN HOXB5A.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

OC Belontiiformes; Adriantichthyidae; Oryziatidae; Oryziatidae.
 OX NCBI_TaxID=8090;
 RN [1]
 RE SEQUENCE FROM N.A.
 RA Kondo S., Naruse K., Shima A.;
 RT "Hox genes of the medakafish *Oryzias latipes*.";
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AB026959; BAA6242.1; -.
 DR HSRP; P02833; 9ANT.
 DR InterPro; IPR01356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR ProDom; PD00010; Homeobox; 1.
 DR SMART; SMO0389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KM DNA-binding; Homeobox; Nuclear protein.
 FT NON TER 1 1
 ST SEQUENCE 82 AA; 9939 MW; 6B6828D280511888 CRC64;
 Query Match 64.5%; Score 95.5; DB 13; Length 82;
 Best Local Similarity 60.0%; Pred. No. 9e-07;
 Matches 21; Conservative 1; Mismatches 4; Indels 9; Gaps 1;
 Qy 1 DRQIKWFORRMKMKK-----TALDASALQ 26
 Db 47 ERQIKWFORRMKMKKDKNKMSLRPGASHQ 81
 RESULT 13
 Q09VZ9 PRELIMINARY; PRT; 219 AA.
 ID Q09VZ9;
 AC Q09VZ9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hoxa-7 protein (Homeodomain transcription factor Hoxa-7).
 OS Gallus gallus (chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9931;
 RN [1]
 RE SEQUENCE FROM N.A.
 RA MEDLINE-2125551; PubMed-11357191;
 RA Gaunt S.;
 RT "Gradients and forward spreading of vertebrate Hox gene expression
 RT detected using a Hox/lacZ transgene.";
 RL Dev. Dyn. 221:26-36(2001).
 RN [2]
 RE SEQUENCE FROM N.A.
 RA Oberig K.C., Eichele G.;
 RT "Hox gene expression and regulation in the presumptive wing region of
 RT the chick lateral plate mesoderm (Abstract # 286).";
 RL Dev. Biol. 210:228-228(1999).
 RN [3]
 RE SEQUENCE FROM N.A.
 RA Oberig K.C., Piza C.U., Creamer D.H., Revelle J.-P., Eichele G.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AJ291729; CAC37629.1; -.
 DR EMBL; AF408695; AAL01899.1; -.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRODOM; PD00010; Homeobox; 1.
 DR SMART; SMO0389; HOX; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.

KM DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 219 AA; 24952 MW; 4BA8046D52C0705 CRC64;
 Query Match 64.2%; Score 95; DB 13; Length 219;
 Best Local Similarity 70.8%; Pred. No. 2.9e-06;
 Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 DRQIKWFORRMKMKKKTALDASA 24
 Db 170 ERQIKWFORRMKMKKHKHSS 193
 RESULT 14
 Q057359 PRELIMINARY; PRT; 43 AA.
 ID Q057359;
 AC Q057359;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hox5 protein (Fragment).
 OS HOXB5 OR HOXA5.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RE SEQUENCE FROM N.A.
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;
 RT "Zebrafish hox genes: genomic organization and modified collinear
 RT expression patterns in the trunk.";
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; Y14526; CAA74861.1; -.
 DR ZFIN; ZDB-GENE-000823-6; hox5b.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD00010; Homeobox; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KM DNA-binding; Homeobox; Nuclear protein.
 FT NON TER 1 1
 ST SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;
 Query Match 63.9%; Score 94.5; DB 13; Length 43;
 Best Local Similarity 67.9%; Pred. No. 6.5e-07;
 Matches 19; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
 Qy 1 DRQIKWFORRMKMKKKTALDASALQ 27
 Db 9 ERQIKWFORRMKMKKDKNKMSLST 36
 RESULT 15
 Q05008 PRELIMINARY; PRT; 80 AA.
 ID Q05008;
 AC Q05008;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Antp protein (Fragment).
 OS ANTP.
 OS Artemia sanctificana (Brine shrimp) (Artemia franciscana).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
 OC Artemiidae; Artemia.
 OX NCBI_TaxID=6661;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC STRAIN=North arm of Great Salt Lake;
 RA Auerof M., Akam M.;
 RT "Hox/Hox genes in a crustacean: implication for the origin of insect
 RT and crustacean body plans.";

```

RL  Curr Biol. 3:73-78(1993).
CC  -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR  EMBL; X70077; CAA49682.1; -.
DR  HSSP; P02833; 9ANT.
DR  InterPro; IPR001356; Homeobox.
DR  Pfam; PF00046; homeobox; 1.
DR  PRINTS; PR00024; HOMEBOX.
DR  ProDom; PD000010; Homeobox; 1.
DR  SMART; SM00389; HOX; 1.
DR  PROSITE; PS00027; HOMEBOX_1; 1.
DR  PROSITE; PS00071; HOMEBOX_2; 1.
KW  DNA-binding; Homeobox; Nuclear protein.
FT  NON_TER
SQ  SEQUENCE 80 AA; 9878 MW; 48472705CEDFCE7 CRC64;

Query Match      63.9%; Score 94.5; DB 5; Length 80;
Best Local Similarity 64.3%; Pred. No. 1.2e-06;
Matches 18; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Qy  1 DROIKIFQNRMRKWK--KTALDASAL 25
    :|||||:|||||:|:|:|
Db  42 ERQIKWFQNRMRKWKENKSKVDGCL 69

```

Search completed: February 18, 2004, 14:36:01
 Job time : 81.0526 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 30.7632 Seconds

(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKWFGNRBRMKNKKTALDASALQTE 26

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.76:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	69.6	81	2	B29585 homeotic protein H
2	103	69.6	96	2	A05266 homeotic protein H
3	103	69.6	97	2	C27176 homeotic protein H
4	103	69.6	224	2	S26400 homeotic protein H
5	103	69.6	224	2	A31324 homeotic protein H
6	100	67.6	105	2	A27471 homeotic protein H
7	100	67.6	119	2	A03314 homeotic protein m
8	100	67.6	229	2	A28329 homeotic protein H
9	99	66.9	75	2	I51341 homeo box protein
10	98	66.2	86	2	S08303 homeotic protein H
11	97	65.5	60	2	PC2339 antennapedia-1like
12	97	65.5	60	2	PC2400 antennapedia-1like
13	96.5	65.2	96	2	S08639 homeotic protein z
14	96	64.9	234	1	S00992 homeotic protein H
15	95	64.2	66	2	S15536 homeotic protein H
16	95	64.2	103	2	A32167 homeotic protein H
17	95	64.2	153	1	WJHUC homeotic protein H
18	95	64.2	153	1	WJMSX6 homeotic protein H
19	95	64.2	230	2	S00592 homeotic protein H
20	95	64.2	234	1	S02014 homeotic protein H
21	95	64.2	235	2	A56568 homeotic protein H
22	95	64.2	235	2	S72429 homeotic protein H
23	95	64.2	242	1	A39164 homeotic protein H
24	94.5	63.9	118	2	A24777 homeotic protein H
25	94.5	63.9	118	2	UT0273 homeotic protein H
26	94.5	63.9	118	2	B24777 homeotic protein H
27	94.5	63.9	269	1	A43551 homeotic protein H
28	94.5	63.9	269	1	A45578 homeotic protein H
29	94.5	63.9	275	1	WJZFX2 homeotic protein H

30	94	63.5	33	2	S57235 antennapedia prote
31	94	63.5	42	2	I65241 homeotic protein H
32	94	63.5	45	2	PC1216 homeotic protein D
33	94	63.5	48	2	I51439 homeobox protein -
34	94	63.5	66	2	S15538 homeotic protein H
35	94	63.5	71	2	JC1161 homeotic protein 3
36	94	63.5	71	2	A60084 homeotic protein H
37	94	63.5	74	2	D34510 homeotic protein H
38	94	63.5	75	2	S58852 homeotic protein S
39	94	63.5	76	2	C43559 homeotic protein R
40	94	63.5	78	2	I51342 homeo box protein
41	94	63.5	81	2	S47605 homeotic protein H
42	94	63.5	82	2	S08302 homeotic protein H
43	94	63.5	83	2	S47603 homeotic protein H
44	94	63.5	83	2	S50066 homeotic protein H
45	94	63.5	86	2	A34510 homeotic protein H

ALIGNMENTS

RESULT 1

B29585

homeotic protein Hox 2.2 precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997

C/Accession: B29585

R:Lonai, P.; Arman, E.; Czornak, H.; Ruddle, F.H.; Blatt, C.

DNA 6, 409-418, 1987

A:Title: New murine homeoboxes: structure, chromosomal assignment, and differential ex

A:Reference number: A29585; PMID:88054465; PMID:2890503

A:Accession: B29585

A:Molecule type: DNA

A:Residues: 1-81 <LON>

A:Cross-references: GB:M18167

A>Note: the authors translated the codon CAG for residue 69 as Glu

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:4-60/Domain: homeobox homology <Hox>

Query Match 69.6%; Score 103; DB 2; Length 81;
Best Local Similarity 70.0%; Pred. No. 4.5e-08;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

OY 1 DRQIKWFGNRBRMKNKKTALDASALQTE 28

DB 44 EROIKWFGNRBRMKNKKTALDASALQTE 73

RESULT 2

A05266

homeotic protein Hox B6 - human (fragment)

N:Alternate names: homeotic protein Hox 2B; homeotic protein Hu2

C:Species: Homo sapiens (man)

C>Date: 05-Jun-1987 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997

C/Accession: A05266; S15537

R:Levine, M.; Rudin, G.M.; Tjian, R.

Cell 38, 667-673, 1984

A:Title: Human DNA sequences homologous to a protein coding region conserved between h

A:Reference number: A05265; PMID:85024858; PMID:6091895

A:Accession: A05266

A:Molecule type: DNA

A:Residues: 1-96 <LEV>

A:Cross-references: EMBL:X02571

A>Note: this reading frame extends between two stop codons and does not begin with a s

R:Boncinelli, E.; Acampora, D.; Parnase, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; S

Genome 31, 745-756, 1989

A:Title: Organization of human class I homeobox genes

A:Reference number: S15036; PMID:90215256; PMID:2576652

A:Accession: S15537

A:Molecule type: DNA

A:Residues: 18-19, 'R', 21-83 <RON>

C:Genetics:

A:Gene: GDB:H0XB6
 A:Cross-references: GDB:120659; OMIM:142961
 A:Map position: 17q21.3-17q21.3
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:19-75/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 96;
 Best Local Similarity 70.0%; Pred. No. 5.3e-08;
 Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DROIKIFQNRMRMKKTKTA--LDASALQTE 28
 :|||||
 Db 59 ERQIKIFQNRMRMKKTKLSASQLSAR 88

RESULT 3

homeotic protein Hox 2.2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Sep-1999
 C:Accession: C27176
 R:Hart, C.P.; Painhod, A.; Ruddle, F.H.
 Genomtics 1, 182-195, 1987
 A:Title: Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes: evolutionary
 A:Reference number: A27176; PMID:88085193; PMID:2891608
 A:Accession: C27176
 A:Molecule type: DNA
 A:Residues: 1-97 <HAR>
 A:Cross-references: GB:M18401; NID:G193936; PIDN:AACT7130.1; PID:G3335322
 C:Genetics:
 A:Gene: Hox-2.2
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:20-76/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 97;
 Best Local Similarity 70.0%; Pred. No. 5.4e-08;
 Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DROIKIFQNRMRMKKTKTA--LDASALQTE 28
 :|||||
 Db 60 ERQIKIFQNRMRMKKTKLSASQLSAR 89

RESULT 4

homeotic protein Hox 2.2 (variant 1) - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Nov-2000
 C:Accession: S26400; S26401
 R:Shen, W.; Derner, K.; Simionitch-Eason, T.A.; Lawrence, H.J.; Largman, C.
 Nucleic Acids Res. 19, 539-545, 1991
 A:Title: Alternative splicing of the Hox 2.2 homeobox gene in human hematopoietic cells
 A:Reference number: S26400; PMID:91187672; PMID:1672751
 A:Accession: S26400
 A:Molecule type: DNA
 A:Residues: 1-224 <SHE>
 A:Cross-references: EMBL:X58431; NID:G32369; PIDN:CAA41335.1; PID:G32370
 A:Experimental source: tissue-type placenta
 A:Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue 60 &
 A:Note: the authors did not translate the codons for residues 139, and 140
 C:Genetics:
 A:introns: 139/1
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulation
 F:147-203/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 224;
 Best Local Similarity 70.0%; Pred. No. 1.3e-07;
 Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DROIKIFQNRMRMKKTKTA--LDASALQTE 28
 :|||||
 Db 187 ERQIKIFQNRMRMKKTKLSASQLSAR 216

RESULT 5

homeotic protein Hox 2.2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 24-Sep-1999
 C:Accession: A31324
 R:Schughart, K.; Utecht, M.P.; Awgulewitsch, A.; Ruddle, F.H.
 Proc. Natl. Acad. Sci. U.S.A. 85, 5582-5586, 1988
 A:Title: Structure and expression of Hox-2.2, a murine homeobox-containing gene.
 A:Reference number: A31324; PMID:88289762; PMID:2899893
 A:Accession: A31324
 A:Molecule type: RNA
 A:Residues: 1-224 <SCH>
 A:Cross-references: GB:A03782; NID:G193929; PIDN:AAA37843.1; PID:G387203
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:147-203/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 224;
 Best Local Similarity 70.0%; Pred. No. 1.3e-07;
 Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DROIKIFQNRMRMKKTKTA--LDASALQTE 28
 :|||||
 Db 187 ERQIKIFQNRMRMKKTKLSASQLSAR 216

RESULT 6

homeotic protein R5 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-May-1997
 C:Accession: A27471
 R:Palzon, M.; Sanderson, N.; Chung, S.Y.
 Gene 54, 23-32, 1987
 A:Title: Cloning and expression of rat homeo-box-containing sequences.
 A:Reference number: A91576; PMID:87277429; PMID:2886401
 A:Accession: A27471
 A:Molecule type: DNA
 A:Residues: 1-105 <PAL>
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:6-62/Domain: homeobox homology <HOX>

Query Match 67.6%; Score 100; DB 2; Length 105;
 Best Local Similarity 70.4%; Pred. No. 1.6e-07;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DROIKIFQNRMRMKKTKTALDASALQTE 27
 :|||||
 Db 46 ERQIKIFQNRMRMKKTKENHDESGAP 72

RESULT 7

homeotic protein m6 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Jul-1997
 C:Accession: A03314; S14043
 R:Colberg-Poley, A.M.; Voss, S.D.; Chowdhury, K.; Gruss, P.
 Nature 314, 713-718, 1985
 A:Title: Structural analysis of murine genes containing homeo box sequences and their
 A:Reference number: A03314; PMID:85188311; PMID:2966010

A/Accession: A03314
A/Molecule type: DNA
A/Residues: 1-119 <COL>
R/Beiler, G.; Bucan, M.; Francke, U.; Colberg-Poley, A.M.; Gruss, P.
EMBO J. 5, 2209-2215, 1986
A/Title: Sequential expression of murine homeo box genes during F9 EC cell differentiation
A/Reference number: 153785; MUID:8705860; PMID:2877873
A/Accession: S14063
A/Molecule type: DNA
A/Residues: 19-48, 'RT', 51-87 <BRE>
C/Genetics:
A/Gene: m6
C/Superfamily: unassigned homeobox proteins; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F/20-76/Domain: homeobox homology <Hox>

Query Match 67.6%; Score 100; DB 2; Length 119;
Best Local Similarity 70.4%; Pred. No. 1.8e-07;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRKMKKKTALDASALQT 27
:|||||
Db 60 ERQIKWIFQNRKMKKCKKHDSQAPT 86

RESULT 8
A28329
homeotic protein Hox A7 - mouse
N/Alternate names: homeotic protein Hox 1.1; m6 homeotic protein
C/Species: Mus musculus (house mouse)
C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
C/Accession: A28329, I49131
R/Kessel, M.; Schulze, F.; Fild, M.; Gruss, P.
Proc. Natl. Acad. Sci. U.S.A. 84, 5306-5310, 1987
A/Title: Primary structure and nuclear localization of a murine homeodomain protein.
A/Reference number: A28329; MUID:87260976; PMID:2885847
A/Accession: A28329
A/Molecule type: mRNA
A/Residues: 1-229 <RES>
A/Cross-references: GB:M17192; NID:g193906; PIDN:AAA37833.1; PID:g309313
R/Perikh, H.; Shah, S.; Hilt, D.; Peterkofsky, A.
Gene 154, 237-242, 1995
A/Title: Organization, sequence and regulation of expression of the murine Hoxa-7 gene.
A/Reference number: I49131; MUID:95197009; PMID:7850170
A/Accession: I49131
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-42, 'GAG', 46-229 <RES>
A/Cross-references: EMBL:U15972; NID:g664757; PIDN:AAC52160.1; PID:g664758
C/Genetics:
A/Gene: Hoxa7
A/Intons: 126/1
C/Species: Salmo gairdneri (Atlantic salmon)
C/Superfamily: homeotic protein Hox A7; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F/130-186/Domain: homeobox homology <Hox>

Query Match 67.6%; Score 100; DB 2; Length 229;
Best Local Similarity 70.4%; Pred. No. 3.6e-07;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRKMKKKTALDASALQT 27
:|||||
Db 170 ERQIKWIFQNRKMKKCKKHDSQAPT 196

RESULT 9
I51341
homeo box protein - Atlantic salmon (fragment)
C/Species: Salmo gairdneri (Atlantic salmon)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
C/Accession: I51341
R/Fjose, A.; Molven, A.; Eiken, H.G.
Gene 62, 141-152, 1988

A/Title: Molecular cloning and characterization of homeobox-containing genes from Acta
A/Reference number: I51341; MUID:88226009; PMID:2897318
A/Accession: I51341
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-75 <FO>
A/Cross-references: GB:M18903; NID:g213797; PIDN:AAA49559.1; PID:g213798
C/Superfamily: unassigned homeobox proteins; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F/2-58/Domain: homeobox homology <Hox>

Query Match 66.9%; Score 99; DB 2; Length 75;
Best Local Similarity 75.0%; Pred. No. 1.6e-07;
Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRKMKKKTALDASA 24
:|||||
Db 42 ERQIKWIFQNRKMKKCKKHDS 65

RESULT 10
S08303
homeotic protein Hox 2.2 - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 17-Oct-1997
C/Accession: S08303
R/Wedden, S.E.; Pang, K.; Eichele, G.
Development 105, 639-650, 1989
A/Title: Expression pattern of homeobox-containing genes during chick embryogenesis.
A/Reference number: S08302; MUID:90126373; PMID:2575515
A/Accession: S08303
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-86 <WED>
A/Cross-references: EMBL:X16847
C/Superfamily: unassigned homeobox proteins; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F/10-66/Domain: homeobox homology <Hox>

Query Match 66.2%; Score 98; DB 2; Length 86;
Best Local Similarity 66.7%; Pred. No. 2.6e-07;
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWIFQNRKMKKKTALDASALQTE 28
:|||||
Db 50 ERQIKWIFQNRKMKKCKKHDS 79

RESULT 11
PC2399
antennapedia-like homeotic protein Ahox 2 - sea squirt (Styela clava) (fragment)
C/Species: Styela clava
C/Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jul-2000
C/Accession: PC2399
R/Ge, T.; Lee, H.; Tomlinson, C.R.
Gene 147, 219-222, 1994
A/Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela
A/Reference number: PC2399; MUID:95011617; PMID:7926803
A/Accession: PC2399
A/Molecule type: DNA
A/Residues: 1-60 <GRT>
A/Cross-references: GB:S73920; NID:g693714; PIDN:AAA33061.2; PID:g7387472
A/Note: The authors translated the codon ATT for residue 47 as Glu
C/Superfamily: unassigned homeobox proteins; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F/2-58/Domain: homeobox homology <Hox>

Query Match 65.5%; Score 97; DB 2; Length 60;
Best Local Similarity 94.1%; Pred. No. 2.5e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRKMKK 17
:|||||

Db 42 DROVKIWFQNRMRMKKK 58

RESULT 12

PC2400 antennapedia-like homeotic protein Ahox 3 - sea squirt (Styela plicata) (fragment)

C/Species: Styela plicata

C/Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 17-Oct-1997

C/Accession: PC2400

R/Gene: T.; Lee, H.; Tomlinson, C.R.

Gene 147, 219-222, 1994

A/Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela cl

A/Reference number: PC2399; MUID:95011617; PMID:7926803

A/Accession: PC2400

A/Molecule type: DNA

A/Residues: 1-60 <GCT>

A/Note: The authors translated the codon ATA for residue 47 as Glu

C/Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/2-58/Domain: homeobox homology <HOX>

Query Match 65.5%; Score 97; DB 2; Length 60;

Best Local Similarity 94.1%; Pred. No. 2.5e-07;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMRMKKK 17

Db 42 DROVKIWFQNRMRMKKK 58

RESULT 13

S08639 homeotic protein zf-61 - zebra fish

C/Species: Brachydanio rerio (zebra fish)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999

C/Accession: S08639

R/NJ01etad, P.R.; Molven, A.; Apold, J.; Fjose, A.

EMBO J. 9, 515-524, 1990

A/Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory

A/Reference number: S08639; MUID:90151628; PMID:1968004

A/Accession: S08639

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-96 <NCO>

A/Cross-references: EMBL:X17266; NID:962538; PIDN:CAA35170.1; PID:el6657; PID:g1334622

C/Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/8-66/Domain: homeobox homology <HOX>

Query Match 65.2%; Score 96.5; DB 2; Length 96;

Best Local Similarity 69.0%; Pred. No. 4.8e-07;

Matches 20; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 1 DROIKIWFQNRMRMKKK-TALDASALQTE 28

Db 48 ERQIKIWFQNRMRMKKKETLSTVPGTE 76

RESULT 14

S00992 homeotic protein Hox 1 - African clawed frog

N/Alternate names: development-controlling protein; homeotic protein AC1; homeotic prote

C/Species: Xenopus laevis (African clawed frog)

C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 11-Jan-2002

C/Accession: S00992; S00993; A03116; S00590; T01066

R/Cho, K.W.Y.; Goetz, J.; Wright, C.V.E.; Fritz, A.; Hardwicke, J.; de Robertis, E.M.

EMBO J. 7, 2139-2149, 1988

A/Title: Differential utilization of the same reading frame in a Xenopus homeobox gene

A/Reference number: S00991; MUID:88329002; PMID:2901347

A/Accession: S00992

A/Molecule type: DNA

A/Residues: 1-234 <CHO>

A/Cross-references: EMBL:X12500; NID:g64743; PIDN:CAA31021.1; PID:g64744

A/Note: 216-Ser and 225-Gln were also found and are interpreted as minor allelic diffe

A/Accession: S00993

A/Molecule type: DNA

A/Residues: 83-215, 'S', 217-224, 'Q', 226-234 <CHW>

A/Cross-references: EMBL:X12499; NID:g64740; PIDN:CAA1020.1; PID:g64742

R/Carrasco, A.E.; McGinnis, W.; Gehring, W.J.; De Robertis, E.M.

Cell 37, 409-414, 1984

A/Title: Cloning of a Xenopus laevis gene expressed during early embryogenesis coding

A/Reference number: A03116; MUID:84205675; PMID:6327066

A/Accession: A03116

A/Molecule type: DNA

A/Residues: 134-138, 'S', 140-200 <CAR>

A/Cross-references: GB:K01943; NID:g214242; PIDN:AAA9743.1; PID:g214243

R/Fritz, A.; de Robertis, E.M.

Nucleic Acids Res. 16, 1453-1469, 1988

A/Title: Xenopus homeobox-containing cDNAs expressed in early development.

A/Reference number: S00590; MUID:88157707; PMID:2894634

A/Accession: S00590

A/Molecule type: mRNA

A/Residues: 121-215, 'S', 217-224, 'Q', 226-234 <PRI>

A/Cross-references: EMBL:X07101; NID:g64738; PIDN:CAA30122.1; PID:g1334649

C/Genetics:

A/Gene: AC1

C/Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/1-234/Product: homeotic protein Hbox1, allelic version PRI #status predicted <MAT>

F/83-215/Product: homeotic protein Hbox1, allelic version PRI #status predicted <MAT>

F/142-198/Domain: homeobox homology <HOX>

Query Match 64.9%; Score 96; DB 2; Length 234;

Best Local Similarity 72.0%; Pred. No. 1.4e-06;

Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMRMKKKTALDASAL 25

Db 182 ERQIKIWFQNRMRMKKKESVLSSTL 206

RESULT 15

S15536 homeotic protein Hox A7 - human (fragment)

N/Alternate names: homeotic protein Hox 1A

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997

C/Accession: S15536

R/Boncinelli, E.; Acampora, D.; Pannese, M.; d'Episcopo, M.; Somma, R.; Gaudino, G.; S

Genome 31, 745-756, 1989

A/Title: Organization of human class I homeobox genes.

A/Reference number: S15036; MUID:90215256; PMID:2576652

A/Accession: S15536

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-66 <BON>

C/Genetics:

A/Gene: GDB:HOXA7

A/Cross-references: GDB:120647; OMIM:142950

A/Map position: 7p15.3-7p15.3

C/Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/2-58/Domain: homeobox homology <HOX>

Query Match 64.2%; Score 95; DB 2; Length 66;

Best Local Similarity 81.0%; Pred. No. 5.4e-07;

Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMRMKKKTALD 21

Db 42 ERQIKIWFQNRMRMKKKSHKD 62

Search completed: February 18, 2004, 14:38:53

Job time : 30.7632 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:16:39 ; Search time 32.9737 Seconds
(Without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKWFOQRKMKKKTALDASALQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	64.2	24	4 US-09-419-826-34	Sequence 34, Appl
2	95	64.2	27	4 US-09-040-725A-2	Sequence 2, Appl
3	94	63.5	34	4 US-09-347-504-79	Sequence 79, Appl
4	94	63.5	61	2 US-08-202-044-3	Sequence 3, Appl
5	94	63.5	61	3 US-08-751-344B-3	Sequence 3, Appl
6	94	63.5	61	3 US-08-751-344B-6	Sequence 6, Appl
7	94	63.5	61	3 US-08-751-344B-9	Sequence 9, Appl
8	93	62.8	22	4 US-09-051-363C-50	Sequence 50, Appl
9	93	62.8	27	3 US-09-051-934-51	Sequence 51, Appl
10	93	62.8	27	3 US-09-051-934-52	Sequence 52, Appl
11	93	62.8	61	3 US-08-751-344B-7	Sequence 7, Appl
12	93	62.2	16	2 US-08-928-958-7	Sequence 7, Appl
13	92	62.2	16	2 US-08-810-540-3	Sequence 3, Appl
14	92	62.2	16	2 US-08-810-540-6	Sequence 6, Appl
15	92	62.2	16	2 US-09-072-429-7	Sequence 7, Appl
16	92	62.2	16	3 US-08-964-302A-6	Sequence 6, Appl
17	92	62.2	16	3 US-09-116-294-4	Sequence 4, Appl
18	92	62.2	16	3 US-08-964-614A-4	Sequence 4, Appl
19	92	62.2	16	3 US-08-849-486-1	Sequence 1, Appl
20	92	62.2	16	3 US-08-849-486-4	Sequence 4, Appl
21	92	62.2	16	3 US-09-208-966-54	Sequence 54, Appl
22	92	62.2	16	3 US-09-308-935-8	Sequence 8, Appl
23	92	62.2	16	3 US-09-441-416A-6	Sequence 6, Appl
24	92	62.2	16	4 US-09-296-089-33	Sequence 33, Appl
25	92	62.2	16	4 US-09-419-826-35	Sequence 35, Appl
26	92	62.2	16	4 US-09-302-305C-10	Sequence 10, Appl
27	92	62.2	16	4 US-09-346-847-1	Sequence 1, Appl

28	92	62.2	16	4 US-09-346-847-25	Sequence 25, Appl
29	92	62.2	16	4 US-09-057-363C-47	Sequence 47, Appl
30	92	62.2	16	4 US-09-043-560B-3	Sequence 3, Appl
31	92	62.2	17	4 US-09-346-847-17	Sequence 17, Appl
32	92	62.2	17	4 US-09-346-847-17	Sequence 20, Appl
33	92	62.2	17	4 US-09-346-847-22	Sequence 22, Appl
34	92	62.2	17	4 US-09-346-847-22	Sequence 27, Appl
35	92	62.2	18	3 US-08-838-545-20	Sequence 20, Appl
36	92	62.2	18	3 US-09-349-532-20	Sequence 20, Appl
37	92	62.2	19	4 US-09-346-847-23	Sequence 23, Appl
38	92	62.2	19	4 US-09-658-517C-7	Sequence 7, Appl
39	92	62.2	20	4 US-09-466-772-3	Sequence 3, Appl
40	92	62.2	20	4 US-09-346-847-16	Sequence 16, Appl
41	92	62.2	20	4 US-09-346-847-18	Sequence 18, Appl
42	92	62.2	20	4 US-09-346-847-30	Sequence 8, Appl
43	92	62.2	20	4 US-09-658-517C-8	Sequence 28, Appl
44	92	62.2	22	4 US-09-346-847-28	Sequence 4, Appl
45	89	60.1	42	3 US-08-751-344B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-419-826-34
Sequence 34, Application US/09419826
Patent No. 6306832
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDE ANTINEOGEN COMPOSITIONS AND METHODS
FOR TREATING BREAST CANCER
NUMBER OF SEQUENCES: 39
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/419,826
FILING DATE: 14-OCT-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/07711
FILING DATE: 14-APR-1998
APPLICATION NUMBER: US 60/043,545
FILING DATE: 14-APR-1997
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 19
OTHER INFORMATION: /note= "X = Phosphorylation"
US-09-419-826-34
Query Match 64.2%; Score 95; DB 4; Length 24;
Best local similarity 85.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
DB 1 RQIKWFOQRKMKKKTALD 21
QY 2 RQIKWFOQRKMKKKTALD 21
US-09-040-725A-2
Sequence 2, Application US/09040725A
Patent No. 6399584
GENERAL INFORMATION:
APPLICANT: Institut Curie
APPLICANT: CNRS

APPLICANT: Arpin, Monique
APPLICANT: Crepaldi, Tiziana
APPLICANT: Gautreau, Alexis
APPLICANT: Louvard, Daniel
TITLE OF INVENTION: Pharmaceutical composition containing ezrin mutated
TITLE OF INVENTION: on tyrosine 353
FILE REFERENCE: 39108200100
CURRENT APPLICATION NUMBER: US/09/040.725A
CURRENT FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (122)
OTHER INFORMATION: Xaa = tyrosine or a phosphorylated tyrosine
US-09-040-725A-2

Query Match 64.2%; Score 95; DB 4; Length 27;
Best Local Similarity 66.7%; Pred. No. 1.2e-07;
Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 2 ROIKIWFQNRMRKMKKTALDASALQTE 28
Db 1 ROIKIWFQNRMRKMKKRLQDXEERTK 27

RESULT 3
US-09-347-504-79
Sequence 79, Application US/09347504
Patent No. 6399075

GENERAL INFORMATION:
APPLICANT: Howley, Peter M.
APPLICANT: Benson, John
APPLICANT: Kasukawa, Hiroaki
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
FILE REFERENCE: HMV-041.01
CURRENT APPLICATION NUMBER: US/09/347.504
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 79
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
US-09-347-504-79

Query Match 63.5%; Score 94; DB 4; Length 34;
Best Local Similarity 94.1%; Pred. No. 2.3e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKWFONRMRKMKK 17
Db 1 ERQIKWFONRMRKMKK 17

RESULT 4
US-08-202-044-3
Sequence 3, Application US/08202044
Patent No. 5858973
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square

CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,044
FILING DATE: 23-FEB-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: MGH-124XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-202-044-3

Query Match 63.5%; Score 94; DB 2; Length 61;
Best Local Similarity 94.1%; Pred. No. 4.3e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKWFONRMRKMKK 17
Db 43 ERQIKWFONRMRKMKK 59

RESULT 5
US-08-751-344B-3
Sequence 3, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wilcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-NOV-6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-751-344B-3

Query Match 63.5%; Score 94; DB 3; Length 61;
Best Local Similarity 94.1%; Pred. No. 4.3e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFONRRMKWK 17
:|||||

Db 43 EROIKIWFONRRMKWK 59

RESULT 6
US-08-751-344B-6
Sequence 6, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-NO. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-751-344B-6

Query Match 63.5%; Score 94; DB 3; Length 61;
Best Local Similarity 94.1%; Pred. No. 4.3e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFONRRMKWK 17

Db 43 EROIKIWFONRRMKWK 59

RESULT 7
US-08-751-344B-9
Sequence 9, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-NO. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-751-344B-9

Query Match 63.5%; Score 94; DB 3; Length 61;
Best Local Similarity 94.1%; Pred. No. 4.3e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFONRRMKWK 17
:|||||

Db 43 EROIKIWFONRRMKWK 59

RESULT 8
US-09-057-363C-50
Sequence 50, Application US/09057363C
Patent No. 6551994
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle

STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,363C
FILING DATE: 08-Apr-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Christensen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 100066.406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-057-363C-50

Query Match 62.8%; Score 93; DB 4; Length 22;
Best Local Similarity 94.1%; Pred. No. 2e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RQIKWIFONRRMKKK 17
:|||||
Db 6 RQIKWIFONRRMKKK 22

RESULT 9
US-09-051-934-51
Sequence 51, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 27
TYPE: PRT
ORGANISM: phosphotyrosine binding domain
US-09-051-934-51

Query Match 62.8%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. No. 2.5e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 RQIKWIFONRRMKKKTALD 21
:|||||
Db 1 RQIKWIFONRRMKKKHIE 20

RESULT 10
US-09-051-934-52

Sequence 52, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52
LENGTH: 27
TYPE: PRT
ORGANISM: phosphotyrosine binding domain
FEATURE:
NAME/KEY: MOD RES
LOCATION: (24)
OTHER INFORMATION: Phosphorylated at Tyr
US-09-051-934-52

Query Match 62.8%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. No. 2.5e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 RQIKWIFONRRMKKKTALD 21
:|||||
Db 1 RQIKWIFONRRMKKKHIE 20

RESULT 11
US-08-751-344B-7
Sequence 7, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener, M.D., Joel F.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wilcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-NO. 6210960-1996
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9110
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-751-344B-7

Query Match 62.2%; Score 93; DB 3; Length 61;
Best Local Similarity 88.2%; Pred. No. 6e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKIWFQNRRMKWKK 17
DB 43 ERQVKIWFQNRMRMKWKK 59

RESULT 12

US-08-928-958-7
Sequence 7, Application US/08928958
Patent No. 5877282
GENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
APPLICANT: CLEAVELAND, JEFFREY S.
APPLICANT: BLAKE, JAMES
APPLICANT: HAFER, OMAR K.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
TITLE OF INVENTION: TRANSLLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026978
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-928-958-7

Query Match 62.2%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKIWFQNRRMKWKK 17
DB 1 RQIKIWFQNRRMKWKK 16

RESULT 13

US-08-810-540-3
Sequence 3, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-3

Query Match 62.2%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKIWFQNRRMKWKK 17
DB 1 RQIKIWFQNRRMKWKK 16

RESULT 14

US-08-810-540-6
Sequence 6, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-6

Query Match 62.2%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ROIKIWPNRRMKKK 17
DB 1 ROIKIWPNRRMKKK 16

RESULT 15
US-09-072-429-7
Sequence 7, Application US/09072429
Patent No. 5962415
GENERAL INFORMATION:
APPLICANT: Nadler, Steven G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN
TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,429
FILING DATE: 04-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Klein, Christopher A.
REGISTRATION NUMBER: 34,363
REFERENCE/DOCKET NUMBER: ON0141b
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 252-3714
TELEFAX: (609) 252-4526
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-072-429-7

Query Match 62.2%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ROIKIWPNRRMKKK 17
DB 1 ROIKIWPNRRMKKK 16

Search completed: February 18, 2004, 14:41:52
Job time : 32.9737 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 81.0526 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162
Sequence: 1 DRQIKIMFQNRKMKKRLADMSWLQTE 28

Scoring table: BLASTUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL_23:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101.5	62.7	274	5	Q9XYT7
2	97	59.9	60	5	Q26375
3	97	59.9	108	11	Q8JZW2
4	97	59.9	181	5	Q26611
5	97	59.9	194	5	Q26478
6	97	59.9	435	5	Q817C8
7	95.5	59.0	90	5	Q817C9
8	94	58.0	39	13	Q57368
9	94	58.0	43	13	Q57359
10	94	58.0	46	13	Q9PVR9
11	94	58.0	51	5	Q27413
12	94	58.0	51	5	Q23743
13	94	58.0	51	5	Q26407
14	94	58.0	57	13	Q9PVR8
15	94	58.0	58	5	Q9Y188
16	94	58.0	58	5	Q25208

17	94	58.0	58	13	Q57362	Q57362 brachydanio
18	94	58.0	59	5	Q8RWM9	Q8RWM9 lithobius a
19	94	58.0	59	5	Q9NB42	Q9NB42 anopheles g
20	94	58.0	59	13	Q9PVR5	Q9PVR5 oryzias lat
21	94	58.0	60	5	Q77143	Q77143 archegozete
22	94	58.0	60	5	Q77139	Q77139 archegozete
23	94	58.0	60	13	Q8QGL5	Q8QGL5 petromyzon
24	94	58.0	60	13	Q8QGL3	Q8QGL3 petromyzon
25	94	58.0	60	13	Q8QGL6	Q8QGL6 petromyzon
26	94	58.0	60	13	Q8QGL2	Q8QGL2 petromyzon
27	94	58.0	60	13	Q8QGL8	Q8QGL8 petromyzon
28	94	58.0	60	13	Q8QGL7	Q8QGL7 petromyzon
29	94	58.0	61	5	Q27910	Q27910 polyandroca
30	94	58.0	63	5	Q77138	Q77138 archegozete
31	94	58.0	63	5	Q8KMB2	Q8KMB2 holopneuste
32	94	58.0	66	13	Q57356	Q57356 brachydanio
33	94	58.0	69	5	Q9U9T4	Q9U9T4 nereis vires
34	94	58.0	69	5	Q9BMF7	Q9BMF7 halloctis a
35	94	58.0	70	5	Q967W5	Q967W5 folioma ca
36	94	58.0	71	13	Q9PVS3	Q9PVS3 oryzias lat
37	94	58.0	71	13	Q9PVS1	Q9PVS1 oryzias lat
38	94	58.0	73	5	Q9Y186	Q9Y186 priapulid c
39	94	58.0	74	13	Q57367	Q57367 brachydanio
40	94	58.0	75	5	Q25209	Q25209 junonia coe
41	94	58.0	75	13	Q9PVR6	Q9PVR6 oryzias lat
42	94	58.0	76	5	Q44257	Q44257 ethmostigm
43	94	58.0	77	5	Q44260	Q44260 ethmostigm
44	94	58.0	77	5	Q9Y187	Q9Y187 priapulid c
45	94	58.0	77	5	Q9U9Z4	Q9U9Z4 lingula ung

ALIGNMENTS

RESULT 1

ID	Q9XYT7	PRELIMINARY;	PRT;	274 AA.
AC	Q9XYT7	Q9XYT7		
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Scor-3 homeodomain protein (Fragment).			
GN	SCOX-3.			
OS	Casaliopsea xamachana.			
OC	Eukaryota; Metazoa; Chordata; Scyphozoa; Rhizostomaeae; Casaliopidae;			
OC	Casaliopidae.			
OX	NCBI_TaxID=12993;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kuhn K., Streif B., Schlierwater B.;			
RT	"Isolation of Hox genes from the scyphozoan Casaliopsea xamachana:			
RT	Implications for the early evolution of Hox genes."			
RL	J. Exp. Zool. 0:0-0(1999).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
DR	EMBL; AF124593; AAD32577.1; -.			
DR	HSSP; P02833; 9ANT.			
DR	InterPro; IPR001356; Homeobox.			
DR	InterPro; IPR000047; HTH_lambdarepressor.			
DR	Pfam; PF00046; homeobox_1.			
DR	PRINTS; PRO0024; HOMEBOX.			
DR	PRINTS; PRO0031; HTHREPRESSR.			
DR	ProDom; PD000010; Homeobox; 1.			
DR	SMART; SM00389; Hox; 1.			
DR	PROSITE; PS00027; HOMEBOX_1; 1.			
DR	PROSITE; PS00071; HOMEBOX_2; 1.			
KW	DNA-binding; Homeobox; Nuclear protein.			
FT	NON_TER			
SQ	SEQUENCE	1	1	
	274 AA;	31041 MM;	58E991FE6B540C3A9 CRC64;	

Query Match 62.7%; Score 101.5; DB 5; Length 274;
Best local similarity 64.5%; Pred. No. 7e-06;
Matches 20; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

Qy 1 DROIKIFQNRMMKK--TALDMSWLOT 28
 Db 182 EROIKIFQNRMMKKGGTTSIDANELERE 212

RESULT 2

ID Q26375 PRELIMINARY; PRT; 60 AA.
 AC Q26375;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE DNA binding protein AHOX2 (Fragment).
 GN AHOX2.
 OS Styela clava (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Styelidae; Styela.
 OX NCBI_TaxId=7725;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95011617; PubMed=7926803;
 RA Ge T., Lee H., Tomlinson C.R.;
 RT "Identification of an antennapedia-like homeobox gene in the ascidians
 RL Styela clava and S. plicata."
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; S73920; AA033061.2; -
 DR HSSP; P02833; NANT.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_1ambdrepresr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRODOM; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 FT NON_TER 60
 SQ SEQUENCE 60 AA; 7630 MW; F506301B979BA25 CRC64;

Query Match 59.9%; Score 97; DB 5; Length 60;
 Best Local Similarity 94.1%; Pred. No. 6.3e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIFQNRMMKK 17
 Db 42 DROIKIFQNRMMKK 58

RESULT 3

ID Q8JZW2 PRELIMINARY; PRT; 108 AA.
 AC Q8JZW2;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Struhsberg R.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC036986; AA036986.1; -
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_1ambdrepresr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.

DR PRINTS; PR00031; HTHREPRESSR.
 DR Prodom; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 108 AA; 13070 MW; 123A78FCDD0E7D90 CRC64;

Query Match 59.9%; Score 97; DB 11; Length 108;
 Best Local Similarity 70.4%; Pred. No. 1.1e-05;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DROIKIFQNRMMKKKTALDMSWLOT 27
 Db 49 EROIKIFQNRMMKKKHEDSAPT 75

RESULT 4

ID Q26611 PRELIMINARY; PRT; 181 AA.
 AC Q26611;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Homeobox protein (Fragment).
 OS Styela plicata (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Styelidae; Styela.
 OX NCBI_TaxId=7726;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ascidian;
 RA Ge T., Lee H., Tomlinson C.R.;
 RT "Identification of an Antennapedia-like Homeobox Gene in the Ascidians
 RL Styela clava and plicata."
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; U05600; AA016288.1; -
 DR HSSP; P02833; NANT.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_1ambdrepresr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRODOM; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 FT NON_TER 181
 SQ SEQUENCE 181 AA; 20873 MW; AF39911408F06672 CRC64;

Query Match 59.9%; Score 97; DB 5; Length 181;
 Best Local Similarity 94.1%; Pred. No. 1.9e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIFQNRMMKK 17
 Db 80 DROIKIFQNRMMKK 96

RESULT 5

ID Q26478 PRELIMINARY; PRT; 194 AA.
 AC Q26478;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Homeobox protein (Fragment).
 OS Styela clava (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Styelidae; Styela.


```

OX NCB1_TaxID=7725;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Ascidian;
RA Ge T., Lee H., Tomlinson C.R.;
RT "Identification of an Antennapedia-like Homeobox Gene in the Ascidians
  Styela clava and Plicata."
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U05571; AA16226.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_LambdaRepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS0071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER
SQ SEQUENCE 194 AA; 2186 MW; 8AD1B15B3E4800BC CRC64;

Query Match 59.9%; Score 97; DB 5; Length 194;
Best Local Similarity 94.1%; Pred. No. 2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFFQNRKMKWK 17
ID :|||||
AC 52 DRQKIMFQNRKMKWK 68
DB

RESULT 6
QY 0817C8 PRELIMINARY; PRT; 435 AA.
ID 0817C8;
AC 0817C8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative homeobox protein Hox10.
GN HOX10.
OS Clona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Clona.
OX NCB1_TaxID=7719;
RN (1)
RP SEQUENCE FROM N.A.
RA Spagnuolo A., Ristoreto F., Di Gregorio A., Anello F., Branno M.,
  Di Lauro R.;
RT "Unusual number and genomic organization of Hox genes in the tunicate
  Clona intestinalis."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ535675; CAD59671.1; -.
KW Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 435 AA; 48739 MW; D8D0F579C02BC9E2 CRC64;

Query Match 59.9%; Score 97; DB 5; Length 435;
Best Local Similarity 94.1%; Pred. No. 4.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFFQNRKMKWK 17
ID :|||||
AC 295 DRQKIMFQNRKMKWK 311
DB

RESULT 7
QY 0817C9 PRELIMINARY; PRT; 90 AA.
ID 0817C9;
AC 0817C9;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

```

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DE Putative homeobox protein Hox6/7 (Fragment).
GN Hox6/7.
OS Clona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Clona.
OX NCB1_TaxID=7719;
RN (1)
RP SEQUENCE FROM N.A.
RA Spagnuolo A., Ristoreto F., Di Gregorio A., Anello F., Branno M.,
  Di Lauro R.;
RT "Unusual number and genomic organization of Hox genes in the tunicate
  Clona intestinalis."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ535674; CAD59670.1; -.
KW Homeobox; DNA-binding; Nuclear protein.
FT NON_TER
SQ SEQUENCE 90 AA; 11352 MW; CAAD6B261FE908E CRC64;

Query Match 59.0%; Score 95.5; DB 5; Length 90;
Best Local Similarity 57.6%; Pred. No. 1.5e-05;
Matches 19; Conservative 3; Mismatches 6; Indels 5; Gaps 1;

QY 1 DRQIKWFFQNRKMKKTALDWS----WLTQE 28
ID :|||||
AC 57 ERQIKWFFQNRKMKKENDIAESNNWECRE 89
DB

RESULT 8
QY 057368 PRELIMINARY; PRT; 39 AA.
ID 057368;
AC 057368;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hox5 protein (Fragment).
GN Hox5A OR Hox5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCB1_TaxID=7955;
RN (1)
RP SEQUENCE FROM N.A.
RA Prince V.B., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
  expression patterns in the trunk."
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14539; CAA74874.1; -.
DR ZFIN; ZDB-GENE-980526-533; hox5a.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_LambdaRepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS0071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER
SQ SEQUENCE 39 AA; 4827 MW; 592A0FEC12B58860 CRC64;

Query Match 58.0%; Score 94; DB 13; Length 39;
Best Local Similarity 94.1%; Pred. No. 1e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFFQNRKMKWK 17
ID :|||||
AC 13 BRQIKWFFQNRKMKWK 29
DB

RESULT 9

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057359          PRELIMINARY;      PRT;      43 AA.
ID 057359
AC 057359
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hoxa5 protein (Fragment).
GN Hoxb5b OR Hoxa5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
RT expression patterns in the trunk."
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14526; CA74861.1; -.
DR ZFIN; ZDB-GENE-000823-6; hoxb5b.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KM DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;

Query Match          58.0%; Score 94; DB 13; Length 43;
Best Local Similarity 94.1%; Pred. No. 1.1e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIFQNRMMKKK 17
   :|||||
Db 9 EROIKIFQNRMMKKK 25

RESULT 10
Q9PVR9          PRELIMINARY;      PRT;      46 AA.
ID Q9PVR9
AC Q9PVR9
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hoxc5a (Fragment).
GN Hoxc5a.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OC NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kondo S., Naruse K., Shima A.;
RT "Hox genes of the medaka fish Oryzias latipes."
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AB026960; BAA86243.1; -.
DR HSSP; P02833; IHOM.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KM DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 46 AA; 5955 MW; 60399999ED4294D03 CRC64;

```

```

Query Match          58.0%; Score 94; DB 13; Length 46;
Best Local Similarity 94.1%; Pred. No. 1.2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIFQNRMMKKK 17
   :|||||
Db 22 EROIKIFQNRMMKKK 38

RESULT 11
Q27413          PRELIMINARY;      PRT;      51 AA.
ID Q27413
AC Q27413
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE LOX5 ORTHOLOG homeobox (Fragment).
GN CTS-LOX5.
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.
OC NCBI_TaxID=40316;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94356262; Pubmed=7915607;
RX DICK M.H., Bues L.W.;
RA DICK M.H., Bues L.W.;
RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
RT (Annelida: Polychaeta)."
RL Mol. Phylogenet. Evol. 3:146-158(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA DICK M.H., Bues L.W.;
RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U26629; AAC46851.1; -.
DR EMBL; S76226; AAB31777.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepress.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KM DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 51 AA; 6278 MW; 88C8F65161E94A22 CRC64;

Query Match          58.0%; Score 94; DB 5; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIFQNRMMKKK 17
   :|||||
Db 22 EROIKIFQNRMMKKK 38

RESULT 12
Q23743          PRELIMINARY;      PRT;      51 AA.
ID Q23743
AC Q23743
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Deformed ortholog homeobox (Fragment).
GN CTS-DFD.
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.

```

OX NCBI_TaxID=40316;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=94356262; PubMed=7915607;
RA Dick M.H., Bues L.W.;
RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
RL (Annelida: Polychaeta).";
RMol. Phylogenet. Evol. 3:146-158(1994).
RN
RP SEQUENCE FROM N.A.
RA Dick M.H., Bues L.W.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC EMBL; U08627; AAC46849.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepressor.
DR Pfam; PF00046; homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT SEQUENCE 51 AA; 6533 MW; 9EDB50C927FBCBD5 CRC64;
SQ
Query Match 58.0%; Score 94; DB 5; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DROIKIFQNRMRMKK 17
Db 22 EROIKIFQNRMRMKK 38
RESULT 13
Q26407 PRELIMINARY; PRT; 51 AA.
ID Q26407
AC Q26407;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Cts-Did protein (fragment).
GN CTS-DPD.
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.
OC NCBI_TaxID=40316;
OX
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=94356262; PubMed=7915607;
RA Dick M.H., Bues L.W.;
RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
RL (Annelida: Polychaeta).";
RMol. Phylogenet. Evol. 3:146-158(1994).
CC EMBL; S76416; AAB31775.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepressor.
DR Pfam; PF00046; homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT SEQUENCE 51 AA; 6533 MW; 9EDB50C927FBCBD5 CRC64;
SQ

Query Match 58.0%; Score 94; DB 5; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DROIKIFQNRMRMKK 17
Db 22 EROIKIFQNRMRMKK 38
RESULT 14
Q9PVR8 PRELIMINARY; PRT; 57 AA.
ID Q9PVR8
AC Q9PVR8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE HOXA5A (Fragment).
GN HOXA5A.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygia; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN
RP SEQUENCE FROM N.A.
RA Kondo S., Naruse K., Shima A.;
RT "Hox genes of the medaka fish Oryzias latipes.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC EMBL; AB026961; BAA86244.1; -.
DR HSSP; P02833; 1HOW.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT SEQUENCE 57 AA; 6891 MW; 5A6430320F68C04 CRC64;
SQ
Query Match 58.0%; Score 94; DB 13; Length 57;
Best Local Similarity 94.1%; Pred. No. 1.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DROIKIFQNRMRMKK 17
Db 22 EROIKIFQNRMRMKK 38
RESULT 15
Q9Y188 PRELIMINARY; PRT; 58 AA.
ID Q9Y188
AC Q9Y188;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hbl homeodomain protein (fragment).
GN Hbl.
OS Priapulus caudatus.
OC Eukaryota; Metazoa; Priapulida; Priapulidae; Priapulins.
OC NCBI_TaxID=37621;
OX
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=99318125; PubMed=10391241;
RA de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adoutte A., Akam M.,
RA Carroll S.B., Balavoine G.;
RT "Hox genes in brachiopods and priapulids and protostome evolution.";
RL Nature 399:772-776(1999).
CC EMBL; AF144888; AAD40644.1; -.
DR HSSP; P02833; 9ANT.
SQ

DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepressr.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00721; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 58 AA; 7323 MW; 572F30DA57C9A513 CRC64;

Query Match 58.0%; Score 94; DB 5; Length 58;
Best Local Similarity 94.1%; Pred. No. 1.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRQIKWFOHRRMKWK 17
:|||||
Db 23 ERQIKWFOHRRMKWK 39

Search completed: February 18, 2004, 14:36:01
Job time : 83.0526 secs

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OM protein - protein search, using SW model

Run on: February 18, 2004, 13:39:39 ; Search time 16.5789 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162
Sequence: 1 DRQIKWIFQNRMRMKKTALDMSWLQTE 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	59.9	105	1 HXAT_RAT	P09634 ratnus novy
2	97	59.9	229	1 HXAT_MOUSE	P02830 mus musculus
3	96	59.3	75	1 HXSA_SALSA	P09636 salmo salar
4	95	58.6	224	1 HXBE_HUMAN	P17509 homo sapien
5	95	58.6	224	1 HXBE_MOUSE	P09623 mus musculus
6	95	58.6	230	1 HXAT_HUMAN	P31568 homo sapien
7	94	58.0	48	1 HXBE_XENLA	P31559 xenopus lae
8	94	58.0	49	1 HXAS_SHEEP	P02859 ovis aries
9	94	58.0	71	1 HXAT_SHEEP	P02850 ovis aries
10	94	58.0	71	1 HXCS_NOTVI	P31562 notophthalm
11	94	58.0	74	1 HM90_APIME	P15860 apis mellif
12	94	58.0	76	1 HXCA_RAT	P18865 ratnus novy
13	94	58.0	78	1 HXAS_SALSA	P09637 salmo salar
14	94	58.0	80	1 HXAT_LINSA	P81192 linus sang
15	94	58.0	81	1 HXSL_BRARE	P09013 brachydantio
16	94	58.0	82	1 HXBS_CHICK	P14838 gallus gall
17	94	58.0	84	1 HXBE_CHICK	P14839 gallus gall
18	94	58.0	86	1 SCR_APIME	P15859 apis mellif
19	94	58.0	87	1 HXCS_XENLA	P09020 xenopus lae
20	94	58.0	93	1 HXBE_PIG	P09078 sus scrofa
21	94	58.0	96	1 HXCS_BRARE	P15862 brachydantio
22	94	58.0	105	1 HXBA_BRARE	P22574 brachydantio
23	94	58.0	112	1 HXBT_RAT	P18864 ratnus novy
24	94	58.0	148	1 HXAS_LAMBE	P50208 ambystoma m
25	94	58.0	153	1 HXCS_SHEEP	P49925 ovis aries
26	94	58.0	208	1 HXAT_HETFR	P91325 heterodontu
27	94	58.0	209	1 HXAT_XENLA	P09071 xenopus lae
28	94	58.0	217	1 HXBT_BOVIN	P09078 sus scrofa
29	94	58.0	217	1 HXBT_HUMAN	P09024 mus musculus
30	94	58.0	217	1 HXBT_MOUSE	P09024 mus musculus
31	94	58.0	220	1 HB7A_XENLA	P04476 xenopus lae
32	94	58.0	220	1 HB7B_XENLA	P04476 xenopus lae
33	94	58.0	222	1 HXCS_HUMAN	P00444 homo sapien

34	94	58.0	222	1 HXCS_MOUSE	P32043 mus musculus
35	94	58.0	225	1 HXAT_MORSA	P09644 morone saxa
36	94	58.0	228	1 HXBE_BRARE	P15861 brachydantio
37	94	58.0	229	1 HXAS_HETFR	P09019 heterodontu
38	94	58.0	230	1 HXBS_XENLA	P09092 mus musculus
39	94	58.0	232	1 HXBE_MOUSE	P09070 xenopus lae
40	94	58.0	232	1 HXAT_XENLA	P09071 xenopus lae
41	94	58.0	232	1 HXCS_BRARE	P09074 brachydantio
42	94	58.0	233	1 HXAS_RAT	P52949 ratnus novy
43	94	58.0	233	1 HXBA_HUMAN	P31267 homo sapien
44	94	58.0	234	1 HXCS_NOTVI	P14858 notophthalm
45	94	58.0	234	1 HXCS_XENLA	P02832 xenopus lae

ALIGNMENTS

RESULT 1
HXAT_RAT
ID HXAT_RAT STANDARD; PRT; 105 AA.
AC P09634;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (Hox-1.1) (R3) (Fragment).
GN HOXA7 OR HOXA-7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=87277429; PubMed=2886401;
RA Falson M., Sanderson N., Chung S.Y.;
RT "Cloning and expression of rat homeo-box-containing sequences."
RL Gene 54:23-32(1987).
CC
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC SPECIFIC POSITIONAL REGULATOR SYSTEM THAT PROVIDES CELLS WITH
CC SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: M16807; -!- NOT_ANNOTATED_CDS.
CC PIR: A27471; A27471.
CC
CC HSSP: P02833; NANT.
CC
CC TRANSFAC: T01707; -!
CC INTERPRO: IPR001827; Antennapedia.
CC INTERPRO: IPR001356; Homeobox.
CC Pfam: PF00046; homeobox.1.
CC PRINTS: PR00024; HOMEOBOX.
CC PRODOM: PD000010; Homeobox.1.
CC SMART: SM00389; HOX.1.
CC PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
CC PROSITE: PS00027; HOMEOBOX_1; 1.
CC PROSITE: PS00711; HOMEOBOX_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC transcription regulation.
CC NON_TER 1
CC FT DNA_BIND 5 64 HOMEOBOX.
CC FT DOMAIN 91 105 GLU-RICH (ACIDIC).
CC SQ SEQUENCE 105 AA; 12552 MW; 106CIDP938F2864B CRC64;
Query Match 59.9%; Score 97; DB 1; Length 105;
Best Local Similarity 70.4%; Pred. No. 1.1e-06;

Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DROIKIWFONRRMKKKTALDMSWLOT 27
 Db 46 EROIKIWFONRRMKKKEHDESOAPT 72

RESULT 2
 HXA7 MOUSE STANDARD; PRT; 229 AA.

AC P02830;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-A7 (Hox-1.1) (M6-12) (M6).
 GN HXA7 OR HXA7-7 OR HXA7-1.1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87260976; PubMed=2885847;
 RA Kessel M., Schultze F., Fibi M., Gruss P.;
 RT "Primary structure and nuclear localization of a murine homeobox domain protein";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5306-5310(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=95197009; PubMed=7890170;
 RA Parikh H., Shah S., Hilt D., Peterkofsky A.;
 RT "Organization, sequence and regulation of expression of the murine Hoxa-7 gene";
 RL Gene 154:237-242(1995).
 RN [3]
 RP SEQUENCE OF 126-229 FROM N.A.
 RX MEDLINE=85188311; PubMed=2986010;
 RA Colberg-Poley A.M., Voos S.D., Chowdhury K., Gruss P.;
 RT "Structural analysis of murine genes containing homeo box sequences and their expression in embryonal carcinoma cells";
 RL Nature 314:713-718(1985).
 RN [4]
 RP SEQUENCE OF 129-197 FROM N.A.
 RX MEDLINE=87053860; PubMed=2877873;
 RA Breier G., Bucan M., Francke U., Colberg-Poley A.M., Gruss P.;
 RT "Sequential expression of murine homeo box genes during F9 EC cell differentiation";
 RL EMBO J. 5:1209-2215(1986).
 RL -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC -----
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 CC -----
 DR EMBL; M17192; AAA37833.1; -;
 DR EMBL; U15972; AAC52160.1; -;
 DR PIR; A03314; A03314.
 DR PIR; A28329; A28329.
 DR HSSP; P02833; 9ANT.
 DR TRASNFAIC; T01278; -;
 DR MGD; MGI:96179; Hoxa7.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.

DR PRINTS; PR00025; ANTENNAPEIDIA.
 DR PRINTS; PR00024; HOMEOBOX.
 DR PRODOM; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00032; ANTENNAPEIDIA; 1.
 DR PROSITE; PS00027; HOMEOBOX_1; 1.
 DR PROSITE; PS00071; HOMEOBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT SITE 118 123 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 129 188 HOMEOBOX.
 FT DOMAIN 156 159 POLY-ARG.
 FT DOMAIN 211 229 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 215 229 POLY-GLU.
 FT CONFLICT 43 45 GAG -> APA (IN REF. 1).
 SQ SEQUENCE 229 AA; 25682 MW; D3E6BD61D8D5C6F CRC64;

Query Match Score 97; DB 1; Length 229;
 Best Local Similarity 70.4%; Fred. No. 2.4e-06;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DROIKIWFONRRMKKKTALDMSWLOT 27
 Db 170 EROIKIWFONRRMKKKEHDESOAPT 196

RESULT 3
 HNSA SALSA STANDARD; PRT; 75 AA.

AC P09636;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein S12-A (Fragment).
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OC NCBI_TaxId=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88226009; PubMed=2897318;
 RA Fjose A., Mølven A., Eiken H.G.;
 RT "Molecular cloning and characterization of homeo-box-containing genes from Atlantic salmon";
 RL Gene 62:141-152(1988).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC -----
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 CC -----
 DR EMBL; M18903; AAA49559.1; -;
 DR PIR; I51341; I51341.
 DR HSSP; P02833; 9ANT.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRODOM; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEOBOX_1; 1.
 DR PROSITE; PS00071; HOMEOBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
 FT NON_TER 1 1
 FT DNA_BIND 1 60 HOMEOBOX.
 FT NON_TER 75 75
 SQ SEQUENCE 75 AA; 9330 MW; FC02C3672F35475D CRC64;

Query Match Score 96; DB 1; Length 75;

Best Local Similarity 78.3%; Pred. No. 1e-06;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRBMKKTALDWS 23
Db 42 EROIKIWFQNRBMKKTALDWS 64

RESULT 4
HXB6_HUMAN STANDARD; PRT; 224 AA.
AC P17509; P09068; Q9H811; Q9UGH2;
DT 01-NOV-1988 (Rel. 09, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Homeobox protein Hox-B6 (Hox-2.2) (HU-2).
GN HOBX6 OR HOBX2B.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Placenta;
RX MEDLINE=91187672; PubMed=1672751;
RA Shen W.-F., Detmer K., Simonitch T.A., Lawrence H.J.,
RA Laryman C.;
RT "Alternative splicing of the HOX 2.2 homeobox gene in human
RT hematopoietic cells and murine embryonic and adult tissues";
RL Nucleic Acids Res. 19:539-545(1991).
[2]
RP SEQUENCE FROM N.A.
RA Frezza D., D'Esposito M., Migliaccio E., Santini S.M., Fruscalzo A.;
RT "Expression of HOX genes in T lymphocytes and hairy leukemia cell
RT lines";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Kidd K.K., Buysyina V., Demille M.M.C., Speed W.C., Ruggeri V.,
RA Kidd J.R., Pakestis A.J.;
RT "Overall linkage disequilibrium in 33 populations for highly
RT informative multiallelic haplotypes spanning the HOXB gene cluster";
RL Am. J. Hum. Genet. 67:235-235(2000).
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusik K., Farmer A.A., Casavant T.L., Schaefer T.E.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schaefer T.E.,
RA Brownstein M.J., Uddin T.B., Toohyuk S., Carrinchi P., Prange C.,
RA Raha S.S., Loguelfino N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Phelan J., Helton E., Kettner M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RP SEQUENCE OF 135-224 FROM N.A.
RX MEDLINE=90046832; PubMed=2573064;
RA Shen W.-F., Laryman C., Lowney P., Corral J.C., Detmer K.,
RA Hauser C.A., Simonitch T.A., Hack P.M., Lawrence H.J.;
RT "Lineage-restricted expression of homeobox-containing genes in human

RT hematopoietic cell lines";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).
[6]
RP PRELIMINARY SEQUENCE OF 136-240 FROM N.A.
RX MEDLINE=85024858; PubMed=6091895;
RA Levine M., Rubin G.M., Tjian R.;
RT "Human DNA sequences homologous to a protein coding region conserved
RT between homeotic genes of Drosophila";
RL Cell 38:667-673(1984).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P17509-1; Sequence=Displayed;
CC Name=2; Synonym=Homeobox-1e88;
CC IsoId=P17509-2; Sequence=VSP_002389, VSP_002389;
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.

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CC or send an email to license@isb-sib.ch).

DR EMBL; X58431; CAA41335.1; -
DR EMBL; X58431; CAA41336.1; -
DR EMBL; AJ270993; CAB65909.1; -
DR EMBL; AF287967; AAG31552.1; -
DR EMBL; BC014651; AAH14651.1; -
DR EMBL; M30597; AAA36004.1; -
DR EMBL; X02571; -; NOT_ANNOTATED_CDS.
DR PIR; S26400; S26400.
DR HSSP; P02833; IHOM.
DR TRANSFAC; T01732; -
DR Genew; HGNC:5117; HOXB6.
DR MIM; 142961; -
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003700; F:transcription factor activity; NAS.
DR GO; GO:0008595; P:determination of anterior/posterior axis, e...; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; HOMEBOX.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX; 1; 1.
DR PROSITE; PS50071; HOMEBOX; 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation; Alternative splicing.
KW SITE 127 132
FT DNA BIND 146 205
FT DOMAIN 216 220
FT VARSPLIC 140 140
FT FTID=VSP_002389.
FT VARSPLIC 141 224
FT FTID=VSP_002389.
FT CONFLICT 24 25
FT CONFLICT 33 33
FT CONFLICT 60 60
FT CONFLICT 73 73
FT CONFLICT 149 150
SQ SEQUENCE 224 AA; 25427 MW; D8F96AFAC93D878 CRC64;
Query Match 58.6%; Score 95; DB 1; Length 224;
Best Local Similarity 66.7%; Pred. No. 4.5e-06;

Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Oy 1 DROIKIFQNRBMKWKTA--LDMSWQTE 28
 Db 187 EROIKIFQNRBMKWKESKLSASQLSAE 216

RESULT 5
 ID HXB6 MOUSE STANDARD; PRT; 224 AA.

AC P09023; 01-NOV-1988 (Rel. 09, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-B6 (Hox-2.2) (MH-22A).
 GN HOXB6 OR HOXB-6 OR HOX-2.2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88289762; PubMed=2899893;
 RA Schughart K., Utset M.F., Awgulewitsch A., Ruddle P.H.;
 RT "Structure and expression of Hox-2.2, a murine homeobox-containing gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:5582-5586(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91187672; PubMed=1672751;
 RA Shen W.F., Detmer K., Simionitch-Bason T.A., Lawrence H.U.,
 RA Largman C.;
 RT "Alternative splicing of the HOX 2.2 homeobox gene in human hematopoietic cells and murine embryonic and adult tissues.";
 RL Nucleic Acids Res. 19:539-545(1991).
 RN [3]
 RP SEQUENCE OF 144-224 FROM N.A.
 RX MEDLINE=88054465; PubMed=2890503;
 RA Lomai P., Arman E., Czosenek H., Ruddle P.H., Blatt C.;
 RT "New murine homeoboxes: structure, chromosomal assignment, and differential expression in adult erythropoiesis.";
 RL DNA 6:409-418(1987).
 RN [4]
 RP SEQUENCE OF 140-224 FROM N.A.
 RX MEDLINE=88085193; PubMed=2891608;
 RA Hart C.P., Fainrod A., Ruddle P.H.;
 RT "Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes: evolutionary and structural comparisons.";
 RL Genomics 1:182-195(1987).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
 CC -----
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 CC -----
 DR EMBL; M18166; AAA37844.1; -;
 DR EMBL; X56459; CAA39834.1; -;
 DR EMBL; M18401; AAC27130.1; ALT_SEQ.
 DR EMBL; J03782; AAA37843.1; -;
 DR PIR; A31324; A31324.
 DR HSSP; P02833; 1HOM.
 DR TRASPAC; T01733; -;
 DR MGD; MGI:96187; Hoxb6.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.

DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR Prodom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT SITE 127 132 ANTP-TYPE HEXAPEPTIDE.
 FT DNA BIND 146 205 HOMEBOX.
 FT DOMAIN 216 220 POLY-GLU.
 FT CONFLICT 186 186 T -> P (IN REF. 3).
 SQ SEQUENCE 224 AA; 25310 MW; E8FC0BDB57F5C3D CRC64;

Query Match 58.6%; Score 95; DB 1; Length 224;
 Best Local Similarity 66.7%; Pred. No. 4; Se-06;
 Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Oy 1 DROIKIFQNRBMKWKTA--LDMSWQTE 28
 Db 187 EROIKIFQNRBMKWKESKLSASQLSAE 216

RESULT 6
 ID HXA7 HUMAN STANDARD; PRT; 230 AA.

AC P1256; 043368; 043486; 095655; Q9NSC8; Q9UDM1;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-A7 (Hox-1A) (Hox 1.1).
 GN HOXA7 OR HOX1A.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Polakowska R., Lacelle P.T.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9903755; PubMed=9804983;
 RA McMillan M.A., Bremner P.S., McMullin M.F., Maxwell A.P.,
 RA Winter P.C., Lappin T.R.;
 RT "Sequence characterisation and expression of homeobox HOX A7 in the multi-potential erythroleukaemic cell line TF-1.";
 RL Biochim. Biophys. Acta 1442:329-333(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Bradshaw H., Hinds K., Keppeler D.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20369265; PubMed=10911612;
 RA Kim M.H., Jin H., Seol E.Y., Yoo M., Park H.W.;
 RT "Sequence analysis and tissue specific expression of human HOXA7.";
 RL Mol. Biotechnol. 14:19-24(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Albrechtsen R., Wewer U.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 1-91 FROM N.A.
 RA Cho M., Kim M.H., Hwang C.Y., Min W.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 130-195 FROM N.A.
 RX MEDLINE=90215256; PubMed=2576652;
 RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,

RA Gaudio G., Stornaiuolo A., Cafiero M., Falella A., Simeone A.;
 RT "Organization of human class I homeobox genes.";
 RL Genome 31:745-756(1989).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL, REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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 CC -----
 DR EMBL; AF026397; AAB94604.1; -;
 DR EMBL; AF005814; CAA06713.1; -;
 DR EMBL; AC004080; -; NOT ANNOTATED_CDS.
 DR EMBL; AF032095; AAD01339.2; -;
 DR EMBL; U92543; AAD00727.1; -;
 DR EMBL; X64803; CAA59270.1; -;
 DR EMBL; X64804; CAA59270.1; JOINED.
 DR PIR; S1536; S1536.
 DR HSSP; P02833; 9ANT.
 DR TRASPAC; T01705; -;
 DR Genew; HGNC:5108; HOXA7.
 DR MIM; 142950; -;
 DR GO; GO:0003700; F:transcription factor activity; TAS.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PRO0025; ANTENNAPEDIA.
 DR PRINTS; PRO0024; HOMEOBOX.
 DR Prodom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00027; HOMEOBOX 1; 1.
 DR PROSITE; PS50071; HOMEOBOX 2; 1.
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT SITE 119 124 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 130 189 HOMEOBOX.
 FT DOMAIN 157 160 POLY-ARG.
 FT DOMAIN 196 199 POLY-ALA.
 FT DOMAIN 214 230 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 223 230 POLY-GLU.
 FT CONFLICT 18 18 T->A (IN REF. 3).
 FT CONFLICT 75 76 DA->RR (IN REF. 6).
 FT CONFLICT 78 78 MISSING (IN REF. 5).
 FT CONFLICT 174 174 I->V (IN REF. 4).
 FT CONFLICT 194 195 PT->RL (IN REF. 5).
 FT CONFLICT 195 195 T->I (IN REF. 7).
 FT CONFLICT 222 222 D->Y (IN REF. 5).
 SQ SEQUENCE 230 AA; 25385 MW; 6E2F1991F1BBED21 CRC64;
 Query Match 58.6%; Score 95; DB 1; Length 230;
 Best Local Similarity 81.0%; Pred. No. 4.6e-06;
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DRQIKIWFQNRMRMKKKTALD 21
 DB 171 ERQIKIWFQNRMRMKKCKEHD 191
 RESULT 7
 ID HXB6_XENLA STANDARD; PRT; 48 AA.
 AC P31256;
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Homeobox protein Hox-B6 (XlHox-2.2) (Fragment).
 GN HOXB6 OR XLHOX-2.2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxId=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93043517; PubMed=1384809;
 RA Leroy P., de Robertis E.M.;
 RT "Effects of ilthium chloride and retinoic acid on the expression of
 RT genes from the Xenopus laevis Hox 2 complex.";
 RL Dev. Dyn. 194:21-32(1992).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL, REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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 CC -----
 DR EMBL; M91587; AAA49750.1; -;
 DR PIR; I51439; I51439.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PRO0024; HOMEOBOX.
 DR Prodom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEOBOX 1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
 DR PROSITE; PS50071; HOMEOBOX 2; 1.
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT NON_TER 1 1
 FT DNA_BIND 1 1 HOMEOBOX.
 FT SEQUENCE 48 AA; 5716 MW; BC39E36822EDD2A CRC64;
 Query Match 58.0%; Score 94; DB 1; Length 48;
 Best Local Similarity 94.1%; Pred. No. 1.2e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRQIKIWFQNRMRMKK 17
 DB 11 ERQIKIWFQNRMRMKK 27
 RESULT 8
 ID HXAS_SHEEP STANDARD; PRT; 49 AA.
 AC Q28559;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-A5 (Fragment).
 GN HOXA5 OR HOXA-5.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxId=9940;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Roche P.J.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF

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CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF:
CC 5'-CYNATATATGTY-3'.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U61978; AAB04754.1; -.
DR HSSP; P02833; IHOM.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1
FT DNA_BIND 1
FT NON_TER 49
FT SEQUENCE 49 AA; 6331 MW; 1EE702315E7C099B CRC64;
SQ
Query Match 58.0%; Score 94; DB 1; Length 49;
Best Local Similarity 94.1%; Pred. No. 1.2e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DROIKTFQNRMRMKKK 17
:|||||
DB 31 EROIKTFQNRMRMKKK 47

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DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR00047; HTH_LambdaRepressor.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1
FT DNA_BIND 1
FT NON_TER 49
FT SEQUENCE 49 AA; 6331 MW; 1EE702315E7C099B CRC64;
SQ
Query Match 58.0%; Score 94; DB 1; Length 71;
Best Local Similarity 94.1%; Pred. No. 1.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DROIKTFQNRMRMKKK 17
:|||||
DB 45 EROIKTFQNRMRMKKK 61

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FT  DNA_BIND 4 63 HOMEBOX.
FT  NON_TER 71
SQ  SEQUENCE 71 AA; 8979 MW; 079999FDE89995B42 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 71;
Best Local Similarity 94.1%; Pred. No. 1.9e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMMKKK 17
   :|||||
Db 45 EROIKIWFQNRMMKKK 61

RESULT 11
HM90_APIME STANDARD; PRT; 74 AA.
ID HM90_APIME
AC P15860;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein H90 (Fragment).
DE Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apoidea; Apis.
OC NCBI_TaxID=7460;
RX MEDLINE=9009384; PubMed=2574865;
RA Walldorf U., Fleig R., Gehring W.J.;
RT "Comparison of homeobox-containing genes of the honeybee and
RT Drosophila."
RL Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).
CC CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M29493; AAA27728.1; -.
DR PIR; D34510; D34510.
DR HSSP; P02833; IHOM.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1 1
FT DNA_BIND 8 67 HOMEBOX.
FT NON_TER 74
SQ SEQUENCE 74 AA; 9263 MW; 5FC9F84F723D837 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 74;
Best Local Similarity 94.1%; Pred. No. 1.9e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMMKKK 17
   :|||||
Db 49 EROIKIWFQNRMMKKK 65

RESULT 12
HXCA_RAT STANDARD; PRT; 76 AA.
ID HXCA_RAT
AC P18865;
DT 01-NOV-1990 (Rel. 16, Created)

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DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C4 (R3) (Fragment).
GN HOXC4 OR HOXC-4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=8921502; PubMed=2907739;
RA Falzon M., Chung S.Y.;
RT "The expression of rat homeobox-containing genes is developmentally
RT regulated and tissue specific."
RL Development 103:601-610(1988).
CC CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC CC -1- SUBCELLULAR LOCATION: Nuclear.
CC CC -1- TISSUE SPECIFICITY: PREDOMINANTLY SPINAL CORD AND KIDNEY.
CC CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC CC "DERIVED" SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M37567; AAA41343.1; -.
DR PIR; C43559; C43559.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR00047; HTH_Lambdaressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 11 70 HOMEBOX.
FT SEQUENCE 76 AA; 9293 MW; 5235F65C0672385 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 76;
Best Local Similarity 94.1%; Pred. No. 1.9e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMMKKK 17
   :|||||
Db 52 EROIKIWFQNRMMKKK 68

RESULT 13
HXAS_SALSA STANDARD; PRT; 78 AA.
ID HXAS_SALSA
AC F09637;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A5 (S12-B) (Fragment).
GN HOXA5.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

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OX NCB1_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88226009; PubMed=2897318;
RA Fjose A., Molven A., Eiken H.G.;
RT "Molecular cloning and characterization of homeo-box-containing genes
   from Atlantic salmon";
RL Gene 62:141-152(1988).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
   A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
   SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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CC -----
DR EMBL; M18904; AAA49560.1; -.
DR PIR; I51342; I51342.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KM Transcription regulation.
FT DNA_BIND 1 60 HOMEOBOX.
FT NON_TER 1 60
SQ SEQUENCE 78 AA; 9489 MW; 82BDEBD778AC20 CRC64;

Query Match          58.0%; Score 94; DB 1; Length 78;
Best local similarity 94.1%; Pred. No. 2e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DROIKIWFQRRMKKK 17
DB 42 EROIKIWFQRRMKKK 58

RESULT 14
HX44_LINSA STANDARD; PRT; 80 AA.
ID HX44_LINSA
AC P81192;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A4 (Lshox 4) (Fragment).
GN HOXA4.
OS Lineus sanguineus (Ribbon worm).
OC Eukaryota; Metazoa; Nemertea; Anopla; Heteronemertea; Lineidae;
OC Lineus.
OX NCB1_TaxID=48190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98169491; PubMed=9501210;
RA Kmlta-Cunliffe M., Looisli F., Blerne J., Gehring W.J.;
RT "Homeobox genes in the ribbonworm Lineus sanguineus: evolutionary
   implications";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3030-3035(1998).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
   A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
   SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
   SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC "DEFORMED" SUBFAMILY.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_Jamrepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEOBOX.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KM Transcription regulation.
FT DNA_BIND 1 80 HOMEOBOX.
FT NON_TER 1 80
SQ SEQUENCE 80 AA; 9860 MW; F2CE1B01CB8042F1 CRC64;

Query Match          58.0%; Score 94; DB 1; Length 80;
Best local similarity 94.1%; Pred. No. 2.1e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DROIKIWFQRRMKKK 17
DB 52 EROIKIWFQRRMKKK 68

RESULT 15
HX5L_BRARE STANDARD; PRT; 81 AA.
ID HX5L_BRARE
AC P09013;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B5 like (ZP-54) (Fragment).
GN HOXB5B OR ZP54 OR ZP-54.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Brachydanio; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCB1_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89016617; PubMed=2902580;
RA Njolatad P.R., Molven A., Hordvik I., Apold J., Fjose A.;
RT "Primary structure, developmentally regulated expression and
   potential duplication of the zebrafish homeobox gene ZP-21";
RL Nucleic Acids Res. 16:9097-9113(1988).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
   A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
   SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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CC -----
DR EMBL; X12803; CAA31291.1; -.
DR HSSP; P02833; 1SAN.
DR ZFIN; ZDB-GENE-000823-6; hoxb5b.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEOBOX.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
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DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 6 65 HOMEBOX.
SQ SEQUENCE 81 AA; 9977 MW; B769BAFFEB3C6B4 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 81;
Best Local Similarity 94.1%; Pred. No. 2.1e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKIWFQNRKMKKK 17
:|||||
Db 47 ERQIKIWFQNRKMKKK 63

Search completed: February 18, 2004, 14:28:14
Job time : 16.5789 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-17
Perfect score: 41
Sequence: 1 LDMWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp Vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriophage: *
17: sp_archaeop: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	95.1	513	2 Q8VPV8	Q8VPV8 synchococc
2	37	90.2	107	9 Q9FZX5	Q9FZX5 bacterioph
3	37	90.2	274	16 Q8DKO6	Q8DKO6 synchococc
4	37	90.2	282	16 Q8D354	Q8D354 wigleswort
5	37	90.2	288	2 Q8VTT4	Q8VTT4 pseudomonas
6	37	90.2	308	2 Q8K2S2	Q8K2S2 acetobacter
7	37	90.2	311	5 Q94380	Q94380 caenorhabdi
8	37	90.2	313	2 Q8VU06	Q8VU06 pseudomonas
9	37	90.2	318	16 Q8ZC58	Q8ZC58 yersinia pe
10	37	90.2	329	16 Q8XVB4	Q8XVB4 ralsionia s
11	37	90.2	331	16 Q91427	Q91427 pseudomonas
12	37	90.2	341	16 Q8G3A8	Q8G3A8 bruceella su
13	37	90.2	344	16 Q8YEH7	Q8YEH7 bruceella me
14	37	90.2	353	16 Q9A7F0	Q9A7F0 caulobacter
15	37	90.2	377	17 Q59445	Q59445 pyrococcus
16	37	90.2	378	17 Q8U022	Q8U022 pyrococcus

17	37	90.2	379	17 Q9V1M1	Q9V1M1 pyrococcus
18	37	90.2	386	16 Q92U27	Q92U27 rhizobium m
19	37	90.2	393	16 Q987Z1	Q987Z1 rhizobium 1
20	37	90.2	399	16 Q8PFO8	Q8PFO8 xanthomonas
21	37	90.2	404	17 Q57734	Q57734 pyrococcus
22	37	90.2	405	17 Q9UXV2	Q9UXV2 pyrococcus
23	37	90.2	1291	5 Q9VP46	Q9VP46 dictyostella
24	37	90.2	1449	5 Q8MNA4	Q8MNA4 dictyostella
25	37	90.2	1578	5 Q81BF7	Q81BF7 plasmidium
26	37	90.2	2283	5 Q81C35	Q81C35 plasmidium
27	36	87.8	82	17 Q26213	Q26213 methanobact
28	36	87.8	162	16 Q53756	Q53756 mycobacteri
29	36	87.8	313	16 Q8FU02	Q8FU02 corynebacte
30	36	87.8	322	16 Q8YK7	Q8YK7 bruceella me
31	36	87.8	347	16 Q98KR3	Q98KR3 rhizobium 1
32	36	87.8	347	16 Q92QP5	Q92QP5 rhizobium m
33	36	87.8	347	16 Q8G1B0	Q8G1B0 bruceella su
34	36	87.8	348	16 Q8UPX0	Q8UPX0 agrobacteri
35	36	87.8	414	16 Q9KL94	Q9KL94 vibrio chol
36	36	87.8	439	2 Q93Q61	Q93Q61 klebsiella
37	36	87.8	443	16 Q8ZDM7	Q8ZDM7 yersinia pe
38	36	87.8	451	16 Q8D0S7	Q8D0S7 yersinia pe
39	36	87.8	618	15 Q88284	Q88284 snakehead r
40	36	87.8	740	6 Q9SKV1	Q9SKV1 bos taurus
41	36	87.8	745	11 Q8CBT3	Q8CBT3 mus musculu
42	36	87.8	756	6 Q9SKV0	Q9SKV0 bos taurus
43	36	87.8	764	16 Q8U6N1	Q8U6N1 agrobacteri
44	36	87.8	1120	16 Q8ZRA5	Q8ZRA5 salmonella
45	36	87.8	1120	16 Q8ZRT6	Q8ZRT6 salmonella

ALIGNMENTS

RESULT 1

Q8VPV8 ID Q8VPV8 PRELIMINARY; PRT; 513 AA.
AC Q8VPV8; 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE NADH3 dehydrogenase subunit 4.
GN NADH3.
OS Synchococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7942;
RA Maeda S., Badger M.R., Price G.D.,
RT "Identification of ChpX and ChpY, catalyzing light-dependent CO2
hydration involved in CO2 uptake in Cyanobacteria."
RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029338; AAK37764.1; -
DR InterPro; IPR003918; NADH3_oxred4.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
DR PRINTS; PR01437; NUOXDRDTASB4.
DR NAD; Oxidoreductase; Plastocyanine.
SQ SEQUENCE 513 AA; 54237 MW; 2732576B55224AB CRC64;

Query Match 95.1%; Score 39; DB 2; Length 513;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMWL 6
Db 59 IDMWL 64
RESULT 2
Q9FZX5 PRELIMINARY; PRT; 107 AA.

AC Q9FZK5; 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 12.6 kDa protein.
 OS Bacteriophage GA-1.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
 OC phi-29-like viruses.
 OX NCBI_TaxId=12345;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97094855; PubMed=8940089;
 RA Freire R., Serrano M., Salas M., Hermoso J.;
 RT "Activation of replication origins in phi29-related phages requires
 RT the recognition of initiation proteins to specific nucleoprotein
 RT complexes.";
 RL J. Biol. Chem. 271:31000-31007(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97123975; PubMed=8969297;
 RA Iliana B., Blanco L., Salas M.;
 RT "Functional characterization of the genes coding for the terminal
 RT protein and DNA polymerase from bacteriophage GA-1. Evidence for a
 RT sliding-back mechanism during protein-primed GA-1 DNA replication.";
 RL J. Mol. Biol. 264:453-464(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99370049; PubMed=10438592;
 RA Horcajadas J.A., Monsalve M., Rojo F., Salas M.;
 RT "The switch from early to late transcription in phage GA-1:
 RT characterization of the regulatory protein p4G.";
 RL J. Mol. Biol. 290:917-928(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20280072; PubMed=10773070;
 RA Gascon I., Lazaro J.M., Salas M.;
 RT "Differential functional behavior of viral phi29, NF and GA-1 SSB
 RT proteins.";
 RL Nucleic Acids Res. 28:2034-2042(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Melijer W.J.J., Horcajadas J.A., Salas M.;
 RT "The phi29 family of phages.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Horcajadas J.A., Melijer W.J.J., Rojo F., Salas M.;
 RT "Transcriptional map of the Bacillus bacteriophage GA-1. Analysis of
 RT the viral C2 promoter.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X96987; CAC21518.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 107 AA; 12636 MW; ABEF24B68A255B02 CRC64;

Query Match 90.2%; Score 37; DB 9; Length 107;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMEWL 6
 DB 100 DMEWL 104

RESULT 3
 Q8DK06 PRELIMINARY; PRT; 274 AA.
 ID Q8DK06; AC Q8DK06;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cdbv family protein.
 GN TR80803.
 OS *Synechococcus elongatus* (Thermosynechococcus elongatus).

OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxId=32046;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BP-1;
 RX MEDLINE=22225144; PubMed=12240834;
 RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
 RA Watanabe A., Iriyuchi M., Kawashima K., Kimura T., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
 RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the thermophilic cyanobacterium
 RT Thermosynechococcus elongatus BP-1.";
 RL DNA Res. 9:123-130(2002).
 DR EMBL; AP005371; BAC08354.1; -.
 KW Complete proteome.
 SQ SEQUENCE 274 AA; 30329 MW; 021D35F51D8AB77E CRC64;

Query Match 90.2%; Score 37; DB 16; Length 274;
 Best Local Similarity 100.0%; Pred. No. 2,2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMEW 5
 DB 49 LDMEW 53

RESULT 4
 Q8D354 PRELIMINARY; PRT; 282 AA.
 ID Q8D354; AC Q8D354;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CyoA protein.
 GN CYOA.
 OS *Wigglesworthia brevipalpis*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Wigglesworthia.
 OX NCBI_TaxId=164609;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22297718; PubMed=12219091;
 RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
 RA Aksoy S.;
 RT "Genome sequence of the endocellular obligate symbiont of tsetse
 RT flies, *Wigglesworthia glossinidia*.";
 RL Nat. Genet. 32:402-407(2002).
 DR EMBL; AB063521; BAC24293.1; -.
 KW Complete proteome.
 SQ SEQUENCE 282 AA; 32500 MW; 39CC286285F3B35 CRC64;

Query Match 90.2%; Score 37; DB 16; Length 282;
 Best Local Similarity 83.3%; Pred. No. 2,3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMEW 6
 DB 134 LDMEW 139

RESULT 5
 Q8VTT4 PRELIMINARY; PRT; 288 AA.
 ID Q8VTT4; AC Q8VTT4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cytochrome o ubiquinol oxidase A (Fragment).
 GN CYOA.
 OS *Pseudomonas putida*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxId=303;

[1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=PM1;
 RA Syn C.K.C., Liew C.F., Swarup S.;
 RT "Pseudomonas putida cytochrome o ubiquinol oxidase A, B, C, and D
 genes";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF321090; AAL57192.1; -;
 DR InterPro; IPR001505; Copper_Cua.
 DR InterPro; IPR006333; CytoA_II.
 DR ProDom; PD000131; Copper_Cua; 1.
 DR TIGRFAMs; TIGR01433; CytoA; 1.
 FT NON_TER 1
 SQ SEQUENCE 288 AA; 31882 MW; 60E40B3A36516BFC CRC64;
 Query Match 90.2%; Score 37; DB 2; Length 288;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDWEMWL 6
 Db 108 LDWKMWL 113

RESULT 6

Q8KZS2 PRELIMINARY; PRT; 308 AA.
 AC Q8KZS2;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Ubiquinol oxidase subunit II.
 OS Acetobacter pasteurianus (Acetobacter turbidans).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Acetobacteraceae; Acetobacter.
 OX NCBI_TaxId=438;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NCT 1193;
 RA Takakura N., Yamane K., Oda Y., Tsukamoto Y., Ohnishi M.;
 RT "Identification of the acetic acid bacterium NCT 1193 and nucleotide
 RT sequences of the genes encoding enzymes related to acetic acid
 production";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB086015; BAB97173.1; -;
 DR InterPro; IPR001505; Copper_Cua.
 DR InterPro; IPR006333; CytoA_II.
 DR InterPro; IPR002429; Cyt_C_ox_2.
 DR Pfam; PF00116; COX2; 1.
 DR PRINTS; PR01166; CYCOX1DASEII.
 DR ProDom; PD000131; Copper_Cua; 1.
 DR TIGRFAMs; TIGR01433; CytoA; 1.
 KW Oxidoreductase.

SO SEQUENCE 308 AA; 33988 MW; F93006DBE528AD2C CRC64;

Query Match 90.2%; Score 37; DB 2; Length 308;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDWEMWL 6
 Db 135 LDWKMWL 140

RESULT 7

Q94380 PRELIMINARY; PRT; 311 AA.
 AC Q94380;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ZC47.13 protein.
 GN ZC47.13.

OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditicoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA McMurray A.A.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology";
 RT Science 282:2012-2018(1998).
 DR EMBL; Z81141; CAB03488.2; -;
 DR WormPep; ZC47.13; CE25668.
 DR InterPro; IPR002900; DUF38.
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF01827; FTH; 1.
 SQ SEQUENCE 311 AA; 36603 MW; 92846420868C48B CRC64;

Query Match 90.2%; Score 37; DB 5; Length 311;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDWEMWL 6
 Db 295 LDWKMWL 300

RESULT 8

Q8VU06 PRELIMINARY; PRT; 313 AA.
 AC Q8VU06;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Cytochrome o oxidase A.
 GN CYOA.

OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxId=303;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=KT2442;
 RA Fukumori F., Kishii M.;
 RT "Characterization of the toluene-sensitive mutants of Pseudomonas
 RT putida KT2442TOL";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB066295; BAB83593.1; -;
 DR InterPro; IPR001505; Copper_Cua.
 DR InterPro; IPR006333; CytoA_II.
 DR InterPro; IPR002429; Cyt_C_ox_2.
 DR Pfam; PF00116; COX2; 1.
 DR ProDom; PD000131; Copper_Cua; 1.
 DR TIGRFAMs; TIGR01433; CytoA; 1.
 KW Oxidoreductase.

SO SEQUENCE 313 AA; 34557 MW; 193B3F78EBDA2B CRC64;

Query Match 90.2%; Score 37; DB 2; Length 313;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDWEMWL 6
 Db 133 LDWKMWL 138

RESULT 9

Q8ZC58


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ID 082C58 PRELIMINARY; PRT; 318 AA.
AC 082C58;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cytochrome o ubiquinol oxidase subunit II (EC 1.10.3.-).
GN CYO OR YFOJ164 OR Y1021.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
CX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titchell R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltham T., Hamlin N., Holtroyd S., Jagers K., Kariyeh A.V.,
RA Leather S., Moul S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.,
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=21242430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Brubaker R.R., Plano G.V.,
RA Staley S.C., McDonough K.A., Niles M.L., Mason J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AJ414155; CAC92339.1; -
DR EMBL; AE013705; AAM84602.1; -
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006533; CyoA_II.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyoA; 1.
DR Oxidoreductase; Complete proteome.
KW SEQUENCE 318 AA; 35049 MW; E2947941923016D3 CRC64;
SQ
Query Match 90.2%; Score 37; DB 16; Length 318;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDWEMT 6
Db 135 LDWKWL 140

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RA Chandler M., Choiane N., Claudel-Renard C., Cumac S., Demange N.,
RA Gaspin C., Lavie W., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissendbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
RN EMBL; AL646072; CAD16624.1; -
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006533; CyoA_II.
DR InterPro; IPR002429; Cyt_cox_2.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00116; COX2; 1.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyoA; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 329 AA; 35781 MW; 08DA178C39A5964A CRC64;
SQ
Query Match 90.2%; Score 37; DB 16; Length 329;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDWEMT 6
Db 133 LDWKWL 138

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RESULT 11
ID 091427 PRELIMINARY; PRT; 331 AA.
AC 091427;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cytochrome o ubiquinol oxidase subunit II.
GN CYO OR PA1317.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
CX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stever C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Brody L.L., Goltzy L., Tolentino B., Westbrook-Wadman S., Yuan Y.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saiter M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
RN EMBL; AB004561; AAG04706.1; -
DR HSSP; P18400; IGYW.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006533; CyoA_II.
DR InterPro; IPR002429; Cyt_cox_2.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00116; COX2; 1.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyoA; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Complete proteome.
SQ SEQUENCE 331 AA; 36623 MW; DC4449ED0F0BB66 CRC64;
SQ
Query Match 90.2%; Score 37; DB 16; Length 331;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDWEMT 6
Db 133 LDWKWL 138

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RESULT 12

Q8G3A8 PRELIMINARY; PRT; 341 AA.

ID Q8G3A8

AC Q8G3A8

DT 01-MAR-2003 (TRENBLREL. 23, Created)

DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)

DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)

DE Ubiqinol oxidase, subunit II.

GN CYOA OR BR0042.

OS Brucella suis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Brucellaceae; Brucella.

OX NCBI_TaxID=29461;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=1330 / Biovar 1;

RX MEDLINE=22247741; PubMed=12271122;

RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

RA Daugherty S.C., Debroy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,

RA Riedmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,

RT "The Brucella suis genome reveals fundamental similarities between

RT animal and plant pathogens and symbionts."

RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).

RX EMBL, AE014319; AAN28999.1; -.

DR TIGR, BR0042; -.

KW Complete proteome.

SQ SEQUENCE 341 AA; 38563 MW; 38856F0751223F5D CRC64;

QY 1 LDWENTL 6

DB 138 LDMKWL 143

RESULT 13

Q8YEH7 PRELIMINARY; PRT; 344 AA.

ID Q8YEH7

AC Q8YEH7

DT 01-MAR-2002 (TRENBLREL. 20, Created)

DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)

DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)

DE Cytochrome O ubiqlinol oxidase subunit II (BC 1.10.3.-).

GN BME11901.

OS Brucella melitensis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Brucellaceae; Brucella.

OX NCBI_TaxID=29459;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=16M / ATCC 23456 / Biotype 1;

RX MEDLINE=20020109; PubMed=1175668;

RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mufet C., Los T.,

RA Ivanova N., Anderson I., Bhattacharya A., Lykakis A., Resnik G.,

RA Jablonki L., Larsen N., D'Souza W., Bernal A., Mazur M., Goldsman E.,

RA Selikov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

RA Haselkorn R., Kyriides N., Overbeek R.,

RT "The genome sequence of the facultative intracellular pathogen

RT Brucella melitensis."

RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

RX EMBL, AE009623; AAL53082.1; -.

DR InterPro, IPR001505; Copper_Gua.

DR InterPro, IPR006333; CyOA_II.

DR ProDom, PD000131; Copper_Gua; 1.

DR TIGRFAW, TIGR01433; CyOA; 1.

KW Oxidoreductase; Complete proteome.

SQ SEQUENCE 344 AA; 38948 MW; B643C91321B600EC CRC64;

Query Match

Best Local Similarity 83.3%; Score 37; DB 16; Length 344;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWENTL 6

DB 141 LDMKWL 146

RESULT 14

Q9A7F0 PRELIMINARY; PRT; 353 AA.

ID Q9A7F0

AC Q9A7F0

DT 01-JUN-2001 (TRENBLREL. 17, Created)

DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)

DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)

DE Ubiqinol oxidase subunit II.

GN CC1773.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;

OC Caulobacteraceae; Caulobacter.

OX NCBI_TaxID=155892;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 19089 / CB15;

RX MEDLINE=21173698; PubMed=11259647;

RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA Debroy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Uterback T., Tran K., Wolf A., Vamathavan J., Ermlaeva M., White O.,

RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,

RT "Complete genome sequence of Caulobacter crescentus."

RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

RX EMBL, AE005851; AAK23749.1; -.

DR HSP, P18400; ICYW.

DR TIGR, CC1773; -.

DR InterPro, IPR001505; Copper_Gua.

DR InterPro, IPR006333; CyOA_II.

DR ProDom, PD000131; Copper_Gua; 1.

DR TIGRFAW, TIGR01433; CyOA; 1.

KW Complete proteome.

SQ SEQUENCE 353 AA; 38817 MW; 607AF178B2AD184D CRC64;

QY 1 LDWENTL 6

DB 146 LDMKWL 151

RESULT 15

OS9445 PRELIMINARY; PRT; 377 AA.

ID OS9445

AC OS9445

DT 01-AUG-1998 (TRENBLREL. 07, Created)

DT 01-JAN-1999 (TRENBLREL. 09, Last sequence update)

DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)

DE 377A long hypothetical sarcosine oxidase.

GN PH1751.

OS Pyrococcus horikoshii.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

OC Pyrococcus.

OX NCBI_TaxID=53953;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=OT3;

RX MEDLINE=98344137; PubMed=9679194;

RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosegi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb P.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.,
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3.";
 RL DNA Res. 5:55-76 (1998).
 DR EMBL: AP000007; BAA30865.1; -;
 DR InterPro: IPR006076; IPR006076.
 DR Pfam: PF01266; DAO; 1.
 KW Complete proteome.
 SQ SEQUENCE 377 AA; 42421 MW; FA9B0965328EA097 CRC64;

Query Match 90.2%; Score 37; DB 17; Length 377;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEM 5
 Db 354 LDWEM 358

Search completed: February 18, 2004, 14:35:59
 Job time : 18.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41

Sequence: 1 LDMEWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	95.1	501	1 YB06_YEAST	P38081 saccharomyc
2	37	90.2	210	1 KTHY_SCHPO	P36590 echizosacch
3	37	90.2	281	1 Y373_MYCPN	P75227 mycoplasma
4	37	90.2	296	1 CY0A_BUCAI	P57544 buchnera ap
5	37	90.2	307	1 QOX2_ACBAE	P50653 acetobacter
6	37	90.2	314	1 CY0A_PSEPU	P95071 pseudomonas
7	37	90.2	488	1 YK11_CABEL	P34312 caenorhabdi
8	37	90.2	1275	1 RPRC_MYXXA	P50864 myxococcus
9	36	87.8	289	1 Y250_CORGL	P42459 corynebacte
10	36	87.8	290	1 CY0A_BUCAP	P48393 buchnera ap
11	36	87.8	745	1 IKKA_HUMAN	P15111 h inhibitor
12	36	87.8	745	1 IKKA_MOUSE	P06680 m inhibitor
13	36	87.8	756	1 IKKE_HUMAN	P14920 homo sapien
14	36	87.8	757	1 IKKE_MOUSE	P08351 mus musculi
15	36	87.8	757	1 IKKE_RAT	P09478 rattus norv
16	35	85.4	385	1 YPSC_BACSU	P50840 bacillus su
17	34	82.9	191	1 GDIR_CABEL	P02091 caenorhabdi
18	34	82.9	470	1 NOS2_ONCMY	P92091 oncorhynch
19	34	82.9	473	1 LAGC_LACAC	P50977 lactobacill
20	34	82.9	844	1 AMPW_LACHE	P10730 lactobacill
21	34	82.9	1113	1 Y140_MYCGE	P47386 mycoplasma
22	34	82.9	1113	1 Y140_MYCPN	P75033 mycoplasma
23	34	82.9	1120	1 KEPA_ECOLI	P73338 escherichia
24	33	80.5	94	1 FIXX_AZOVI	P53658 azotobacter
25	33	80.5	125	1 VG61_BPMD2	P64253 mycobacteri
26	33	80.5	156	1 RNH_PHOIU	P08677 photorhabdu
27	33	80.5	152	1 PHZE_PSERU	P51768 pseudomonas
28	33	80.5	223	1 WNT1_STRPU	P28094 strongyloce
29	33	80.5	387	1 INTD_ECOLI	P24218 escherichia
30	33	80.5	418	1 HLT_VIBPA	P09289 vibrio para
31	33	80.5	468	1 WNTG_DROME	P09615 drosophila
32	33	80.5	483	1 ENGA_BRUME	P08412 brucella me
33	33	80.5	547	1 SPAK_HUMAN	P09466 homo sapien

34	33	80.5	553	1 SPAK_RAT	O08506 rattus norv
35	33	80.5	556	1 SPAK_MOUSE	O921w9 mus musculi
36	33	80.5	725	1 AREA_PENCI	O01582 penicillium
37	33	80.5	807	1 PHK_RHIO	O086v7 rhizobium 1
38	33	80.5	860	1 AREA_PENRO	O13508 penicillium
39	33	80.5	865	1 AREA_PENRO	O02269 penicillium
40	33	80.5	866	1 AREA_ASFOR	O13415 aspergillus
41	33	80.5	876	1 AREA_EMENT	P17429 emericella
42	33	80.5	878	1 SVY_METUA	O58413 methanococc
43	33	80.5	882	1 AREA_ASPNG	O13412 aspergillus
44	33	80.5	891	1 SVY_PYPAB	O94y55 pyrococcus
45	33	80.5	891	1 SVY_PYPHO	O58052 pyrococcus

ALIGNMENTS

RESULT 1
YB06_YEAST STANDARD; PRT; 501 AA.
AC P38081;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 57.8 kDa protein in PRP6-MDM2 intergenic region.
GN YBR056W OR YBR0510.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX NCBI_Taxid=4932;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95321020; PubMed=7597852;
RA Aljinovic G., Pohl T.M.;
RT "Sequence and analysis of 24 kb on chromosome II of Saccharomyces
cerevisiae.";
RL Yeast 11:475-479(1995).
CC -1 SIMILARITY: BELONGS TO CELLULOSE FAMILY A (FAMILY 5 OF GLYCOSYL
HYDROLASES).
CC
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or send an email to license@sib-sib.ch).
CC
CC EMBL; 235925; CAA84999.1; -.
DR EMBL; 246260; CAA86399.1; -.
DR PIR; S45914; S45914.
DR SGD; S0000260; YBR056W.
DR InterPro; IPR001547; Glyco_hydro_5.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; FALSE_NEG.
KW Hypothetical protein; Hydrolase; Glycosylase.
FT ACT_SITE 236 236 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 333 333 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 501 AA; 57822 MW; 5133A161736ADD3 CRC64;

Query Match 95.1%; Score 39; DB 1; Length 501;
Best Local Similarity 83.3%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEWL 6
:|||||
Db 109 IDMEWL 114

RESULT 2
KTHY_SCHPO STANDARD; PRT; 210 AA.
AC P36590; O74528;

DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thymidylate kinase (EC 2.7.4.9) (dTMP kinase).
 GN TMP OR SPCCT0.07C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 CX NCBI_TaxId=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9300330; PubMed=1327149;
 RA Adair L.T., Yeh Y.I., Jong A.Y.;
 RT "Functional and structural conservation of Schizosaccharomyces pombe
 RT dTMP kinase gene."
 RL Biochim. Biophys. Acta 1132:222-224(1992).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltham D., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA Jones K., Jones L., Jones M., Leathers S., McDonald S., McLean J.,
 RA Mooney P., Mouton S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voiclaert G., Aert R., Robben J., Grympey B.,
 RA Wellens I., Vanstraelen E., Rieger M., Schefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leinich H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mortier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Roche M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Fribourg S.L.,
 RA Cerutti L., Lowe T., McComb W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nuree P.;
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: Catalyzes the conversion of dTMP to dUMP.
 CC -1- CATALYTIC ACTIVITY: ATP + thymidine 5'-phosphate = ADP + thymidine
 CC 5'-diphosphate.
 CC -1- PATHWAY: Biosynthesis of dTMP from dUMP.
 CC -1- SIMILARITY: BELONGS TO THE THYMIDYLATE KINASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X65868; CAA46698.1; -;
 DR EMBL; AL023794; CAA19357.1; -;
 DR PIR; T41553; T41553.
 DR HSP; P00572; ITMK.
 DR GeneDB Spombe; SPCCT0.07C; -;
 DR InterPro; IPR000062; Thymidylate_kin.
 DR Pfam; PF02223; Thymidylate_kin; 1.
 DR TIGRFAMs; TIGR00041; dTMP_kinase; 1.
 DR PROSITE; PS01331; THYMIDYLATE_KINASE; 1.
 FT Transferrase; Kinase; Nucleotide biosynthesis; ATP-binding.
 FT NP BIND 14 21 ATP (POTENTIAL).
 FT CONFLICT 33 39 SGEKAE -> LMKRLK (IN REF. 1).

FT CONFLICT 59 59 K -> T (IN REF. 1).
 FT CONFLICT 80 93 T T O Y I E Q I N K V T -> P S I Y Y R A N Q O R C N (IN REF.
 FT CONFLICT 125 125 P -> T (IN REF. 1).
 FT CONFLICT 164 164 P -> L (IN REF. 1).
 FT CONFLICT 186 186 S -> Y A (IN REF. 1).
 FT CONFLICT 191 191 H -> D (IN REF. 1).
 FT CONFLICT 191 191 H -> D (IN REF. 1).
 SQ SEQUENCE 210 AA; 24249 MW; 42661444ABDAB6C0 CRC64;
 Query Match 90.2%; Score 37; DB 1; Length 210;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMEW 5
 DB 112 LDMEW 116
 RESULT 3
 Y373 MYCPN STANDARD; PRT; 261 AA.
 AC P75237;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Hypothetical protein MG373 homolog (G12_orf281).
 GN MFN551 OR MP291.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 CX NCBI_TaxId=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae."
 RL Nucleic Acids Res. 24:4420-4449(1996).
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 CC -----
 DR EMBL; AB000027; AAB95939.1; -;
 DR PIR; S73617; S73617.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 281 AA; 32569 MW; FC70957510D7BEF3 CRC64;
 Query Match 90.2%; Score 37; DB 1; Length 281;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DMEWL 6
 DB 271 DMEWL 275
 RESULT 4
 CYOA BUCAI STANDARD; PRT; 296 AA.
 ID CYOA BUCAI
 AC P57544;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Ubiquinol oxidase poly(ubiquitin) precursor (EC 1.10.3.-) (Cytochrome O
 DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
 DE subunit 2).
 GN CYOA OR BU472.

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OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum)
OC Bacterioides; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118099;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-Tokyo 1998;
RA MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
CC GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
-----
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-----
DR EMBL; AP001119; BAB13169.1; -.
DR HSSP; P18400; 1CWM.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CytoC.
DR InterPro; IPR002429; Cyt_cox_2.
DR InterPro; IPR000437; Prok_LipoProc.
DR Pfam; PF00116; COX2; 1.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRfam; TIGR01433; CytoC; 1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE NEG.
DR Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
KW Signal; Lipoprotein; Complete proteome.
FT SIGNAL 1 15
FT CHAIN 1 296
FT LIPID 16 296
FT DOMAIN 16 33
FT TRANSMEM 34 54
FT DOMAIN 55 78
FT TRANSMEM 79 99
FT DOMAIN 100 296
FT SIGNAL 296 34180
SQ SEQUENCE 296 AA; 34180 MW; 1AB2B4F0408FBAC CRC64;

Query Match 90.2%; Score 37; DB 1; Length 296;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWML 6
DB 125 LDMKWL 130

RESULT 5
ID COX2_ACEAC STANDARD; PRT; 307 AA.
AC P50653;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome
DE A1 subunit 2) (Oxidase BA(3) subunit 2).
GN CYAB.
OS Acetobacter aceti.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Acetobacter.

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OX NCBI_TaxID=435;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=1023;
RX MEDLINE=93322308; PubMed=8392509;
RA Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H.,
RA Kawamura Y., Horiuchi S., Beppu T.;
RT "Characterization of a cytochrome a1 that functions as a ubiquinol
RT oxidase in Acetobacter aceti.";
RL J. Bacteriol. 175:4307-4314(1993).
CC -1- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: SOME TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
-----
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-----
DR EMBL; D13185; BAA02480.1; -.
DR PIR; A36885; A36885.
DR HSSP; P18400; 1CWM.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CytoC.
DR InterPro; IPR002429; Cyt_cox_2.
DR Pfam; PF00116; COX2; 1.
DR PRINTS; PR01166; CYCOXIDASEII.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRfam; TIGR01433; CytoC; 1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Oxidoreductase; Transmembrane; Respiratory chain; Signal;
KW Lipoprotein.
FT SIGNAL 1 23
FT CHAIN 24 307
FT LIPID 24 24
FT TRANSMEM 46 66
FT TRANSMEM 87 107
SQ SEQUENCE 307 AA; 33921 MW; B6734B84410996D CRC64;

Query Match 90.2%; Score 37; DB 1; Length 307;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWML 6
DB 135 LDMKWL 140

RESULT 6
ID CYOA_PSEPU STANDARD; PRT; 314 AA.
AC Q9WWR1;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
DE subunit 2).
GN CYOA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=IH-2000;
RX MEDLINE=99085656; PubMed=9868765;
RA Hirayama H., Takami H., Inoue A., Horikoshi K.;

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RT "Isolation and characterization of toluene-sensitive mutants from
RT Pseudomonas putida IH-2000."
RL FEMS Microbiol. Lett. 169:219-225(1998).
CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
CC GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
CC
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CC
CC -----
CC EMBL: AB016787; BAA76356.1; -.
CC DR HSSP: P18400; ICYM.
CC DR InterPro: IPR001505; Copper_Gua.
CC DR InterPro: IPR006333; Cyto_O.
CC DR InterPro: IPR002423; Cyt_c-ox_2.
CC DR Pfam: PF00116; COX2; 1.
CC DR ProDom: PD000131; Copper_Gua; 1.
CC DR TIGRFAMs: TIGR01433; Cyto_O.
CC DR PROSITE: PS00013; PROXR LIPOPROTEIN; 1.
CC K0 OXidoreductase; Respiratory chain; Electron transport; Transmembrane;
CC Inner membrane; Signal; Lipoprotein.
CC FT SIGNAL 1 23
CC FT CHAIN 1 23
CC FT LIPID 24 314
CC FT LIPID 24 314
CC FT DOMAIN 24 42
CC FT TRANSSEM 43 63
CC FT DOMAIN 64 86
CC FT TRANSSEM 87 107
CC FT DOMAIN 108 314
CC FT DOMAIN 108 314
CC SQ SEQUENCE 314 AA; 34702 MW; 96EB04FC3AA77F07 CRC64;
CC
CC Query Match 90.2%; Score 37; DB 1; Length 314;
CC Best Local Similarity 83.3%; Pred. No. 37;
CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 LDWEML 6
CC DB 133 LDWEML 138
CC
CC RESULT 7
CC YKTL CABEL STANDARD; PRT; 488 AA.
CC ID YKTL CABEL
CC AC P34312;
CC DT 01-FEB-1994 (Rel. 28, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Hypothetical protein C07A9.1 in chromosome III precursor.
CC GN C07A9.1.
CC OS Caenorhabditis elegans.
CC OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabditoidea;
CC OC Rhabdilita; Pelodermata; Caenorhabditis.
CC OX NCBI_TaxID=6239;
CC OX NCB1_TaxID=6239;
CC
CC SEQUENCE FROM N.A.
CC RP STRAIN=Bristol N2;
CC RX MEDLINE=94150718; PubMed=7906398;
CC RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
CC Bonfield J., Burton J., Connell M., Copestake T., Cooper J., Coulson A.,
CC Cretton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
CC Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
CC Johnson L., Jones M., Kersey J., Karsen J., Laisner N.,
CC Lacroix P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
CC Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Snowken R.,

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RA Sims M., Smailson N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Suleston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Watson R., Watson A., Weinstein L., Wilkinson-Sproat J.,
RA Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC
CC -----
CC EMBL: Z29094; CA82340.1; -.
CC DR PIR: S40706; S40706.
CC DR HSSP: P23807; LIXX.
CC DR WormPep: C07A9.1; CE00502.
CC DR InterPro: IPR002619; CX.
CC DR InterPro: IPR01104; Lectin_C.
CC DR Pfam: PF00059; Lectin_c; 1.
CC DR ProDom: PD006744; CX; 1.
CC DR SMART: SM00034; CLECT; 1.
CC DR PROSITE: PS00615; C TYPE LECTIN 1; FALSE_NEG.
CC DR PROSITE: PS50041; C TYPE LECTIN 2; 1.
CC KW Hypothetical protein; Lectin; Signal.
CC FT SIGNAL 1 49
CC FT CHAIN 1 49
CC FT CHAIN 50 488
CC FT DOMAIN 224 341
CC FT CARBOHYD 187 187
CC FT CARBOHYD 237 237
CC FT CARBOHYD 409 409
CC FT SEQUENCE 488 AA; 54717 MW; 9022691E47078814 CRC64;
CC
CC Query Match 90.2%; Score 37; DB 1; Length 488;
CC Best Local Similarity 100.0%; Pred. No. 56;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 2 DWEML 6
CC DB 287 DWEML 291
CC
CC RESULT 8
CC RFB_C MYXA STANDARD; PRT; 1275 AA.
CC ID RFB_C MYXA
CC AC O50864;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 01-NOV-1997 (Rel. 35, Last annotation update)
CC DE O-antigen biosynthesis protein rfbC.
CC GN RFB_C.
CC OS Myxococcus xanthus.
CC OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
CC OC Cytiobacteriinae; Myxococcaceae; Myxococcus.
CC OX NCBI_TaxID=34;
CC OX NCB1_TaxID=34;
CC
CC SEQUENCE FROM N.A.
CC RP STRAIN=DK6640;
CC RX MEDLINE=96198166; PubMed=8626291;
CC RA Guo D., Bowden M.G., Perahad R., Kaplan H.B.;
CC RT "The Myxococcus xanthus rfbABC operon encodes an ATP-binding cassette
CC transporter homolog required for O-antigen biosynthesis and
CC multicellular development."
CC RT J. Bacteriol. 178:1631-1639(1996).
CC CC -1- FUNCTION: INVOLVED IN O-ANTIGEN BIOSYNTHESIS.
CC -----
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Query Match 87.8%; Score 36; DB 1; Length 290;
 Best Local Similarity 83.3%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 LDMEWL 6
 134 LDMRWL 139

RESULT 11
 IKKA_HUMAN STANDARD; PRT; 745 AA.
 ID IKKA_HUMAN 015111; 014666; Q13132; G92467;
 AC 015111; 014666; Q13132; G92467;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase subunit (IC 2.7.1.-)
 DE (1-kappa-B kinase alpha) (IKK-alpha) (IKK-A) (Ikkapab kinase
 DE (1-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
 DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1KA).
 GN CHUK OR IKK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RC TISSUE=T-cell;
 RA MEDLINE=97386461; PubMed=9244310;
 RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
 RT "Identification and characterization of an IkappaB kinase-";
 RL Cell 90:373-383(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC MEDLINE=97394468; PubMed=9252186;
 RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
 RT "A cytokine-responsive IkappaB kinase that activates the transcription
 RT factor NF-kappaB-";
 RL Nature 368:548-554(1997).
 RN [3]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
 RP SER-176.
 RC TISSUE=Cervical carcinoma;
 RA MEDLINE=98008813; PubMed=9346484;
 RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
 RT NF-kappaB activation-";
 RL Science 278:860-866(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA MEDLINE=99032998; PubMed=9813230;
 RA Hu M.C.-T., Wang Y.-P.;
 RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 RT embryonic tissues but localized to different human chromosomes-";
 RL Gene 223:31-40(1998).
 RN [5]
 RP SEQUENCE OF 32-745 FROM N.A.
 RC TISSUE=Cervical carcinoma;
 RA MEDLINE=96258427; PubMed=8777433;
 RA Connelly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain-";
 RL Cell. Mol. Biol. Res. 41:537-549(1995).
 RN [6]
 RP PHOSPHORYLATION BY MAPK14/NIK, AND MUTAGENESIS OF SER-176; THR-179
 RP AND SER-180.
 RA MEDLINE=98186283; PubMed=9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of

RT Ser-176-";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 RN [7]
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RA MEDLINE=99413720; PubMed=10485710;
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
 RA Donner D.B.;
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt
 RT serine-threonine kinase-";
 RL Nature 401:82-85(1999).
 RN [8]
 RP IKKA-IKKB BINDING.
 RA MEDLINE=99212441; PubMed=10195894;
 RA Delnase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation-";
 RL Science 284:309-313(1999).
 RN [9]
 RP IKK PHOSPHORYLATION.
 RA MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase-";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [10]
 RP REVIEW.
 RA MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection-";
 RL Am. J. Physiol. 278:C451-C462(2000).
 RN [11]
 RP SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKKB AND IKKGA.
 RA MEDLINE=21968797; PubMed=11971985;
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 RA O'Malley B.W.;
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
 RT activity by I kappa B kinase-";
 RL Mol. Cell. Biol. 22:3549-3561(2002).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-GAMMA/MEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAPK14/NIK, MEKK1, IKAP and IKK-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- PTM: Phosphorylated by MAPK14/NIK, AKT and to a lesser extent by
 CC MEKK1, and dephosphorylated by PP2A. Auto-phosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC
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 CC or send an email to license@sib-sb.ch).
 CC
 CC EMBL; AF012890; AAC51662.1; -
 CC EMBL; AF009225; AAC51671.1; -
 CC EMBL; AF080157; AAC08996.1; -
 CC EMBL; U22512; AAC50713.1; -
 CC HSSP; O63450; 1A06.
 CC GeneW; HGNC:1974; CHUK.
 CC MIM; 600664; -.

DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0008384; P:ikappab kinase activity; TAS.
 DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
 DR GO; GO:0007352; P:I-kappab phosphorylation; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR000719; P:Protein kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; P:kinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; P:Protein kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 302 PROTEIN KINASE.
 FT 455 476 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 738 743 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 PHOSPHORYLATION (BY PKB/AKT1).
 FT MOD_RES 23 23 PHOSPHORYLATION (BY MAP3K14).
 FT MOD_RES 176 176 T->A: LOSS OF PHOSPHORYLATION AND
 FT MUTAGEN 23 23 DECREASE OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->M: LOSS OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->M: LOSS OF AUTOPHOSPHORYLATION.
 FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF
 FT ACTIVITY.
 FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
 FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
 FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
 FT CONFLICT 543 543 E -> G (IN REF. 2).
 FT CONFLICT 604 604 L -> R (IN REF. 5).
 FT CONFLICT 679 680 TS -> AY (IN REF. 5).
 FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
 FT CONFLICT 684 684 TS -> DL (IN REF. 5).
 FT SEQUENCE 745 AA; 84653 KM; 7A90B59BC98A56C2 CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 745;
 Best local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMEWL 6
 Db 738 LDMSWL 743

RESULT 12
 ID IKKA_MOUSE STANDARD; PRT; 745 AA.
 AC Q60680; Q9D2X3;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.-)
 DE (I kappa-B kinase alpha) (IKK- α) (IKK- α) (Ikkapab kinase)
 DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
 DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
 GN CHUK OR IKKA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/c;
 RX MEDLINE=9604444; PubMed=7558004;
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 RT chromosome 10 and mouse chromosome 19.";

RL Genomics 27:348-351(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/c;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connolly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=2108560; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kankawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guestinich S., Hall D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilmink L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohno S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=20198447; PubMed=10733566;
 RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R.,
 RA Gelezianus R., Marcu K.B.;
 RT "Functional isoforms of Ikkapab kinase alpha (IKK- α) lacking
 RT leucine zipper and helix-loop-helix domains reveal that IKK- α and
 RT IKK- β have different activation requirements.";
 RL Mol. Cell. Biol. 20:2635-2649(2000).
 RN [5]
 RP PHOSPHORYLATION BY MAP3K14/NIK.
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of Ikkapab kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RP IKKA-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhaese M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of Ikkapab kinase activity through
 RT IKK- β subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [7]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of Ikkapab kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [8]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).

CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEKK1, IKAP and IKB-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKKG and CREBBP (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q06880-1; Sequence=Displayed;
 CC Name=2; Synonyms=Delta LH; Sequence=VSP_004866, VSP_004867;
 CC IsoId=Q06880-2; Sequence=VSP_004866, VSP_004867;
 CC Name=3; Synonyms=Delta H;
 CC IsoId=Q06880-3; Sequence=VSP_004868, VSP_004869;
 CC -1- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
 CC 3 are expressed predominantly in brain and T-lymphocytes.
 CC -1- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
 CC E11, E15 and E17 days. In the limb development, its expression
 CC predominates in the limb buds at E12.5 day.
 CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: U12473; AAC52589.1; -;
 CC EMBL: AK018671; BAB31335.1; -;
 CC PIR: I49101; I49101.
 CC HSSP: Q63450; 1A06.
 CC MGD: MGI:99484; Chuk.
 CC DR InterPro: IPR000719; Prot. Kinase.
 CC DR InterPro: IPR002290; Ser Thr kinase.
 CC DR InterPro: IPR001245; Tyr kinase.
 CC DR Pfam: PF00069; Kinase; 1.
 CC DR PRINTS: PR00109; TRKINASE.
 CC DR PRODOM: PD000001; Prot. Kinase; 1.
 CC DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 CC DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 CC DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 CC DR Transferrase, Serine/threonine-protein kinase; ATP-binding;
 CC Phosphorylation; Alternative splicing.
 CC KW Phosphorylation; Alternative splicing.
 CC FT DOMAIN 15 300
 CC FT DOMAIN 455 476
 CC FT DOMAIN 738 743
 CC FT NP_BIND 21 29
 CC FT BINDING 44 44
 CC FT ACT_SITE 144 144
 CC FT MOD_RES 23 23
 CC FT MOD_RES 176 176
 CC FT VARSPPLIC 452 471
 CC FT VARSPPLIC 472 745
 CC FT VARSPPLIC 577 584
 CC FT VARSPPLIC 577 584

FT VARSPPLIC 585 745 Missing (in isoform 3).
 FT CONFLICT 236 236 /FTId=VSP_004869.
 FT CONFLICT 400 400 K -> E (IN REF. 3).
 FT CONFLICT 400 400 S -> Y (IN REF. 3).
 SQ SEQUENCE 745 AA; 84728 MW; 3PFF5582APF92233 CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 745;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDMEWL 6
 DB 738 LDMSWL 743
 RESULT 13
 ID IKKB HUMAN
 AC 014820; C75327; STANDARD; PRT; 756 AA.
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 15-SEP-2003 (Rel. 42; Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 DE (I-kappa-B kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBKB).
 GN IKKB OR IKKB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=98008813; PubMed=9346484;
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RT "IKK-1 and IKK-2: cytokine-activated Ikappab kinases essential for
 RT NF-kappaB activation";
 RL Science 278:860-866 (1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RX MEDLINE=98008814; PubMed=9346485;
 RA Morioniz J.D., Gao X., Cao Z., Roche M., Goeddel D.V.;
 RT "Ikappab kinase-beta: NF-kappaB activation and complex formation with
 RT Ikappab kinase-alpha and NIK";
 RL Science 278:866-869 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=99032998; PubMed=9813220;
 RA Hu M.C.-T., Wang Y.-P.;
 RT "Ikappab kinase-alpha and -beta genes are coexpressed in adult and
 RT embryonic tissues but localized to different human chromosomes";
 RL Gene 222:31-40 (1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND GENE MAPPING.
 RX MEDLINE=98438415; PubMed=9763654;
 RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
 RT "Assignment of Ikappab kinase beta (IKKB) to human chromosome band
 RT 8p12-->p11 by in situ hybridization";
 RL Cytogenet. Cell Genet. 82:32-33 (1998).
 RN [5]
 RP SEQUENCE OF 1-256 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Krausner R.L., Feinberg F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udell T.B., Tohilyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzaniak M.I., Skalska U., Smalins D.E.,
 RA Scheraga A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RP IKK PHOSPHORYLATION.
 RP MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.,
 RA "Coordinate regulation of I-kappaB kinases by mitogen-activated protein
 RT kinase kinase 1 and NF-kappaB-inducing kinase.";
 RT Mol. Cell. Biol. 18:7336-7343(1998).
 [7]
 RP REVIEW.
 RP MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.,
 RA "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RT Am. J. Physiol. 278:C451-C462(2000).
 [8]
 RP IDENTIFICATION IN A COMPLEX WITH CREBBP, NCOA2, NCOA3, IKKA AND IKKB.
 RP MEDLINE=21968797; PubMed=11971985;
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Teal S.Y., Teal M.J.,
 RA O'Malley B.W.,
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
 RT activity by I kappa B kinase.";
 RT Mol. Cell. Biol. 22:3549-3561(2002).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3 (By similarity).
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50
 CC complex. Phosphorylated IKB-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
 CC and CREBBP.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
 CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and
 CC peripheral blood.
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL, AF028684, AAC51860.1, -;
 CC EMBL, AF080158, AAD08997.1, -;
 CC EMBL, AF031416, AAC64675.1, -;
 CC EMBL, BC006231, AA06231.1, -;
 CC HSSP, 063450, 1A06.
 CC Genew: HGNC:5960; IKKB.
 DR MIM, 603258.
 DR GO, GO:0005737, C:cytoplasm; NAS.
 DR GO, GO:0005524, F:ATP binding activity; NAS.
 DR GO, GO:0004674, F:protein serine/threonine kinase activity; NAS.
 DR GO, GO:0016563, F:transcriptional activator activity; NAS.

DR GO, GO:0006468, P:protein amino acid phosphorylation; NAS.
 DR InterPro, IPR000719, Prot_kinase.
 DR InterPro, IPR002290, Ser_thr_kinase.
 DR Pfam, PF00069, pkinase; 1.
 DR Pfam, PF00240, ubiquitin; 1.
 DR ProDom, PDD00001, Prot_kinase; 1.
 DR PROSITE, PS00107, PROTEIN_KINASE_ATP, FALSE_NEG.
 DR PROSITE, PS00108, PROTEIN_KINASE_ST, 1.
 DR PROSITE, PS50011, PROTEIN_KINASE_DOM, 1.
 KW transferase; Serine/threonine-protein kinase; ATP-binding;
 KW phosphorylation.
 FT DOMAIN 15 300
 FT DOMAIN 458 479
 FT DOMAIN 737 742
 FT NP_BIND 21 29
 FT BINDING 44 44
 FT ACT_SITE 145 145
 FT MOD_RES 23 23
 FT MOD_RES 177 177
 FT MOD_RES 181 181
 FT MOD_RES 44 44
 FT MUTAGEN 177 177
 FT MUTAGEN 177 177
 FT MUTAGEN 181 181
 FT MUTAGEN 181 181
 FT CONFLICT 231 255
 FT CONFLICT 425 425
 FT SEQUENCE 756 AA; 8653 MW; P9CADF671AE9E14E CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 756;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 LDWBL 6
 Db 737 LDWBL 742
 RESULT 14
 ID IKKB MOUSE STANDARD. PRT; 757 AA.
 AC 088351; Q9RLJ6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B-kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFIKB).
 GN IKKB OR IKK2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. AND PHOSPHORYLATION BY MEK1.
 RC STRAIN=C57BL/6; TISSUE=Spleen;
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.,
 RT "Differential regulation of I-kappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase kinase-1.";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 [2]
 RP SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.,
 RT "Murine I-kappaB kinase-B, a developmentally regulated protein kinase that
 RT constitutively phosphorylates serine residues of I-kappaB.";
 RT Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
 [3]
 RP DEVELOPMENTAL STAGE.

RX MEDLINE=99455228; PubMed=10523828;
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates Ikkapab kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 (4)
 RN IKK PHOSPHORYLATION.
 RP MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of Ikkapab kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappa-B-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 [5]
 RN REVIEW.
 RP MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P65-P50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
 CC and CREBBP (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
 CC -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
 CC the mouse embryo, at E9.5 day its expression begins to be
 CC localized to the brain, neural ganglia, neural tube, and in liver
 CC at E12.5 day. At E15.5 day, the expression is further restricted
 CC to specific tissues of the embryo.
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
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 CC
 DR EMBL; AF026524; AAC23557.1; -
 DR EMBL; AF088910; AAD52095.1; -
 DR HSP; Q63450.1A06.
 DR MGI; MGI:1338071; Ikbkb.
 DR InterPro; IPR000719; Prot. kinase.
 DR InterPro; IPR002290; Ser. Thr. kinase.
 DR InterPro; IPR001245; Tyr. kinase.
 DR Pfam; PF00069; Pkinase.1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot. Kinase.1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP. FALSE NEG.
 DR PROSITE; PS00108; PROTEIN KINASE ST.1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM.1.
 KM Transerase; Serine/threonine-protein kinase; ATP-binding;
 KW phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 MEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).

FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 406 406 K -> R (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 757 TLDMWSLQWEDERCSLRQACD -> VTA (IN REF. 2).
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5B CRC64;
 Query Match Score 36; DB 1; Length 757;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDMWML 6
 DB 737 LDMWML 742
 RESULT 15
 ID IKKB RAT STANDARD; PRT; 757 AA.
 AC Q9078; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-.)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid:10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IKK beta in megakaryocyte differentiation.";
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of Ikkapab kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappa-B-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P65-P50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
 CC and CREBBP (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC
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CC -----
 DR EMBL; AF115282; AAF21978.1; -
 DR HSSP; Q63450; 1A06.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; PKinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KM Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 757 AA; 86866 MW; 3AFBE46A7DF91F9C CRC64;

Query Match 87.8%; Score 36; DB 1; Length 757;

Best Local Similarity 83.3%; Pred. No. 1.2e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWEMWL 6

Db 737 LDWEMWL 742

Search completed: February 18, 2004, 14:28:14
 Job time : 4.55263 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09, Search time 6.5921 Seconds
(without alignment)
87.531 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41

Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96166682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	95.1	501	2 S45914	probable glucan 1,
2	37	90.2	210	2 T41553	thymidylate kinase
3	37	90.2	210	2 S28955	dTMP kinase (EC 2.
4	37	90.2	242	2 T27590	hypothetical prote
5	37	90.2	277	1 JCS900	bo-type ubiquinol
6	37	90.2	281	2 S73617	MG373 homolog G12
7	37	90.2	296	2 A84985	cytochrome o ubiqu
8	37	90.2	307	1 A36885	bo-type ubiquinol
9	37	90.2	318	2 AD0384	cytochrome o ubiqu
10	37	90.2	331	2 D83480	cytochrome o ubiqu
11	37	90.2	344	2 AG3489	cytochrome o ubiqu
12	37	90.2	353	2 A87469	ubiquinol oxidase
13	37	90.2	377	2 B71184	probable sarcosine
14	37	90.2	379	2 F75144	sarcosine oxidase,
15	37	90.2	386	2 C96006	probable cytochrom
16	37	90.2	404	2 A71213	alanine-tRNA ligase
17	37	90.2	405	2 G75027	alanine-tRNA synthet
18	37	90.2	488	2 S40706	hypothetical prote
19	37	90.2	1275	2 T18556	O-antigen biosynth
20	36	87.8	82	2 C69013	hypothetical prote
21	36	87.8	162	2 C70829	hypothetical prote
22	36	87.8	270	2 I40724	hypothetical prote
23	36	87.8	332	2 A13395	NADH2 dehydrogenas
24	36	87.8	348	2 AE2733	NADH ubiquinone ox
25	36	87.8	348	2 G97514	NADH dehydrogenase
26	36	87.8	414	2 B82408	hypothetical prote
27	36	87.8	443	2 AE0309	probable sugar tra
28	36	87.8	745	1 I49101	conserved helix-lo
29	36	87.8	764	2 AD3144	formate dehydrogen

30	36	87.8	764	2 H98143	cbhbc protein (U60
31	36	87.8	1120	2 A10561	integral membrane
32	35	85.4	332	2 A42593	cytochrome o ubiqu
33	35	85.4	377	2 B97376	cytochrome ba(3) (
34	35	85.4	378	2 T12895	hypothetical prote
35	35	85.4	385	2 F69941	conserved hypothet
36	35	85.4	420	2 A54759	cytochrome ba(3) c
37	35	85.4	451	2 G82218	benzox histidine k
38	35	85.4	480	2 T24087	hypothetical prote
39	35	85.4	660	2 S66708	probable membrane
40	35	85.4	700	2 T24092	hypothetical prote
41	35	85.4	723	2 T32136	hypothetical prote
42	35	85.4	765	2 T35719	chitinase - Strept
43	35	85.4	783	2 F88808	protein R09E10.3 (
44	35	85.4	854	2 C83905	hypothetical prote
45	35	85.4	903	2 T20804	hypothetical prote

ALIGNMENTS

RESULT 1

S45914

probable glucan 1,3-beta-glucosidase (EC 3.2.1.58) YBR056w - yeast (Saccharomyces cerev

N.Alternate names: hypothetical protein YBR0510

C.Species: Saccharomyces cerevisiae

C.Date: 26-Aug-1994 #sequence revision 09-Sep-1994 #text_change 19-Apr-2002

C.Accession: S45914; S49511; S55855

R.Aljinovic, G.; Pohl, F.M.; Pohl, T.M.

submitted to the Protein Sequence Database, August 1994

A.Reference number: S45906

A.Accession: S45914

A.Molecule type: DNA

A.Residues: 1-501 <AL2>

A.Cross-references: EMBL:Z35925; NID:G536292; PID:G536293; MIPS:YBR056w

A.Experimental source: strain S288C

A.Description: Sequence and analysis of 24 kb on chromosome II of Saccharomyces cerevis

A.Reference number: S49503

A.Accession: S49511

A.Molecule type: DNA

A.Residues: 1-501 <AL2>

A.Cross-references: EMBL:Z46260; NID:G559942; PID:G559952

A.Experimental source: strain S288C

R.Aljinovic, G.; Pohl, T.M.

Yeast 11, 475-479, 1995

A.Title: Sequence and analysis of 24 kb on chromosome II of Saccharomyces cerevisiae.

A.Reference number: S55846; MUID:95321020; PMID:7597852

A.Accession: S55855

A>Status: nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

A.Residues: 1-501 <AL2>

A.Cross-references: EMBL:Z46260; NID:G559942; PID:CA06399.1; PID:G559952

A.Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994

C.Genetics:

A.Cross-references: SGD:S0000260

A.Map position: 2R

C.Keywords: glycosidase; hydrolase

Query Match 95.1% Score 39; DB 2; Length 501;
Best Local Similarity 83.3% Pred. No. 63;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWEWL 6
:|||||
DB 109 LDWEWL 114

RESULT 2

T41553

thymidylate kinase - fission yeast (Schizosaccharomyces pombe)

C.Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
 C/Accession: T41553
 R/Mod: V.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Hartley, D.
 Submitted to the EMBL Data Library, June 1998
 A/Reference number: Z22001
 A/Accession: T41553
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-210 <MOO>
 A/Cross-references: EMBL:AL023794; PIDN:CAA19357.1; GSPDB:GN00068; SPDB:SPCC70.07c
 A/Experimental source: strain 972h-; cosmid c70
 C/Genetics:
 A/Gene: SPDB:SPCC70.07c
 A/Map position: 3
 A/Introns: 45/1; 110/3
 C/Superfamily: dtwp kinase

Query Match 90.2%; Score 37; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEW 5
 |||||
 DB 112 LDMEW 116

RESULT 3
 S28955
 dtwp kinase (EC 2.7.4.9) - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 19-Jan-2001
 C/Accession: S28955
 R/Mod: V.; Yeh, Y.-I.S.; Jong, A.Y.
 Biochim. Biophys. Acta 1132, 222-224, 1992
 A/Title: Functional and structural conservation of Schizosaccharomyces pombe dtwp kinase
 A/Reference number: S28955; MUID:93003330; PMID:1137149
 A/Accession: S28955
 A/Molecule type: mRNA
 A/Residues: 1-210 <ABA>
 A/Cross-references: EMBL:X65868; NID:94973; PIDN:CAA46698.1; PID:94974
 C/Superfamily: dtwp kinase
 C/Keywords: ATP; nucleotide binding; nucleotide biosynthesis; P-loop; phosphotransferase
 P14-21/Region: nucleotide-binding motif A (P-loop)

Query Match 90.2%; Score 37; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEW 5
 |||||
 DB 111 LDMEW 115

RESULT 4
 T27590
 hypothetical protein ZC47.13 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C/Accession: T27590
 R/Mod: V.; Murray, A.
 Submitted to the EMBL Data Library, October 1996
 A/Reference number: Z20391
 A/Accession: T27590
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-242 <WIL>
 A/Cross-references: EMBL:Z81141; PIDN:CA03488.1; CESP:ZC47.13
 A/Experimental source: clone ZC47
 C/Genetics:
 A/Gene: CESP:ZC47.13
 A/Introns: 172/3
 C/Superfamily: Caenorhabditis elegans hypothetical protein ZC47.9

Query Match 90.2%; Score 37; DB 2; Length 242;
 Best Local Similarity 83.3%; Pred. No. 60;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEW 6
 |||||
 DB 226 LDMEW 231

RESULT 5
 JCS900
 bo-type ubiquinol oxidase (EC 1.10.3.-) chain II - Bradyrhizobium japonicum
 C/Species: Bradyrhizobium japonicum
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: JCS900
 R/Mod: V.; Luebben, M.; Møller, R.J.
 Gene 183, 201-206, 1996
 A/Title: The Bradyrhizobium japonicum coxX gene cluster encodes a bo3-type ubiquinol
 A/Reference number: JCS900; MUID:97149299; PMID:8996107
 A/Accession: JCS900
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-277 <SUR>
 C/Genetics:
 A/Gene: coxX
 C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
 C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; re

Query Match 90.2%; Score 37; DB 1; Length 277;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEW 6
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 DB 108 LDMEW 113

RESULT 6
 S73617
 MG373 homolog G12.orf281 - Mycoplasma pneumoniae (strain ATCC 29342)
 C/Species: Mycoplasma pneumoniae
 A/Variant: ATCC 29342
 C/Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
 C/Accession: S73617
 R/Mod: V.; Hilbert, H.; Plagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.
 Nucleic Acids Res. 24, 4420-4449, 1996
 A/Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
 A/Reference number: S73327; MUID:97105885; PMID:8946633
 A/Accession: S73617
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-281 <HIM>
 A/Cross-references: EMBL:AB000027; GB:U00089; NID:91673941; PIDN:AAB95939.1; PID:916731
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 C/Genetics:
 A/Genetic code: SGC3

Query Match 90.2%; Score 37; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWEMW 6
 |||||
 DB 271 DWEMW 275

RESULT 7
 AB4985
 cytochrome o ubiquinol oxidase subunit II [imported] - Buchnera sp. (strain APS)
 C/Species: Buchnera sp.
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2001
 C/Accession: AB4985
 R/Mod: V.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000
 A/Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
 A/Reference number: AB4930; MUID:20445117; PMID:10993077

A/Accession: AB4985
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-296 <STO>
 A/Cross-references: GB:AP000398; GSPDB:GN00144
 A/Experimental source: strain APS
 C/Genetics:

A/Gene: cyoA, BU472
 C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
 C/Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match
 Best Local Similarity 90.2%; Score 37; DB 2; Length 296;
 Pred. No. 74;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWMTL 6
 |||:
 Db 125 LDMKWL 130

RESULT 8
 A/Accession: A36885
 bo-type ubiquinol oxidase (EC 1.10.3.-) chain II precursor - Acetobacter aceti

N/Alternate names: cytochrome a1 chain II

C/Species: Acetobacter aceti
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C/Accession: A36885
 R/Pukaya, M.; Tayama, K.; Tamaki, T.; Edisuya, H.; Okumura, H.; Kawamura, Y.; Horinouchi

J. Bacteriol. 175, 4307-4314, 1993
 A/Title: Characterization of a cytochrome a-1 that functions as a ubiquinol oxidase in A

A/Reference number: A36885; MUID:9332308; PMID:8392509

A/Accession: A36885
 A/Status: preliminary

A/Molecule type: DNA
 A/Residues: 1-307 <FTK>

A/Cross-references: GB:D13185; NID:9409064; PIND:BA02480.1; PID:9433186

A/Experimental source: isolate 1023
 C/Genetics:

A/Gene: cybB
 C/Complex: heterotetramer; chains I, II, III and IV

C/Function: terminal oxidase for ethanol oxidation

C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain

C/Keywords: copper; electron transfer; heterotetramer; membrane-associated complex; oxid

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-307/Product: bo-type ubiquinol oxidase chain II #status predicted <MAT>

F/48-64/Domain: transmembrane #status predicted <TM1>

F/89-105/Domain: transmembrane #status predicted <TM2>

Query Match
 Best Local Similarity 90.2%; Score 37; DB 1; Length 307;
 Pred. No. 77;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWMTL 6
 |||:
 Db 135 LDMKWL 140

RESULT 9
 A/Accession: AD0384
 cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Yersinia pestis (str

C/Species: Yersinia pestis

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

C/Accession: AD0384
 R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Terrage, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,

Nature 413, 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AD0384
 A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-318 <KUR>

A/Cross-references: GB:AL590842; PIND:CAC92399.1; PID:g15961102; GSPDB:GN00175

C/Genetics:

A/Gene: cyoA

C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chat

C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; re

Query Match
 Best Local Similarity 90.2%; Score 37; DB 2; Length 318;
 Pred. No. 80;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWMTL 6
 |||:
 Db 135 LDMKWL 140

RESULT 10
 A/Accession: DB3480
 cytochrome o ubiquinol oxidase subunit II PA1317 [imported] - Pseudomonas aeruginosa (

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C/Accession: DB3480
 R/Stover, C.K.; Pham, X.Q.; Brown, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Liu

Lozy, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat

A/Reference number: AB2950; MUID:20437337; PMID:10984043

A/Accession: DB3480
 A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-331 <STO>

A/Cross-references: GB:AE004561; GB:AE004091; NID:g9947253; PIND:AA04706.1; GSPDB:GN0

A/Experimental source: strain PA01

C/Genetics:

A/Gene: cyoA, PA1317

C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chat

C/Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match
 Best Local Similarity 90.2%; Score 37; DB 2; Length 331;
 Pred. No. 83;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWMTL 6
 |||:
 Db 133 LDMKWL 138

RESULT 11
 A/Accession: AG3489
 cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Brucella melitensis

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 22-Mar-2002

C/Accession: AG3489
 R/DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Lob, T.; Ivanova,

.; Mazur, M.; Goltzman, B.; Selkov, E.; Elzer, P.H.; Hagler, S.; O'Callaghan, D.; Lete

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen Brucella melite

A/Reference number: AD3252; PMID:11756688

A/Accession: AG3489
 A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-344 <KUR>

A/Cross-references: GB:AE00917; PIND:AAL53082.1; PID:g17963945; GSPDB:GN00190

A/Experimental source: strain 16M

C/Genetics:

A/Gene: BME11901

A/Map position: I

C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chat

C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; re

Query Match 90.2%; Score 37; DB 2; Length 344;
 Best Local Similarity 83.3%; Pred. No. 87;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMEWL 6
 |||||
 DB 141 LDMEWL 146

RESULT 12

A87469
 ubiquinol oxidase subunit II [imported] - Caulobacter crescentus

C/Species: Caulobacter crescentus

C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-May-2001

C/Accession: A87469

R/Nieman, W.C.; Feldlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eison, J.; Heidelberg, J.

B.; Laub, M.T.; Debby, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A/Title: Complete Genome Sequence of Caulobacter crescentus.

A/Reference number: A87449; MUID:21173698; PMID:11259647

A/Accession: A87469

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-353 <STO>

A/Cross-references: GB:AE005673; NID:913423199; PIDN:AAK23749.1; GSPDB:GN00148

C/Genetics:

A/Gene: CCI773

C/Superfamily: bc-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain

C/Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.2%; Score 37; DB 2; Length 353;
 Best Local Similarity 83.3%; Pred. No. 89;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMEWL 6
 |||||
 DB 146 LDMEWL 151

RESULT 13

B71184
 probable sarcosine oxidase - Pyrococcus horikoshii

C/Species: Pyrococcus horikoshii

C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000

C/Accession: B71184

R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Seki

M.; Ohnuki, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushiida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A/Reference number: A71000; MUID:98344137; PMID:9679194

A/Accession: B71184

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-377 <KAW>

A/Cross-references: GB:AP000007; NID:93236134; PIDN:BA30865.1; PID:93258182

A/Experimental source: strain Q73

A/Note: this accession replaces an interim accession for a sequence replaced by Genbank

C/Genetics:

A/Gene: PH1751

C/Superfamily: sarcosine oxidase

Query Match 90.2%; Score 37; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMEWL 5
 |||||
 DB 354 LDMEWL 358

RESULT 14

F75144
 sarcosine oxidase, chain beta (soxb) PAB0214 - Pyrococcus abyssi (strain Orsay)

C/Species: Pyrococcus abyssi

C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C/Accession: F75144

R/anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome st

A/Reference number: A75001

A/Accession: F75144

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-379 <KAW>

A/Cross-references: GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CA949237.1; PID:95457

A/Experimental source: strain Orsay

C/Genetics:

A/Gene: soxb

C/Superfamily: sarcosine oxidase

Query Match 90.2%; Score 37; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMEWL 5
 |||||
 DB 356 LDMEWL 360

RESULT 15

C96006
 probable cytochrome o ubiquinol oxidase chain II protein (EC 1.10.3.-) [imported] - St.

C/Species: Stenotrophobacter meliloti

C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C/Accession: C96006

R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hern

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A/Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing en

A/Reference number: A95842; MUID:21396508; PMID:11481431

A/Accession: C96006

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-386 <KUR>

A/Cross-references: GB:AL51985; PIDN:CAK49715.1; PID:915141202; GSPDB:GN00167

A/Experimental source: strain 1021, megaplasmid pSymB

R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Huble

pela, D.; Chain, P.; Cowley, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lela

heault, F.; Vandemol, M.; Vorholter, F.J.; Weidner, S.; Keller, D.H.; Wong, K.; Yeh,

A/Title: The composite genome of the legume symbiont Stenotrophobacter meliloti.

A/Reference number: A96039; MUID:21368234; PMID:11474104

A/Contents: annotation

C/Genetics:

A/Gene: cyoA; SMD21487

A/Genome: plasmid

C/Superfamily: bc-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain

C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; re

Query Match 90.2%; Score 37; DB 2; Length 386;
 Best Local Similarity 83.3%; Pred. No. 98;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMEWL 6
 |||||
 DB 141 LDMEWL 146

Search completed: February 18, 2004, 14:38:52
 Job time : 6.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41

Sequence: 1 LDWEML 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubppa/PCR_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	6	10	US-09-847-940B-17
2	41	100.0	6	11	US-09-847-946A-17
3	41	100.0	6	11	US-09-847-946A-45
4	41	100.0	6	11	US-09-847-946A-117
5	41	100.0	6	11	US-09-847-946A-117
6	41	100.0	6	11	US-09-847-946A-117
7	41	100.0	6	11	US-09-847-946A-117
8	41	100.0	6	11	US-09-847-946A-117
9	41	100.0	6	11	US-09-847-946A-117
10	41	100.0	6	11	US-09-847-946A-117
11	41	100.0	6	11	US-09-847-946A-117
12	41	100.0	6	11	US-09-847-946A-117
13	41	100.0	6	11	US-09-847-946A-117
14	41	100.0	6	11	US-09-847-946A-117
15	39	95.1	471	12	US-10-369-493-12414

15	37	90.2	20	12	US-09-962-756-939	Sequence 939, App
17	37	90.2	20	12	US-10-253-471-939	Sequence 939, App
18	37	90.2	70	9	US-09-864-761-46514	Sequence 46514, A
19	37	90.2	219	12	US-10-369-493-19572	Sequence 19572, A
20	37	90.2	259	12	US-10-369-493-22800	Sequence 22800, A
21	37	90.2	280	12	US-10-369-493-3354	Sequence 3354, A
22	37	90.2	354	15	US-10-166-087-6	Sequence 6, App1
23	37	90.2	462	12	US-10-369-493-8244	Sequence 8244, App
24	36	87.8	6	10	US-09-847-940B-2	Sequence 2, App1
25	36	87.8	6	11	US-09-847-946A-2	Sequence 2, App1
26	36	87.8	7	11	US-09-847-946A-3	Sequence 3, App1
27	36	87.8	6	11	US-09-847-946A-37	Sequence 37, App1
28	36	87.8	8	11	US-09-847-946A-30	Sequence 30, App1
29	36	87.8	8	11	US-09-847-946A-38	Sequence 38, App1
30	36	87.8	9	11	US-09-847-946A-39	Sequence 39, App1
31	36	87.8	9	11	US-09-847-946A-32	Sequence 32, App1
32	36	87.8	9	11	US-09-847-946A-35	Sequence 35, App1
33	36	87.8	9	11	US-09-847-946A-36	Sequence 36, App1
34	36	87.8	10	11	US-09-847-946A-31	Sequence 31, App1
35	36	87.8	10	11	US-09-847-946A-34	Sequence 34, App1
36	36	87.8	11	11	US-09-847-946A-28	Sequence 28, App1
37	36	87.8	11	11	US-09-847-946A-132	Sequence 132, App1
38	36	87.8	11	11	US-09-847-946A-140	Sequence 140, App1
39	36	87.8	13	11	US-09-847-946A-143	Sequence 143, App1
40	36	87.8	13	11	US-09-847-946A-144	Sequence 144, App1
41	36	87.8	13	11	US-09-847-946A-145	Sequence 145, App1
42	36	87.8	13	11	US-09-847-946A-148	Sequence 148, App1
43	36	87.8	17	11	US-09-847-946A-141	Sequence 141, App1
44	36	87.8	17	11	US-09-847-946A-142	Sequence 142, App1
45	36	87.8	17	11	US-09-847-946A-146	Sequence 146, App1

ALIGNMENTS

RESULT 1
US-09-847-940B-17
; Sequence 17, Application US/09847940B
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: Sankar
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-17

Query Match 100.0%; Score 41; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6
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Db 1 LDWEML 6

RESULT 2
US-09-847-946A-17
; Sequence 17, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

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APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-17
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Best Local Similarity 100.0%; Pred. No. 7e+05;
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OY 1 LDWEML 6
DB 1 LDWEML 6
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RESULT 3
US-09-847-946A-45
Sequence 45, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-45
```

```
Query Match          100.0%; Score 41; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 LDWEML 6
DB 1 LDWEML 6
```

```
RESULT 4
US-09-847-946A-117
Sequence 117, Application US/09847946A
Publication No. US20030054999A1
```

```
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 117
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-117
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```
Query Match          100.0%; Score 41; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 LDWEML 6
DB 1 LDWEML 6
```

```
RESULT 5
US-09-847-946A-121
Sequence 121, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 121
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-121
```

```
Query Match          100.0%; Score 41; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 LDWEML 6
DB 1 LDWEML 6
```

```
RESULT 6
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US-09-847-946A-114
; Sequence 114, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIORITY FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-114

Query Match 100.0%; Score 41; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWML 6
Db 3 LDWML 8

RESULT 7
US-09-847-946A-122
; Sequence 122, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIORITY FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-122

Query Match 100.0%; Score 41; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWML 6
Db 1 LDWML 6

RESULT 8
US-09-847-946A-113
; Sequence 113, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIORITY FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-113

Query Match 100.0%; Score 41; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWML 6
Db 1 LDWML 6

RESULT 9
US-09-847-946A-116
; Sequence 116, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIORITY FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-116

Query Match 100.0%; Score 41; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6
| | | | |
Db 1 LDWEML 6

RESULT 10

US-09-847-946A-119
; Sequence 119, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-119

Query Match 100.0%; Score 41; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6
| | | | |
Db 3 LDWEML 8

RESULT 11

US-09-847-946A-120
; Sequence 120, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-120

Query Match 100.0%; Score 41; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWEML 6
| | | | |
Db 2 LDWEML 7

RESULT 12

US-09-847-946A-115
; Sequence 115, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 115
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-115

Query Match 100.0%; Score 41; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6
| | | | |
Db 2 LDWEML 7

RESULT 13

US-09-847-946A-118
; Sequence 118, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-118

US-09-847-946A-118

Query Match 100.0%; Score 41; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 3 LDWEWL 8

RESULT 14

US-09-847-946A-112
; Sequence 112, Application US/09847946A
; Publication No. US2003054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Flindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-112

Query Match 100.0%; Score 41; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 3 LDWEWL 8

RESULT 15
US-10-369-493-12414
; Sequence 12414, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfang
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12414
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure

; LOCATION: (1)..(471)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12414

Query Match 95.1%; Score 39; DB 12; Length 471;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 119 LDWEWL 124

Search completed: February 18, 2004, 15:42:01
Job time : 16.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 / Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41

Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	90.2	334	4	US-09-252-991A-22395
2	36	87.8	439	4	US-09-172-952-14
3	36	87.8	745	2	US-08-887-518-3
4	36	87.8	745	2	US-09-023-321-3
5	36	87.8	745	2	US-08-890-853-4
6	36	87.8	745	2	US-09-032-475-3
7	36	87.8	745	2	US-09-099-125A-4
8	36	87.8	745	2	US-09-099-125A-4
9	36	87.8	745	2	US-09-032-476-4
10	36	87.8	745	3	US-08-890-854-4
11	36	87.8	745	3	US-09-023-324-4
12	36	87.8	745	3	US-09-168-629-2
13	36	87.8	745	3	US-08-910-820-10
14	36	87.8	745	3	US-08-910-820-10
15	36	87.8	745	4	US-09-109-986-4
16	36	87.8	745	4	US-09-844-908-10
17	36	87.8	745	4	US-08-868-758-3
18	36	87.8	756	2	US-08-887-518-4
19	36	87.8	756	2	US-09-023-321-4
20	36	87.8	756	2	US-08-890-853-2
21	36	87.8	756	2	US-09-032-475-4
22	36	87.8	756	2	US-09-099-125A-2
23	36	87.8	756	2	US-09-099-124A-2
24	36	87.8	756	3	US-08-890-854-2
25	36	87.8	756	3	US-09-023-324-2
26	36	87.8	756	3	US-09-168-629-15
27	36	87.8	756	3	US-09-168-629-15

28	36	87.8	756	3	US-08-910-820-9	Sequence 9, Appl1
29	36	87.8	756	4	US-09-109-986-2	Sequence 2, Appl1
30	36	87.8	756	4	US-09-844-908-9	Sequence 9, Appl1
31	36	87.8	756	4	US-09-868-758-4	Sequence 4, Appl1
32	36	87.8	997	4	US-09-417-197-123	Sequence 123, App
33	36	87.8	997	4	US-09-417-197-121	Sequence 121, App
34	34	82.9	38	2	US-08-488-161-55	Sequence 55, Appl1
35	34	82.9	38	2	US-09-273-685-55	Sequence 55, Appl1
36	34	82.9	38	5	PCT-US95-11934-55	Sequence 55, Appl1
37	34	82.9	138	1	US-08-686-878A-33	Sequence 33, Appl1
38	34	82.9	138	4	US-09-175-928-33	Sequence 33, Appl1
39	34	82.9	470	4	US-09-107-532A-4517	Sequence 4517, Ap
40	33	80.5	25	3	US-09-082-279B-1275	Sequence 1275, Ap
41	33	80.5	25	4	US-09-315-304B-1275	Sequence 1275, Ap
42	33	80.5	25	4	US-09-834-784-1275	Sequence 1275, Ap
43	33	80.5	162	4	US-09-199-637A-161	Sequence 161, App
44	33	80.5	162	4	US-09-199-637A-162	Sequence 162, App
45	33	80.5	177	4	US-09-252-991A-20614	Sequence 20614, A

ALIGNMENTS

RESULT 1
US-09-252-991A-22395
Sequence 22395, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,768
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22395
LENGTH: 334
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22395

Query Match 90.2% Score 37; DB 4; Length 334;
Best Local Similarity 83.3% Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 136 LDWKWL 141

RESULT 2
US-09-172-952-14
Sequence 14, Application US/09172952
Patent No. 6368793
GENERAL INFORMATION:
APPLICANT: Hoch, James
TITLE OF INVENTION: METABOLIC SELECTION METHODS
FILE REFERENCE: 234/191
CURRENT APPLICATION NUMBER: US/09/172,952
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 439
TYPE: PRT
ORGANISM: Y14X2
US-09-172-952-14

Query Match 87.8%; Score 36; DB 4; Length 439;
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWML 6
 DB 171 LDWML 176

RESULT 3

US-08-887-518-3
 ; Sequence 3, Application US/08887518
 ; Patent No. 5843721
 ; GENERAL INFORMATION:
 ; APPLICANT: Roche, Mike
 ; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/887,518
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSMAN, RICHARD A
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: T97-008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 745 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-887-518-3

Query Match 87.8%; Score 36; DB 2; Length 745;
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWML 6
 DB 738 LDWML 743

RESULT 4
 US-09-023-321-3
 ; Sequence 3, Application US/09023321
 ; Patent No. 5844073
 ; GENERAL INFORMATION:
 ; APPLICANT: Roche, Mike
 ; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA

COUNTRY: USA
 ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,321
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/887,518
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSMAN, RICHARD A
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: T97-008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 745 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-023-321-3

Query Match 87.8%; Score 36; DB 2; Length 745;
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWML 6
 DB 738 LDWML 743

RESULT 5
 US-08-890-853-4
 ; Sequence 4, Application US/08890853
 ; Patent No. 5851812
 ; GENERAL INFORMATION:
 ; APPLICANT: Goedel, David V.
 ; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/890,853
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSMAN, RICHARD A
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: T97-006-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMEWL 6
DB 738 LDMSWL 743

RESULT 6
US-09-032-475-3
Sequence 3, Application US/09032475
Patent No. 5854003

GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032.475
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMEWL 6
DB 738 LDMSWL 743

RESULT 7
US-09-099-125A-4
Sequence 4, Application US/09099125A
Patent No. 5916760

GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099.125A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMEWL 6
DB 738 LDMSWL 743

RESULT 8
US-09-099-124A-4
Sequence 4, Application US/09099124A
Patent No. 5939302

GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099.124A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-124A-4

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWMTL 6
DB 738 LDWMTL 743

RESULT 9
US-09-032-476-4
Sequence 4, Application US/09032476
Patent No. 6235492
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaoan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-476-4

Query Match 87.8%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWMTL 6
DB 738 LDWMTL 743

RESULT 10
US-08-890-854-4
Sequence 4, Application US/08890854
Patent No. 6235512
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaoan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-854-4

Query Match 87.8%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWMTL 6
DB 738 LDWMTL 743

RESULT 11
US-09-023-324-4
Sequence 4, Application US/09023324
Patent No. 6235513
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaoan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 87.8%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWMTL 6
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DB 738 LDWMTL 743

RESULT 12
US-09-168-629-2
; Sequence 2, Application US/09168629
; Patent No. 6242253
; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: Didonato, Joseph A.
; APPLICANT: Rothwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
; FILE REFERENCE: P-UD 1395
; CURRENT APPLICATION NUMBER: US/09/168,629
; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,470
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-168-629-2

Query Match 87.8%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWMTL 6
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DB 738 LDWMTL 743

RESULT 13
US-08-910-820-10
; Sequence 10, Application US/08910820
; Patent No. 6258579
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; APPLICANT: Zhu, Hengyi
; APPLICANT: Barbosa, Miguel
; APPLICANT: Li, Gian
; APPLICANT: Murray, Brian W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-910-820-10

Query Match 87.8%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWMTL 6
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DB 738 LDWMTL 743

RESULT 14
US-08-810-131A-2
; Sequence 2, Application US/08810131A
; Patent No. 6268194
; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: Didonato, Joseph A.
; APPLICANT: Rothwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using
; TITLE OF INVENTION: Same
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California

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; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,131A
; FILING DATE: 25-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-810-131A-2

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Query Match      87.8%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 LDMEWL 6
DB      738 LDMSWL 743

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RESULT 15
US-09-109-986-4
; Sequence 4, Application US/09109986
; Patent No. 6479266
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Cao, Zhaden
; APPLICANT: R. gnter, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,986
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: 197-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-109-986-4

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Query Match      87.8%; Score 36; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 LDMEWL 6
DB      738 LDMSWL 743

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Search completed: February 18, 2004, 14:41:51
Job time : 7.06579 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignment)
79.423 Million cell updates/sec

Title: US-09-643-260-16

Perfect score: 40

Sequence: 1 LDWML 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	37	92.5	745	1 IKKA_MOUSE	O0680 m inhibitor
3	37	92.5	756	1 IKKB_HUMAN	O14820 homo sapien
4	37	92.5	757	1 IKKB_MOUSE	O08351 mus musculu
5	37	92.5	757	1 IKKB_RAT	O09378 rattus norv
6	36	90.0	524	1 CP72_CATRO	O05047 cattharantlu
7	36	90.0	656	1 VEXE_SALTI	P43112 salmonelela
8	36	90.0	840	1 VPHI_YEAST	P32563 saccharomyc
9	35	87.5	290	1 CYOA_BUCAR	O08393 buchiera ap
10	35	87.5	296	1 CYOA_BUCAT	P57544 buchiera ap
11	35	87.5	307	1 OOX2_ACEAC	P50653 acetobacter
12	35	87.5	314	1 CYOA_PEEPU	O9wrt1 pseudomonas
13	34	85.0	99	1 NOS3_SHEEP	P79209 ovls arles
14	34	85.0	262	1 LY4A_MOUSE	O06051 mus musculu
15	34	85.0	263	1 KLR4_MOUSE	O06051 mus musculu
16	34	85.0	914	1 GUX2_CLOSR	P50300 clostridium
17	34	85.0	1167	1 ITAE_MOUSE	O60677 mus musculu
18	34	85.0	1201	1 NOS3_MOUSE	P70313 mus musculu
19	34	85.0	1202	1 NOS3_HUMAN	P29474 homo sapien
20	34	85.0	1204	1 NOS3_BOVIN	P29474 homo sapien
21	34	85.0	1204	1 NOS3_PIG	O28869 sus scrofa
22	33	82.5	220	1 Y132_METUA	O57596 methanococ
23	33	82.5	300	1 Y223_HAEIN	P44579 haemophilus
24	33	82.5	362	1 DCUP_YEAST	P32547 saccharomyc
25	33	82.5	411	1 CYB_CHRVI	O31215 chromatiu
26	33	82.5	480	1 MTH6_DROME	O9va77 drosophila
27	33	82.5	501	1 YB06_YEAST	P38081 saccharomyc
28	33	82.5	578	1 YC20_METUA	O58617 methanococ
29	33	82.5	583	1 EPA3_CHICK	P29318 gallus gall
30	33	82.5	583	1 EPA3_HUMAN	P29320 homo sapien
31	33	82.5	583	1 EPA3_MOUSE	P29319 mus musculu
32	33	82.5	584	1 EPA3_RAT	O08680 rattus norv
33	33	82.5	1002	1 EPB5_CHICK	O07497 gallus gall

34	33	82.5	1039	1 GUNB_CALSA	P10474 c endogluc
35	32	80.0	83	1 VG41_BPML5	O05252 mycobacteri
36	32	80.0	94	1 VG41_BPM02	O64213 mycobacteri
37	32	80.0	269	1 BAS1_HUMAN	P35613 h basigin p
38	32	80.0	315	1 T2S1_STRAL	O53608 streptomyce
39	32	80.0	336	1 NOSO_BACSU	O34453 bacillus su
40	32	80.0	339	1 RRA1_ECOLI	P27128 escherichia
41	32	80.0	343	1 ZDH4_MOUSE	O9d6h5 mus musculu
42	32	80.0	344	1 ZDH4_HUMAN	O9np98 homo sapien
43	32	80.0	366	1 GCST_SYNEI	O8d4v6 synchococc
44	32	80.0	380	1 APV_MACMU	O97666 macaca mula
45	32	80.0	387	1 MANA_RHIME	P29954 rhizobium m

ALIGNMENTS

RESULT 1
IKKA_HUMAN STANDARD; PRT; 745 AA.
ID IKKA_HUMAN 015111, O14666; Q13132; Q92467;
AC 015111, O14666; Q13132; Q92467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
DE (I-kappa-B kinase alpha) (IKBA) (IKK-alpha) (IKK-A) (Ikkapab kinase)
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIXA).
GN CHUK OR IKKA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=FROM N.A., AND MUTAGENESIS OF LYS-44.
RC TISSUE=T-cell.
RX MEDLINE=97386461; PubMed=9244310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Roche M.,
RT "Identification and characterization of an Ikappab kinase.";
RL Cell 90:373-383(1997).
RN [2]
RP TISSUE=FROM N.A., AND PARTIAL SEQUENCE.
RC MEDLINE=97394468; PubMed=9252186;
RX D'Donato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.,
RT "A cytokine-responsive Ikappab kinase that activates the transcription
RL Nature 388:548-554(1997).
RN [3]
RP TISSUE=FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
RC SER-176.
RX TISSUE=Cervical carcinoma;
RA MEDLINE=97394468; PubMed=9252186;
RX Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.,
RT "IKK-1 and IKK-2: cytokine-activated Ikappab kinases essential for
RL NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [4]
RP TISSUE=Heart;
RC MEDLINE=99032998; PubMed=9813230;
RX Hu M.C.-T., Wang Y.-P.,
RT "Ikappab kinase-alpha and -beta genes are coexpressed in adult and
RL embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40(1998).
RN [5]
RP TISSUE=OP 32-745 FROM N.A.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=96258427; PubMed=8777433;
RA Connelly M.A., Marcu K.B.,
RT "CHUK, a new member of the helix-loop-helix and leucine zipper
RL families of interacting proteins, contains a serine-threonine kinase
RL catalytic domain.";

RL Cell. Mol. Biol. Res. 41:537-549(1995).
 RN [6]
 RP PHOSPHORYLATION BY MAP3K4/NIK, AND MUTAGENESIS OF SER-176; THR-179
 RP AND SER-180.
 RX MEDLINE=98188283; PubMed=9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
 Ser-176.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 RN [7]
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RX MEDLINE=99433720; PubMed=10485710;
 RA Ozes O.N., Mayo L.D., Guetin J.A., Pfeffer S.R., Pfeffer L.M.,
 RA Donner D.B.;
 RT "NF-kappaB activation by tumor necrosis factor requires the Akt
 serine-threonine kinase.";
 RL Nature 401:82-85(1999).
 RN [8]
 RP IKKA-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 IkappaB subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [9]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [10]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 RN [11]
 RP SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKKB AND IKBK.
 RX MEDLINE=21968797; PubMed=11971985;
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 RA O'Malley B.W.;
 RT "Regulation of SRC-3 (pCt/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
 activity by I kappa B kinase.";
 RL Mol. Cell. Biol. 22:3549-3561(2002).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 the dissociation of the inhibitor/NF-kappa-B complex and
 ultimately the degradation of the inhibitor. Also phosphorylates
 NCOA3.
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated
 when dephosphorylated.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 also bind to MAP3K14/NIK, MEKK1, IKAP and IKK-alpha-p65-p50
 complex. A weak interaction with TRAF2 cannot be excluded. Part of
 a complex composed of NCOA2, NCOA3, IKKB, IKBK and CREBBP.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
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 or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AF012890; AAC51662.1; -
 DR EMBL; AF009225; AAC51671.1; -
 DR EMBL; AF080157; AAD08996.1; -
 DR EMBL; U22512; AAC50713.1; -
 DR HSRP; Q63450; 1A06.
 DR Genew; HGNC:1974; CHUK.
 DR MIM; 600664; -
 DR GO; GO:0005737; Cytoplasm; TAS.
 DR GO; GO:0008384; FikappaB kinase activity; TAS.
 DR GO; GO:0007345; Ptenryogenesis and morphogenesis; TAS.
 DR GO; GO:0007252; P-I-kappaB phosphorylation; TAS.
 DR GO; GO:0006935; P-immune response; TAS.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR01245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR Prodom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR Trasnferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 302
 FT DOMAIN 455 476
 FT DOMAIN 738 743
 FT NP BIND 21 29
 FT BINDING 44 44
 FT ACT SITE 144 144
 FT MOD RES 23 23
 FT MOD RES 176 176
 FT MUTAGEN 23 23
 FT FT
 FT MUTAGEN 44 44
 FT MUTAGEN 44 44
 FT MUTAGEN 176 176
 FT MUTAGEN 176 176
 FT MUTAGEN 179 179
 FT MUTAGEN 180 180
 FT CONFLICT 543 543
 FT CONFLICT 604 604
 FT CONFLICT 679 680
 FT CONFLICT 684 684
 FT CONFLICT 686 687
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
 Query Match 92.5%; Score 37; DB 1; Length 745;
 Best Local Similarity 83.3%; Pred. No. 76;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LDMAML 6
 Db 738 LDMAML 743
 RESULT 2
 IKKA MOUSE STANDARD; PRT; 745 AA.
 AC Q60680; Q9D2X3; 1
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
 DE (I-kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkkappaB kinase)
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
 kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKIKK).
 GN CHUK OR IKKA.
 OS MUS MUSCULUS (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 NX NCBI_TaxId=10090;

RN [1]
 RC SEQUENCE FROM N.A. (ISOFORM 1).
 RX STRAIN=BAJB/C;
 RA MEDLINE=9604444; Pubmed=7558004;
 RT Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RL "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 10 and mouse chromosome 19.";
 RM Genomics 27:348-351(1995).
 RN [2]
 RC SEQUENCE FROM N.A. (ISOFORM 1).
 RX STRAIN=BAJB/C;
 RA MEDLINE=96258427; Pubmed=8777433;
 RT Connolly M.A., Marcu K.B.;
 RL "CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase catalytic domain.";
 RM Cell. Mol. Biol. Res. 41:537-549(1996).
 RN [3]
 RC SEQUENCE FROM N.A. (ISOFORM 3).
 RX STRAIN=C57BL/6J; TISSUE=Colon;
 RA MEDLINE=21085650; Pubmed=11217851;
 RT Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamazaki I., Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Giesl C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schirml L.M., Staudl R., Suzuki R., Tomita M., Wagner L., Maehiro T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barash G., Blake J., Boffelli D., Bojunga N., Carrinetti P., de Bonaldo M.F., Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M., Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilmberg L., Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y.;
 RL "Functional annotation of a full-length mouse cDNA collection.";
 RM Nature 409:685-690(2001).
 RN [4]
 RC ALTERNATIVE SPLICING.
 RX MEDLINE=20198447; Pubmed=10733566;
 RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R., Gelezianus R., Marcu K.B.;
 RL "Functional isoforms of Ikappab kinase alpha (IKKalpha) lacking leucine zipper and helix-loop-helix domains reveal that IKKalpha and IKKbeta have different activation requirements.";
 RM Mol. Cell. Biol. 20:2635-2649(2000).
 RN [5]
 RC PHOSPHORYLATION BY MAP3K14/NIK.
 RX MEDLINE=98188238; Pubmed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishimura S., Mihara M., Yagita H., Okumura K.;
 RL "Differential regulation of Ikappab kinase alpha and beta by two upstream kinases, NF-kappaB-inducing kinase and mitogen-activated protein kinase/ERK kinase kinase-1.";
 RM Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RC IKK-1/KKB BINDING.
 RX MEDLINE=99212141; Pubmed=1015894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RL "Positive and negative regulation of Ikappab kinase activity through IKKbeta subunit phosphorylation.";
 RM Science 284:309-313(1999).
 RN [7]
 RC IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; Pubmed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RL "Coordinate regulation of Ikappab kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RM Mol. Cell. Biol. 18:7336-7343(1998).

RN [8]
 RC REVIEW.
 RX MEDLINE=20178139; Pubmed=10712233;
 RA Jobin C., Sartor R.B.;
 RL "The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
 RM Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates NCOA3.
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated when dephosphorylated.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but also as an homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-P65-P50 complex. A weak interaction with TRAF2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKK, IKK-gamma (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1:
 CC IsoId=Q60680-1; Sequence=Displayed;
 CC Name=2; Synonyms=Delta LH;
 CC IsoId=Q60680-2; Sequence=VSP_004866; VSP_004867;
 CC Name=3; Synonyms=Delta H;
 CC IsoId=Q60680-3; Sequence=VSP_004868; VSP_004869;
 CC Tissue Specificity: Ubiquitous only for isoform 1, isoforms 2 and 3 are expressed predominantly in brain and T-lymphocytes.
 CC -1- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by E11, E15 and E17 days. In the limb development, its expression predominates in the limb buds at E12.5 day.
 CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by MEK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: U12473; AAC52589.1; -
 CC EMBL: AK018671; BAB31335.1; -
 CC PIR: I49101; I49101.
 CC HSP: G63450; I406.
 CC MGI: MGI:99484; Chuk.
 CC InterPro: IPR000719; Prot kinase.
 CC InterPro: IPR002290; Ser Thr kinase.
 CC InterPro: IPR001245; Tyr-kinase.
 CC Pfam: PF00069; pkinase; 1.
 CC PRINTS: PR00109; TYRKINASE.
 CC PRODOM: PD000001; Prot kinase; 1.
 CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE: PS00108; PROTEIN KINASE ST; 1.
 CC PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC Phosphorylation; Alternative splicing.
 CC DOMAIN 15 300
 CC DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 CC DOMAIN 738 743 NEMO-BINDING.
 CC NP BIND 21 29 ATP (BY SIMILARITY).
 CC BINDING 44 44 ATP (BY SIMILARITY).
 CC ACT_SITE 144 144 BY SIMILARITY.
 CC MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1) (BY SIMILARITY).
 CC MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14) (BY SIMILARITY).

DR HSP; 063450; 1A06.
 DR Genew; HGNC:5960; IKKB.
 DR MIM; 603258; --
 DR GO; GO:0005737; C:cytoplasm; NAS.
 DR GO; GO:0005524; F:ATP binding activity; NAS.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
 DR GO; GO:0016563; F:transcriptional activator activity; NAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00240; ubiquitin; 1.
 DR Prodom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KM Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION.
 FT MOD_RES 181 181 PHOSPHORYLATION.
 FT MOD_RES 44 44 K-2A: LOSS OF KINASE ACTIVITY AND NO EFFECT ON BINDING TO NIK.
 FT MUTAGEN 177 177 S-2A: DECREASE OF ACTIVITY.
 FT MUTAGEN 177 177 S-2E: FULL ACTIVATION.
 FT MUTAGEN 181 181 S-2A: DECREASE OF ACTIVITY.
 FT MUTAGEN 181 181 S-2E: FULL ACTIVATION.
 FT COMPACT 231 255 WHSKRQSEVDIVSDINGLYWF -> CVRMMPGVVHNS
 FT COMPACT 231 255 CNSTLGGGRGMI (IN REF. 5).
 FT CONFLICT 425 425 Q -> H (IN REF. 1).
 SQ SEQUENCE 756 AA; 86563 MM; P9CADF671A3B3E14E CRC64;

Query Match 92.5%; Score 37; DB 1; Length 756;
 Best Local Similarity 83.3%; Pred. No. 77;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAWL 6
 Db 737 LDMSWL 742

RESULT 4
 IKKB_MOUSE
 ID IKKB_MOUSE STANDARD; PRT; 757 AA.
 AC 088351; Q9RJ6; --
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleota; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RX MEDLINE=9818828; PubMed=9520401;
 RA Okumura K.; Shindo M.; Sakon S.; Nishinaka S.; Mihara M.; Yagita H.;
 RA "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Hu M.C.-T.; Wang Y.-P.; Mikhail A.; Qiu W.R.;
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
 RT constitutively phosphorylates serine residues of Ikb.";
 RL Submitted (Aug-1998) to the EMBL/Genbank/DDJ databases.
 RN [3]
 RX DEVELOPMENTAL STAGE.
 RX MEDLINE=94455228; PubMed=10523628;
 RA Hu M.C.-T.; Wang Y.-P.; Qiu W.R.; Mikhail A.; Meyer C.F.; Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RN IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S.; DiDonato J.A.; Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [5]
 RN REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C.; Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEK1, MAPK14/NIK, IKAP and IKB-ALPHA-P65-P50
 CC complex. Phosphorylated IKB-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
 CC and CREBBP (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
 CC -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
 CC the mouse embryo, at E9.5 day its expression begins to be
 CC localized to the brain, neural ganglia, neural tube, and in liver
 CC at E12.5 day. At E15.5 day, the expression is further restricted
 CC to specific tissues of the embryo.
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAPK14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC or send an email to license@sib-ch).
 CC -----
 DR EMBL; AF026524; AAC23557.1; --
 DR EMBL; AF088910; AAD52095.1; --
 DR HSP; 063450; 1A06.
 DR MGD; MGI:1338071; IKKb.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINIS; PR00109; TYRKINASE.
 DR Prodom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KM Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.

FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 757 TLDMSWTQMEDERCSLEQACD -> VTA (IN REF. 2).
 SQ SEQUENCE 757 AA; 86690 MW; PED962F095449C5E CRC64;
 Query Match 92.5%; Score 37; DB 1; Length 757;
 Best Local Similarity 83.3%; Pred. No. 77;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LDMAML 6
 Db 737 LDMAML 742
 RESULT 5
 ID IKKB_RAT STANDARD; PRT; 757 AA.
 AC 09QY78;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN NM_011911;
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IKK beta in megakaryocyte differentiation";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RX IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein
 RT kinase Kinase Kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection".
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50
 CC complex. Phosphorylated IKB-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
 CC and CREBBP (by similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; AF15282; AAF21978.1; -.
 DR HSSP; Q63450; 1A06.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KM Transferase; Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 757 AA; 86866 MW; 3AFB6A7DF91F9C CRC64;
 Query Match 92.5%; Score 37; DB 1; Length 757;
 Best Local Similarity 83.3%; Pred. No. 77;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LDMAML 6
 Db 737 LDMAML 742
 RESULT 6
 ID CP72_CATRO STANDARD; PRT; 524 AA.
 AC 005047;
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome P450 72A1 (EC 1.3.3.9) (CYP7A1) (Secoiooganin synthase)
 DE (SL5).
 GN CYP72A1 OR CYP72 OR P450CR3.
 OS Cathartacus roseus (Roosevelt's hawk) (Magdascar periwinkle).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Lamiales; Gentianales; Apocynaceae; Rauvolfiaceae; Vincet;
 OC Cathartanthus.
 OX NCBI_TaxID=4058;
 RN NM_011911;
 RP SEQUENCE FROM N.A.
 RA Vetter H.-P., Mangold U., Schroeder G., Warner F.-J.,
 RA Werck-Reichardt D., Schroeder U.;
 RT "Molecular analysis and heterologous expression of an inducible
 RT cytochrome P-450 protein from periwinkle (Cathartanthus roseus L.).";
 RL Plant Physiol. 100:998-1007(1992).
 RN [2]
 SQ SEQUENCE OF 469-524 FROM N.A.

RC STRAIN=cv. G. Don;
 RX MEDLINE=93283641; PubMed=8507838;
 RA Medjfer A.H., Souer E., Verpoorte R., Hoge J.H.C.;
 RT "Isolation of cytochrome P-450 cDNA clones from the higher plant
 Catharanthus roseus by a PCR strategy.";
 RL Plant Mol. Biol. 22:379-383(1993).
 RN [1]
 RP FUNCTION.
 RC STRAIN=cv. CPA,
 RX MEDLINE=20575722; PubMed=11135113;
 RA Imler S., Schroeder G., St-Pierre B., Crouch N.P., Hotze M.,
 RA Schmidt J., Strack D., Matern U., Schroeder J.;
 RT "Indole alkaloid biosynthesis in Catharanthus roseus: new enzyme
 RT activities and identification of cytochrome P450 CYP72A1 as
 RT secologanin synthase.";
 RL Plant J. 24:797-804(2000).
 CC -1- FUNCTION: Converts loganin into secologanin.
 CC -1- CATALYTIC ACTIVITY: Loganin + NADPH + O(2) = secologanin + NADP(+) + 2 H(2)O.
 CC -1- PATHWAY: Indole alkaloids biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Vacuolar membrane (Probable).
 CC -1- TISSUE SPECIFICITY: Upper and lower leaf epidermis.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 CC -----
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 CC -----
 DR EMBL: L10081; AAA33106.1; -;
 DR EMBL: X69775; CA649430.1; -;
 DR PIR: S35168; S35168.
 DR HSSP: P14779; IJPZ.
 DR InterPro: IPR001128; Cytochrome_P450.
 DR Pfam: PF00067; P450.1.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 KW Oxidoreductase; Monooxygenase; Electron transport; Transmembrane;
 KW NADP; Heme; Alkaloid metabolism.
 FT TRANSMEM 12
 FT METIL 470 470
 FT VARIANT 190 190
 FT VARIANT 194 194
 FT VARIANT 223 223
 FT VARIANT 312 312
 FT VARIANT 318 318
 FT VARIANT 403 403
 FT VARIANT 405 405
 FT VARIANT 411 411
 SQ SEQUENCE 524 AA; 60557 MW; EF5D64E43C751E8 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 524;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OS Salmonella typh.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxId=601;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GI910007;
 RX MEDLINE=93322324; PubMed=8331073;
 RA Hashimoto Y., Li N., Yokoyama H., Ezaki T.;
 RT "Complete nucleotide sequence and molecular characterization of Viab
 RT region encoding Vi antigen in Salmonella typh.";
 RL J. Bacteriol. 175:4456-4465(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typh CT18.";
 RL Nature 413:848-852(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=2531367; PubMed=12644504;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodyanski V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typh strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 CC -1- FUNCTION: MAY BE INVOLVED IN TRANSLOCATION OF THE VI ANTIGEN.
 CC -----
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 CC -----
 DR EMBL: D14156; BAA03200.1; -;
 DR EMBL: AL627283; CAD06771.1; -;
 DR EMBL: AE016848; AA071797.1; -;
 DR PIR: A56975; A56975.
 DR InterPro: IPR001440; TPR.
 KW Polysaccharide transport; Transport; Complete proteome.
 KW Polyaccharide export protein VexE.
 SQ SEQUENCE 656 AA; 73652 MW; 26097P9D6F51CED CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 656;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92332542; PubMed=1385813;
 RA Monolion M.F., Proteau D., Preston R.A., Stenbit A., Roberto B.T.,
 RA Hoyt M.A., Preuss D., Mulholland J., Botstein D., Jones E.W.;
 RT "The VP1 gene encodes a 95-kDa integral membrane polypeptide
 RT required for in vivo assembly and activity of the yeast vacuolar
 RT H(+)-ATPase.";
 RL J. Biol. Chem. 267:14294-14303 (1992).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93147685; PubMed=1491220;
 RA Monolion M.F., Proteau D., Jones E.W.;
 RT "Evidence for a conserved 95-120 kDa subunit associated with and
 RT essential for activity of V-ATPases.";
 RL J. Exp. Biol. 172:105-112 (1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=S288C;
 RX MEDLINE=97051594; PubMed=8896271;
 RA Cheret G., Bernardi A., Sor F.J.;
 RT "DNA sequence analysis of the VP1-SNF2 region on chromosome XV of
 RT Saccharomyces cerevisiae.";
 RL Yeast 12:1059-1064 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN=S288C / FY1679;
 RX MEDLINE=97298311; PubMed=9153759;
 RA Polley R., Juntiaux J.C.;
 RT "Sequencing analysis of a 36.8 kb fragment of yeast chromosome XV
 RT reveals 26 open reading frames including Sec63, CDC31, SUG2, GCD1,
 RT RBL2, PNT1, PAC1 and VP1.";
 RL Yeast 13:483-487 (1997).
 CC -1- FUNCTION: REQUIRED FOR ASSEMBLY AND ACTIVITY OF THE VACUOLAR
 CC ATPASE. POTENTIAL ROLE IN DIFFERENTIAL TARGETING AND REGULATION OF
 CC THE ENZYME FOR A SPECIFIC ORGANELLE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.
 CC -1- SIMILARITY: BELONGS TO THE V-ATPASE 116 kDa SUBUNIT FAMILY.
 CC -----
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 CC -----
 DR EMBL; M89778; AAA35211.1; -;
 DR EMBL; X89633; CA6176.1; -;
 DR EMBL; Z75178; CA99494.1; -;
 DR EMBL; Z75179; CA99496.1; -;
 DR PIR; A42970; A42970.
 DR SGD; S0005795; VP1.
 DR GO; GO:0006797; P:polyphosphate metabolism; IMP.
 DR InterPro; IPR002490; V_ATPase_subd16.
 KM Pfam; PF01496; V_ATPase_sub_d_1.
 DR Hydrogen ion transport; Transmembrane; Glycoprotein.
 FT TRANSSEM 1 411
 FT TRANSSEM 412 432
 FT TRANSSEM 433 462
 FT TRANSSEM 463 483
 FT TRANSSEM 484 540
 FT TRANSSEM 541 561
 FT TRANSSEM 562 571
 FT TRANSSEM 572 592
 FT TRANSSEM 593 635
 FT TRANSSEM 636 656
 FT TRANSSEM 657 760
 FT TRANSSEM 761 787
 FT TRANSSEM 788 840
 DOMAIN
 EXTRACELLULAR (POTENTIAL).

FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 840 AA; 95528 MW; 77709A914410CD4D CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 840;
 Best Local Similarity 100.0%; Pred No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDRAW 5
 Db 518 LDRAW 522
 RESULT 9
 ID CYOA_BUCAP STANDARD; PRT; 290 AA.
 AC 08K953;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (BC 1.10.3.-) (Cytochrome O
 DE subunit 2) (Oxidase B0(3) subunit 2) (Cytochrome O ubiquinol oxidase
 DE subunit 2).
 GN CYOA OR BUG5456.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=98794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22084549; PubMed=12089438;
 RA Tamas I., Klason L., Canback B., Naeslund A.K., Eriksson A.-S.,
 RA Werngreen J.J., Sandstrom J.P., Moran N.A., Anderson S.G.E.;
 RT "50 million years of genomic stasis in endosymbiotic bacteria.";
 RL Science 296:2376-2379 (2002).
 CC -1- FUNCTION: Cytochrome O terminal oxidase complex is the component
 CC of the aerobic respiratory chain that predominates when cells are
 CC grown at high aeration (by similarity).
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.
 CC -----
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 CC -----
 DR EMBL; AB014121; AAM6799.1; -;
 DR InterPro; IPR001505; Copper Cua.
 DR InterPro; IPR006333; Cyoa II.
 DR InterPro; IPR002429; Cyt_c_ox_2.
 DR InterPro; IPR000437; Prok_Tlipprot.
 DR Pfam; PF00116; COX2; 1.
 DR PRINTS; PR01166; CYCOXIDASEII.
 DR PRODOM; PD000131; Copper Cua; 1.
 DR TIGRFAMs; TIGR01433; Cyoa.1.
 DR PROSITE; PS00013; PROKAR LIPOPROTEIN; FALSE NEG.
 KM Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
 FT SIGNAL 1 24
 FT SIGNAL 24 24
 FT CHAIN 25 290
 FT LIPID 25 25
 FT LIPID 25 25
 FT LIPID 25 42
 FT TRANSSEM 43 63
 FT TRANSSEM 64 87
 FT TRANSSEM 88 108
 FT TRANSSEM 109 290
 FT TRANSSEM 290 33730 MW; 3D80A02A84732963 CRC64;
 SQ SEQUENCE

Query Match 87.5%; Score 35; DB 1; Length 290;
 Best Local Similarity 83.3%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMWML 6
 DB 134 LDMRWL 139

RESULT 10
 ID_CVOA_BUCAI STANDARD; PRT; 296 AA.
 AC P57344;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase subunit 2).
 GN CVOA OR BU472.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=118099;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. AS.";
 RT Nature 407:81-86(2000).
 CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE GROWN AT HIGH AERATION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.
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 CC -----
 CC EMBL; AF001119; BAB13169.1; -.
 DR HSSP; P18400; 1CYW.
 DR InterPro; IPR001505; Copper_CuA.
 DR InterPro; IPR006333; CyoA_II.
 DR InterPro; IPR002429; Cyt_c_ox_2.
 DR InterPro; IPR000437; Prok_IIPprot.
 DR Pfam; PF00116; COX2; 1.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR TIGRfam; TIGR01433; CyoA; 1.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.
 DR OXidoreductase; Respiratory chain; Electron transport; Transmembrane; Signal; Lipoprotein; Complete proteome.
 KW SIGNAL; Lipoprotein; Complete proteome.
 FT CHAIN 1 15 POTENTIAL.
 FT LIPID 16 236 N-ACYL DIGLYCERIDE POLYPEPTIDE II.
 FT DOMAIN 16 16 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT TRANSMEM 34 54 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 55 78 POTENTIAL.
 FT TRANSMEM 79 99 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 100 296 POTENTIAL.
 FT SEQUENCE 296 AA; 34180 MW; 1AB2BAF0408FFBAC CRC64;
 Query Match 87.5%; Score 35; DB 1; Length 296;

Best Local Similarity 83.3%; Pred. No. 64;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMWML 6
 DB 125 LDMRWL 130

RESULT 11
 ID_COX2_ACCEAC STANDARD; PRT; 307 AA.
 AC P50653;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome A1 subunit 2) (Oxidase BA(3) subunit 2).
 GN CYAB.
 OS Acetobacter aceti.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Acetobacteraceae; Acetobacter.
 OX NCBI_TaxID=435;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=1023;
 RX MEDLINE=9332308; PubMed=8392509;
 RA Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H.,
 RA Kawamura Y., Horinouchi S., Beppu T.;
 RT "Characterization of a cytochrome at that functions as a ubiquinol oxidase in Acetobacter aceti.";
 RT J. Bacteriol. 175:4307-4314(1993).
 CC -1- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
 CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.
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 CC -----
 CC EMBL; D13185; BAA02480.1; -.
 DR PIR; A36885; A36885.
 DR HSSP; P18400; 1CYW.
 DR InterPro; IPR001505; Copper_CuA.
 DR InterPro; IPR006333; CyoA_II.
 DR InterPro; IPR002429; Cyt_c_ox_2.
 DR Pfam; PF00116; COX2; 1.
 DR PRINTS; PR01166; CYCOXIDASRII.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR TIGRfam; TIGR01433; CyoA; 1.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 DR OXidoreductase; Transmembrane; Respiratory chain; Signal; Lipoprotein.
 KW SIGNAL; Lipoprotein.
 FT CHAIN 1 23 POTENTIAL.
 FT LIPID 24 307 N-ACYL DIGLYCERIDE POLYPEPTIDE II.
 FT TRANSMEM 46 66 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT TRANSMEM 87 107 POTENTIAL.
 FT SEQUENCE 307 AA; 33921 MW; E66734B84410996D CRC64;
 Query Match 87.5%; Score 35; DB 1; Length 307;
 Best Local Similarity 83.3%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 12
CYOA_PSEPU          STANDARD;      PRT;      314 AA.
ID_OYMWRI;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
DE subunit 2).
GN CYOA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxId=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IH-2000; PubMed=9868765;
RA Hiraizawa H., Takami H., Inoue A., Horikoshi K.;
RT "Isolation and characterization of toluene-sensitive mutants from
RT Pseudomonas putida IH-2000."
RL FEMS Microbiol. Lett. 169:219-225 (1998).
CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
CC GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
-----
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-----
DR EMBL; AB016787; BAA76356.1; -.
DR HSSP; P18400; ICW.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyOA_II.
DR InterPro; IPR002429; Cyt_cox_2.
DR Pfam; PF00116; COX2; 1.
DR PRODOM; PD000131; Copper_CuA; 1.
DR TIGRPMAS; TIGR01433; CyOA; 1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
KW Inner membrane; Signal; Lipoprotein.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 1 314 UBIQUINOL OXIDASE POLYPEPTIDE II.
FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
FT DOMAIN 24 42 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 43 63 POTENTIAL.
FT DOMAIN 64 86 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 87 107 PERIPLASMIC (POTENTIAL).
FT DOMAIN 108 314 PERIPLASMIC (POTENTIAL).
SQ SEQUENCE 314 AA; 34702 MW; 965E04FC3AA77F07 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 314;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

AC P79209;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
DE II) (NOSII) (Endothelial NOS) (eNOS) (constitutive NOS) (cNOS)
DE (Fragment).
GN NOS3 OR ENOS.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxId=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RA Aguan K., Weiner C.P.;
RT "Effect of hypoxia on the microvasculature of developing fetal
RT brain of sheep: a studies on the expression pattern of
RT constitutive forms of nitric oxide synthase."
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN
CC VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A cGMP-MEDIATED SIGNAL
CC TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH
CC FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND
CC PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
CC nitric oxide + N NADP(+).
CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF PAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME (BY SIMILARITY).
CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY
CC SIMILARITY).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; U76738; AAB40705.1; -.
DR HSSP; P29473; IDOC.
DR InterPro; IPR004030; NO synthase.
DR Pfam; PF02898; NO synthase; 1.
DR PROSITE; PS60001; NOS; PARTIAL.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding;
KW Heme; Multigene family.
FT NON TER 1 1
FT NON TER 99 99
SQ SEQUENCE 99 AA; 11034 MW; 82C3C765557031DA CRC64;

Query Match 85.0%; Score 34; DB 1; Length 99;
Best Local Similarity 80.0%; Pred. No. 33;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 LDWAML 6
DB 133 LDWAML 138

RESULT 13
NOS3_SHEEP          STANDARD;      PRT;      99 AA.
ID_NOS3_SHEEP

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RESULT 14
LY4A_MOUSE          STANDARD;      PRT;      262 AA.
ID_LY4A_MOUSE
AC P20937;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein YEL/48 (T lymphocyte antigen A1) (LY49-A

```


DE antigen).
GN KLR4 OR LY49A OR LY-49A OR LY49 OR LY-49.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89140367; PubMed=2783949;
RX Chan P.-Y., Takei F.;
RT "Molecular cloning and characterization of a novel murine T cell
RT surface antigen, YEL/48".
RN J. Immunol. 142:1727-1736(1989).
RL [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=89309828; PubMed=2787364;
RX Yokoyama W.M., Jacobs L., Kanagawa O., Shevach E.M., Cohen D.I.;
RT "A murine T lymphocyte antigen belongs to a supergene family of type
RT II integral membrane proteins".
RN J. Immunol. 143:1379-1386(1989).
RL [1]
RP FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR H-2D
CC ALLELES. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
CC CELL LYSIS.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- TISSUE SPECIFICITY: HIGH, IN T LYMPHOMA LINES, VERY LOW IN
CC NORMAL LYMPHOCYTES.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
CC EMBL: M25775; AAA40578.1; ALT_SEQ.
DR EMBL; M25812; AAA37242.1; -.
DR PIR; A30573; A30573.
DR PIR; A45813; A45813.
DR PDB; 1003; 02-JAN-00.
DR MGD; MGI:101907; Klr4l.
DR InterPro; IPR001304; Lectin_C.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;
KW Signal-anchor; Lectin; Receptor; Multigene family; 3D-structure.
FT DOMAIN 1 44
FT TRANSMEM 45 66
FT FT 67 262
FT FT 138 257
FT FT 167 253
FT FT 232 245
FT SITE 137 139
FT CARBOHYD 86 86
FT CARBOHYD 103 103
FT CARBOHYD 123 123
FT CONFLICT 76 78
FT CONFLICT 106 106
FT CONFLICT 166 166
FT CONFLICT 223 223
FT SEQUENCE 262 AA; 30498 MW; 3C3328D265F7185E CRC64;
Query Match 85.0%; Score 34; DB 1; Length 262;
Best Local Similarity 80.0%; Freq. No. 82;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 DNAML 6
|||||

DB 207 DNAMI 211
RESULT 15
KLR4_MOUSE
ID KLR4_MOUSE STANDARD; PRT; 263 AA.
AC Q60651; O78026; Q9EPAS;
DT 01-NOV-1997 (Rel. 35; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Killer cell lectin-like receptor 4 (T-cell surface glycoprotein
DE LY-49D) (LY49-D antigen).
GN KLR4 OR LY49D OR LY-49D OR LY49-D.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM D2).
RA STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=94300068; PubMed=8027540;
RA Smith H.R.C., Karthofer F.M., Yokoyama W.M.;
RT "Ly-49 multigene family expressed by IL-2-activated NK cells".
RN J. Immunol. 153:1068-1079(1994).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RA STRAIN=C57BL/6;
RX MEDLINE=96421544; PubMed=8824161;
RA Silver E.T., Elliott J.P., Kane K.P.;
RT "Alternatively spliced Ly-49D and H transcripts are found in IL-2-
RT immunogenetics 44:478-482(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM D1).
RX STRAIN=MOD. and NOR.
RA MEDLINE=20384764; PubMed=10925254;
RA Silver E.T., Gong D.-E., Chang C.S., Amrani A., Santamaria P.,
RA Kane K.P.;
RT "Ly-49D activates NK-mediated lysis by recognizing H-2Dd".
RN J. Immunol. 165:1771-1781(2000).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR CLASS I MHC.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=D1;
CC IsoId=Q60651-1; Sequence=Displayed;
CC Name=D2;
CC IsoId=Q60651-2; Sequence=VSP 003068;
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
CC EMBL; U10090; AA50218.1; -.
DR EMBL; L78247; AAC32667.1; -.
DR EMBL; AF218079; AAF9592.1; -.
DR EMBL; AF218078; AAF9591.1; -.
DR PIR; I49049; I49049.
DR MGD; MGI:101904; Klr44.
DR InterPro; IPR001304; Lectin_C.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;
KW Signal-anchor; Lectin; Receptor; Multigene family;
KW Alternative splicing; Polymorphism.


```

FT DOMAIN 1 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 65 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT 66 263 (POTENTIAL).
FT DOMAIN 139 258 EXTRACELLULAR (POTENTIAL).
FT DISULFID 168 254 C-TYPE LECTIN (LONG FORM).
FT DISULFID 233 246 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 39 41 Missing (in isoform D2).
FT 5 5 /Ftd=VSP_003068.
FT VARIANT 29 5 E -> K (IN STRAINS NOD AND NOR).
FT VARIANT 32 29 R -> W (IN STRAINS NOD AND NOR).
FT VARIANT 35 32 E -> Q (IN STRAINS NOD AND NOR).
FT VARIANT 45 35 R -> G (IN STRAINS NOD AND NOR).
FT VARIANT 60 45 L -> F (IN STRAINS NOD AND NOR).
FT VARIANT 79 60 T -> I (IN STRAINS NOD AND NOR).
FT VARIANT 132 79 K -> Q (IN STRAINS NOD AND NOR).
FT VARIANT 189 132 Y -> S (IN STRAINS NOD AND NOR).
FT VARIANT 189 189 L -> F (IN STRAINS NOD AND NOR).
SQ SEQUENCE 263 AA; 30872 MM; DDA940A089A9F42D CRC64;

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Query Match 85.0%; Score 34; DB 1; Length 263;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 2 DWAUL 6
DB 208 DWAUL 212

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Search completed: February 18, 2004, 14:28:13
 Job time : 3.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-16

Perfect score: 40

Sequence: 1 LDMAML 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	745	1 I49101	conserved helix-lo
2	36	90.0	215	2 D75215	purine phosphoribo
3	36	90.0	251	2 E70521	probable phosphor
4	36	90.0	304	2 F83632	probable cytochrom
5	36	90.0	316	2 AB2931	hypothetical prote
6	36	90.0	316	2 D98351	dipeptide ABC tran
7	36	90.0	516	2 T10000	cytochrome P450 (C
8	36	90.0	524	2 T09999	cytochrome P450 -
9	36	90.0	524	2 T09944	probable cytochrom
10	36	90.0	656	2 A56975	V1 polysaccharide
11	36	90.0	656	2 A10440	VI polysaccharide
12	36	90.0	840	1 A42970	H+-exporting ATPas
13	36	90.0	1212	2 F83153	probable two-compo
14	36	90.0	1575	2 T18545	lysobactin synthe
15	35	87.5	162	2 C70829	hypothetical prote
16	35	87.5	204	2 C83748	hypothetical prote
17	35	87.5	277	1 UC5900	bo-type ubiquinol
18	35	87.5	296	2 A84985	cytochrome o ubiq
19	35	87.5	299	2 B83243	hypothetical prote
20	35	87.5	307	1 A36885	bo-type ubiquinol
21	35	87.5	318	2 AD0384	cytochrome o ubiq
22	35	87.5	331	2 D83480	cytochrome o ubiq
23	35	87.5	337	2 AG2946	hypothetical prote
24	35	87.5	337	2 C98336	probable integral
25	35	87.5	344	2 AG3489	cytochrome o ubiq
26	35	87.5	353	2 A87469	ubiquinol oxidase
27	35	87.5	386	2 C96006	probable cytochrom
28	35	87.5	394	2 C85064	hypothetical prote
29	35	87.5	418	2 DB5064	hypothetical prote

30	35	87.5	443	2 AE0309	probable sugar tra
31	35	87.5	1139	2 A10379	probable potassium
32	34	85.0	260	2 I49049	Ly-49D-GE antigen
33	34	85.0	262	2 I49361	natural killer cel
34	34	85.0	262	2 A30573	T-cell surface gly
35	34	85.0	262	2 A45813	T-cell surface gly
36	34	85.0	267	2 I56866	LGJ-1 - mouse
37	34	85.0	322	2 A13395	NADH2 dehydrogenas
38	34	85.0	348	2 AE2733	NADH ubiquinone ox
39	34	85.0	348	2 G97514	NADH dehydrogenase
40	34	85.0	395	2 E90438	hypothetical prote
41	34	85.0	395	2 B96610	hypothetical prote
42	34	85.0	616	2 C69226	type I restriction
43	34	85.0	1202	2 S71424	nitric-oxide synth
44	34	85.0	1203	1 A47501	nitric-oxide synth
45	34	85.0	1205	1 A38943	nitric-oxide synth

ALIGNMENTS

RESULT 1

I49101

conserved helix-loop-helix ubiquitons kinase (EC 2.7.1.-) CHUK - mouse

C/Species: Mus musculus (house mouse)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 10-Sep-1999

C/Accession: I49101

R/Mock: B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.

A/Title: CHUK, a conserved helix-loop-helix ubiquitons kinase, maps to human chromosome

A/Reference number: I49101; MID:96044444; PMID:7558004

A/Accession: I49101

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-745 <RES>

A/Cross-references: EMBL:U12473; NID:g1079492; PIDD:AAC52589.1; PID:g1079493

C/Genetics:

A/Gene: CHUK

C/Superfamily: mouse conserved helix-loop-helix ubiquitons kinase; protein kinase homo

F/Keywords: ATP; phosphotransferase

F/13-283/Domain: protein kinase homology <KIN>

Query Match 92.5%; Score 37; DB 1; Length 745;

Best Local Similarity 83.3%; Pred. No. 1; 4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAML 6
Db 738 LDMAML 743

RESULT 2

D75215

purine phosphoribosyltransferase PAB2405 - Pyrococcus abyssi (strain Orsay)

C/Species: Pyrococcus abyssi

C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #ext_change 20-Aug-1999

C/Accession: D75215

R/anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome st:

A/Reference number: A75001

A/Accession: D75215

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-215 <KAM>

A/Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDD:CAM49171.1; PID:el515;

A/Experimental source: strain Orsay

C/Genetics:

A/Gene: gpta; PAB2405

Query Match 90.0%; Score 36; DB 2; Length 215;

Best Local Similarity 66.7%; Pred. No. 57;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

A:Experimental source: cv. cp3
C:Genetics: CYP72C
A:Gene: CYP72C
C:Superfamily: unassigned cytochrome P450; cytochrome P450 homology
C:Keywords: heme; iron; metalloprotein
F:318-481/Domain: cytochrome P450 homology <P45>
F:459/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5
Db 17 LDMAW 21

RESULT 8
T09999
cytochrome P450 - Madagascari periwinkle
C:Species: Catharanthus roseus (Madagascari periwinkle)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
C:Accession: T09999
R:Margold, U.; Bichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-plant Sci. 96, 129-136, 1994
A:Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharanth
A:Reference number: Z16915
A:Accession: T09999
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-524 <MAN>
A:Cross-references: EMBL:L19074; NID:g404687; PID:g404688
A:Experimental source: cv. cp3
C:Genetics:
A:Gene: CYP72B
A:Introns: 96/1; 170/3; 252/2; 381/3
C:Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
C:Keywords: heme; iron; metalloprotein
F:329-492/Domain: cytochrome P450 homology <P45>
F:470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5
Db 28 LDMAW 32

RESULT 9
T09944
probable cytochrome P450 protein - Madagascari periwinkle
N:Alternate names: CYP72 protein
C:Species: Catharanthus roseus (Madagascari periwinkle)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
C:Accession: T09944
R:Vetter, H.P.; Margold, U.; Schroeder, G.; Marner, F.J.; Werck-Reichardt, D.; Schroeder-Plant Physiol. 100, 998-1007, 1992
A:Title: Molecular analysis and heterologous expression of an inducible cytochrome P-450
A:Reference number: Z16902
A:Accession: T09944
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-524 <VERT>
A:Cross-references: EMBL:L10081; NID:g167483; PID:g167484
C:Genetics:
A:Gene: CYP72
C:Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
C:Keywords: heme; iron; metalloprotein
F:329-492/Domain: cytochrome P450 homology <P45>
F:470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5
Db 28 LDMAW 32

RESULT 10
A56975
vi polysaccharide capsule transporter Vexx - Salmonella typhi
C:Species: Salmonella typhi
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 11-Jan-2000
C:Accession: A56975
R:Hashimoto, Y.; Li, N.; Yokoyama, H.; Ezaki, T.
J. Bacteriol. 175, 4456-4465, 1993
A:Title: Complete nucleotide sequence and molecular characterization of viab region en
A:Reference number: A56892; MUID:9332324; PMID:8331073
A:Accession: A56975
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-656 <HAS>
A:Cross-references: GB:D14156; NID:g426443; PID:BAA03200.1; PID:d1003709; PID:g426453
C:Genetics:
A:Gene: vexx
C:Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat
F:284-317/Domain: tetratricopeptide repeat homology <TR>
F:318-351/Domain: tetratricopeptide repeat homology <TR>

Query Match 90.0%; Score 36; DB 2; Length 656;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5
Db 411 LDMAW 415

RESULT 11
AF1040
vi polysaccharide export protein [imported] - Salmonella enterica subsp. enterica sero
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AF1040
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churchel
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF1040
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-556 <PAR>
A:Cross-references: GB:AL513382; PID:CAD06771.1; PID:g16505421; GSPDB:GN00176
C:Genetics:
C:Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat

Query Match 90.0%; Score 36; DB 2; Length 656;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5
Db 411 LDMAW 415

RESULT 12
AA2970

H+-exporting ATPase (EC 3.6.3.6) 95k chain, vacuolar - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: protein O5430c; protein YOR270C
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
 C/Accession: A42970; S67167; S67172; S72041
 R:Monolobon, M.P.; Proteau, D.; Preston, R.A.; Stembic, A.; Roberts, B.T.; Hoyt, M.A.; Pz
 J. Biol. Chem. 267, 14294-14303, 1992
 A:Title: The VP1 gene encodes a 95-kDa integral membrane polypeptide required for in vi
 A/Reference number: A42970; MUID:92332542; PMID:1385813
 A/Accession: A42970
 A:Molecule type: DNA
 A:Residues: 1-840 <MAN>
 A/Cross-references: GB:M89778, NID:g173172; PIDN:AAA35211.1; PID:g173173
 A:Experimental source: strain X2180-1b; vacuolar acidification-defective mutants
 A:Note: sequence extracted from NCBI backbone (NCBIN:108529, NCBI:P.108530)
 R:Jumiaux, J.C.; Polrey, R.
 Submitted to the Protein Sequence Database, July 1996
 A/Reference number: S67143
 A/Accession: S67167
 A:Molecule type: DNA
 A:Residues: 1-840 <JAU>
 A/Cross-references: EMBL:Z75178; NID:g1420605; PIDN:CAA9494.1; PID:g1420606; GSPDB:GN0
 A:Experimental source: strain S288C
 R:Cheret, G.; Sor, F.
 Submitted to the Protein Sequence Database, July 1996
 A/Reference number: S67169
 A/Accession: S67172
 A:Molecule type: DNA
 A:Residues: 1-840 <CHE>
 A/Cross-references: EMBL:Z75178; NID:g1420605; PIDN:CAA9494.1; PID:g1420606; GSPDB:GN0
 A:Experimental source: strain S288C
 R:Cheret, G.; Bernat, A.; Sor, F.
 Yeast 12, 1059-1064, 1996
 A:Title: DNA sequence analysis of the VP1-GNF2 region on chromosome XV of *Saccharomyces*
 A/Reference number: S72039; MUID:97051594; PMID:8896271
 A/Accession: S72041
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-840 <CHM>
 A/Cross-references: EMBL:X89633; NID:g1279694; PIDN:CAA61776.1; PID:g1279697
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
 C:Genetics:
 A:Gene: SGD:VP1, MIPS:YOR270C
 A/Cross-references: MIPS:YOR270C; SGD:S0005796
 A:Map position: 15R
 C:Function:
 A:Description: hydrogen ion transport; hydrolase; required for assembly and activity of
 C:Superfamily: vacuolar ATP synthase 95k chain
 C:Keywords: ATP; glycoprotein; hydrogen ion transport; hydrolase; membrane-associated co
 F/407-441/Domain: transmembrane #status predicted <TM1>
 F/457-478/Domain: transmembrane #status predicted <TM2>
 F/539-558/Domain: transmembrane #status predicted <TM3>
 F/565-591/Domain: transmembrane #status predicted <TM4>
 F/635-656/Domain: transmembrane #status predicted <TM5>
 F/733-795/Domain: transmembrane #status predicted <TM6>

Query Match 90.0%; Score 36; DB 1; Length 840;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDRAW 5
 Db 518 LDRAW 522

RESULT 13

R83153
 Probable two-component sensor PA3946 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C:Species: *Pseudomonas aeruginosa*
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C/Accession: F83153
 R:Stover, C.K.; Pham, X.O.; Eryin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bz
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lhm,

.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pat.
 A/Reference number: A82950; MUID:20437337; PMID:10984043
 A/Accession: F83153
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1212 <STO>
 A/Cross-references: GB:AE004812; GB:AE004091; NID:g9950125; PIDN:AA07333.1; GSPDB:GN0
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA3946
 C:Superfamily: evgs protein; response regulator homology

Query Match 90.0%; Score 36; DB 2; Length 1212;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DWAML 6
 Db 47 DWAML 51

RESULT 14

T18545
 Lysoactin synthetase - *Lysoacter* sp. (ATCC 53042) (fragment)
 C:Species: *Lysoacter* sp.
 A:Variety: ATCC 53042
 C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Dec-2000
 C/Accession: T18545
 R:Bernard, F.
 Submitted to the EMBL Data Library, March 1996
 A:Description: Identification of genes encoding for peptide synthetases from Gram-nega
 A/Reference number: Z18962
 A/Accession: T18545
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-1575 <BER>
 A/Cross-references: EMBL:X96558; NID:e991096; PID:e236566; PIDN:CAA65394.1
 A:Experimental source: ATCC 53042
 C:Superfamily: acyl carrier protein homology; acetate-CoA ligase homology
 C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
 F/468-924/Domain: acetate-CoA ligase homology <AC1>
 F/942-1010/Domain: acyl carrier protein homology <ACP>
 F/974/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 1575;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDRAW 5
 Db 601 LDRAW 605

RESULT 15

C70829
 hypothetical protein RY0471C - *Mycobacterium tuberculosis* (strain H37Rv)
 C:Species: *Mycobacterium tuberculosis*
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
 C/Accession: C70829
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
 Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
 A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genom
 A/Reference number: A70500; MUID:98295987; PMID:9634230
 A/Accession: C70829
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-162 <COL>
 A/Cross-references: GB:AL021933; GB:AL123456; NID:g3261529; PIDN:CAA17426.1; PID:e1252;

A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: RV0471c
C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV0471c

Query Match 87.5%; Score 35; DB 2; Length 162;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDNAML 6
|||
Db 63 LDNRWL 68

Search completed: February 18, 2004, 14:38:52
Job time : 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35,929 Million cell updates/sec

Title: US-09-643-260-16

Perfect score: 40

Sequence: 1 LDMANL 6

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	38	95.0	223	4	US-09-107-532A-5762
2	37	92.5	745	2	US-08-887-518-3
3	37	92.5	745	2	US-09-023-321-3
4	37	92.5	745	2	US-08-890-853-4
5	37	92.5	745	2	US-09-032-475-3
6	37	92.5	745	2	US-09-099-125A-4
7	37	92.5	745	2	US-09-099-125A-4
8	37	92.5	745	3	US-09-032-475-4
9	37	92.5	745	3	US-08-890-854-4
10	37	92.5	745	3	US-09-023-324-4
11	37	92.5	745	3	US-09-168-629-2
12	37	92.5	745	3	US-08-910-820-10
13	37	92.5	745	3	US-08-810-131A-2
14	37	92.5	745	4	US-09-109-986-4
15	37	92.5	745	4	US-09-844-908-10
16	37	92.5	745	4	US-09-868-758-3
17	37	92.5	756	2	US-08-887-518-4
18	37	92.5	756	2	US-09-023-321-4
19	37	92.5	756	2	US-08-890-853-2
20	37	92.5	756	2	US-09-032-475-4
21	37	92.5	756	2	US-09-099-125A-2
22	37	92.5	756	2	US-09-099-125A-2
23	37	92.5	756	3	US-09-032-476-2
24	37	92.5	756	3	US-08-890-854-2
25	37	92.5	756	3	US-09-023-324-2
26	37	92.5	756	3	US-09-168-629-15
27	37	92.5	756	3	US-08-910-820-9

28	37	92.5	756	4	US-09-109-986-2	Sequence 2, Appl1
29	37	92.5	756	4	US-09-844-908-9	Sequence 9, Appl1
30	37	92.5	756	4	US-09-868-758-4	Sequence 4, Appl1
31	37	92.5	996	4	US-09-417-197-123	Sequence 123, App
32	37	92.5	997	4	US-09-417-197-121	Sequence 121, App
33	36	90.0	316	4	US-09-252-991A-17312	Sequence 17312, A
34	36	90.0	1627	4	US-09-252-991A-20395	Sequence 20395, A
35	35	87.5	302	4	US-09-252-991A-21655	Sequence 21655, A
36	35	87.5	334	4	US-09-252-991A-22395	Sequence 22395, A
37	35	87.5	439	4	US-09-172-952-14	Sequence 14, Appl1
38	34	85.0	1205	1	US-07-908-245-2	Sequence 2, Appl1
39	34	85.0	1205	2	US-08-319-866-10	Sequence 10, Appl1
40	34	85.0	1205	3	US-09-123-708-6	Sequence 6, Appl1
41	34	85.0	1205	3	US-09-123-624-6	Sequence 6, Appl1
42	34	85.0	1257	2	US-08-750-152A-2	Sequence 2, Appl1
43	33	82.5	100	1	US-08-241-853-28	Sequence 28, Appl1
44	33	82.5	100	1	US-08-241-853-29	Sequence 28, Appl1
45	33	82.5	100	2	US-08-850-917-28	Sequence 28, Appl1

ALIGNMENTS

RESULT 1
US-09-107-532A-5762
Sequence 5762, Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:
APPLICANT: LYNN A Doucette-Stramm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street
CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC
OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A

PRIOR APPLICATION DATA:
FILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Ariadello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277

TELEFAX: (781)893-5007

INFORMATION FOR SEQ ID NO: 5762:
SEQUENCE CHARACTERISTICS:

LENGTH: 223 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...223

SEQUENCE DESCRIPTION: SEQ ID NO: 5762:

US-09-107-532A-5762

Query Match 95.0%; Score 38; DB 4; Length 223;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
DB 184 LDMAML 189

RESULT 2

US-08-887-518-3
Sequence 3, Application US/08887518
Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
DB 738 LDMAML 743

US-09-023-321-3
Sequence 3, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO

STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
DB 738 LDMAML 743

US-08-890-853-4
Sequence 4, Application US/08890853
Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Moronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
DB 738 LDWAWL 743

RESULT 5
US-09-032-475-3

Sequence 3, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
APPLICANT: Roche, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032.475
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/897,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
DB 738 LDWAWL 743

RESULT 6
US-09-099-125A-4
Sequence 4, Application US/09099125A

Patent No. 5916760
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Moronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
DB 738 LDWAWL 743

RESULT 7
US-09-099-124A-4
Sequence 4, Application US/09099124A
Patent No. 5939302
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Moronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,124A

;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/890,853
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-006-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-099-124A-4

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
|||:|
Db 738 LDMAML 743

RESULT 8

US-09-032-476-4
; Sequence 4, Application US/09032476
; Patent No. 6235492

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Cao, Zhaoan

APPLICANT: R gnier, Catherine

TITLE OF INVENTION: IKK-1 Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/032,476

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/890,854

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-032-476-4

Query Match 92.5%; Score 37; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
|||:|
Db 738 LDMAML 743

RESULT 9

US-08-890-854-4
; Sequence 4, Application US/08890854
; Patent No. 6235512

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Cao, Zhaoan

APPLICANT: R gnier, Catherine

TITLE OF INVENTION: IKK-1 Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/890,854

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-890-854-4

Query Match 92.5%; Score 37; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 10

US-09-023-324-4
; Sequence 4, Application US/09023324
; Patent No. 6235513

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Cao, Zhaoan

APPLICANT: R gnier, Catherine

TITLE OF INVENTION: IKK-1 Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 92.5%; Score 37; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
DB 738 LDMAML 743

RESULT 11
US-09-168-629-2
Sequence 2, Application US/09168629
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: Didonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 745
TYPE: PRT
ORGANISM: Homo sapiens
US-09-168-629-2

Query Match 92.5%; Score 37; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
DB 738 LDMAML 743

DB 738 LDMAML 743

RESULT 12
US-08-910-820-10
Sequence 10, Application US/08910820
Patent No. 6258579
GENERAL INFORMATION:
APPLICANT: Mercutio, Frank
APPLICANT: Zhu, Henry
APPLICANT: Barbosa, Miguel
APPLICANT: Li, Gan
APPLICANT: Murray, Brian W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-910-820-10

Query Match 92.5%; Score 37; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
DB 738 LDMAML 743

RESULT 13
US-08-810-131A-2
Sequence 2, Application US/08810131A
Patent No. 6268194
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: Didonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using
TITLE OF INVENTION: Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego

STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,131A
FILING DATE: 25-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-131A-2

Query Match 92.5%; Score 37; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWAML 6
Db 738 LDWAML 743

RESULT 14
US-09-109-986-4
Sequence 4, Application US/09109986
Patent No. 6479266
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaoen
APPLICANT: R. gntier, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,986
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/990,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-109-986-4

Query Match 92.5%; Score 37; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWAML 6
Db 738 LDWAML 743

RESULT 15
US-09-844-908-10
Sequence 10, Application US/09844908
Patent No. 6576437
GENERAL INFORMATION:
APPLICANT: Mercutio, Frank
APPLICANT: Zhu, Hengyi
APPLICANT: Barboza, Miguel
APPLICANT: Li, Gian
APPLICANT: Murray, Brian W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
COMPLEX AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/844,908
FILING DATE: 27-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-844-908-10

Query Match 92.5%; Score 37; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWAML 6
Db 738 LDWAML 743

Search completed: February 18, 2004, 14:41:51
Job time : 7.06579 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds

(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-15

Perfect score: 36

Sequence: 1 LDMSYL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	94.4	98	1	YDAS_ECOLI
2	33	91.7	330	1	YETK_BACSU
3	32	88.9	265	1	PADI_SCHPO
4	32	88.9	445	1	KAB_BACTI
5	32	88.9	476	1	CLG_CLOPE
6	32	88.9	517	1	SEST_CABEL
7	32	88.9	707	1	ORCI_SCHPO
8	32	88.9	734	1	GYSL_RABIT
9	32	88.9	737	1	GYSL_HUMAN
10	32	88.9	737	1	GYSL_HUMAN
11	32	88.9	737	1	GYSL_HUMAN
12	32	88.9	738	1	GYSL_MOUSE
13	32	88.9	2245	1	MYSL_DICDI
14	31	86.1	223	1	BM49_CABEL
15	31	86.1	385	1	O46A_DROME
16	31	86.1	506	1	POFB_SCHPO
17	31	86.1	703	1	GYSL_HUMAN
18	31	86.1	703	1	GYSL_HUMAN
19	31	86.1	745	1	IKKA_HUMAN
20	31	86.1	745	1	IKKA_MOUSE
21	31	86.1	755	1	IKKB_HUMAN
22	31	86.1	757	1	IKKB_MOUSE
23	31	86.1	757	1	IKKB_HUMAN
24	31	86.1	758	1	IKKB_MOUSE
25	31	86.1	758	1	IKKB_HUMAN
26	31	86.1	758	1	IKKB_MOUSE
27	31	86.1	1161	1	CVGC_DROME
28	30	83.3	97	1	PIXX_RHISN
29	30	83.3	121	1	YCF2_VICPA
30	30	83.3	266	1	UPK_FUSNN
31	30	83.3	364	1	KITH_ILTVT
32	30	83.3	366	1	ALP_NEUCR
33	30	83.3	417	1	CPB2_HUMAN

34	30	83.3	419	1	CBPA_BOVIN	P00730	bos taurus
35	30	83.3	446	1	PIV2_ADE40	P48752	human adeno
36	30	83.3	452	1	PIV2_ADE12	P12540	human adeno
37	30	83.3	482	1	AR12_CABEL	Q22431	caenorhabdl
38	30	83.3	492	1	AR12_MOUSE	Q92166	mus musculu
39	30	83.3	493	1	AR12_HUMAN	Q95376	homo sapien
40	30	83.3	509	1	AR12_DROME	O76924	drosophila
41	30	83.3	528	1	YCT9_MYCTU	Q11038	mycobacteri
42	30	83.3	675	1	CPAA_BACTJ	O87906	bacillus th
43	30	83.3	691	1	TOKI_YEAST	P40310	saccharomyc
44	30	83.3	1179	1	ATX1_ARATH	O91002	arabidopsis
45	29	80.6	103	1	Y131_METJA	Q57595	methanococ

ALIGNMENTS

RESULT 1	YDAS_ECOLI	STANDARD;	PRT;	98 AA.
ID	YDAS_ECOLI	STANDARD;	PRT;	98 AA.
AC	P76063;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Hypothetical protein ydas precursor.			
GN	YDAS OR B1357.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG1655;			
RX	MEDLINE=97426617; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Berna N.T., Burland V.,			
RA	Riley M., Colado-Vides J., Glaeser J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12."			
RL	Science 277:1453-1474(1997).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-bdb.ch/announce/			
CC	or send an email to license@isb-bdb.ch).			
CC	-----			
DR	EMBL; AE000233; AAC74439.1; -.			
DR	PIR; H64885; H64885.			
DR	Ecogene; EG1361; ydas.			
KW	Hypothetical protein; Signal; Complete proteome.			
FT	STGNL			
FT	CHAIN 1 32			
FT	POTENTIAL			
FT	HYPOTHETICAL PROTEIN YDAS.			
SQ	SEQUENCE 98 AA; 10975 MW; 397F00BA459E3BC4 CRC64;			
Query Match	94.4%; Score 34; DB 1; Length 98;			
Best local similarity	83.3%; Pred. No. 10;			
Matches	5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
OY	1 LDMSYL 6			
Db	67 LDMSYL 72			
RESULT 2	YETK_BACSU	STANDARD;	PRT;	330 AA.
ID	YETK_BACSU	STANDARD;	PRT;	330 AA.
AC	P15430;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			

DE Hypothetical transport protein yerk.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
RN NCBI_taxid=1423;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunze F., Ogaawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azavedo V., Bertero M.G., Bessières P., Bolotin A., Borchert S.,
RA Boveris R., Boulter L., Brans A., Braun M., Brigelli S.C., Bron S.,
RA Brouillet S., Bruchet C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummins N.J., Daniel R.A.,
RA Denton F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fader C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grand G.,
RA Guisepi G., Guy B.J., Haga K., Hahne J., Harwood C.R., Henaut A.,
RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Jorjens B., Karamata D., Kaashara Y., Klaerr-Blancharde M., Klein C.,
RA Kobayashi Y., Koester P., Koningsstein G., Krohn S., Kumano M.,
RA Kurita K., Lapidus A., Lardinou S., Lauber J., Lazaretti V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauei C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Priesen B., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivoira C., Rocha R., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeder R., Scofield P.,
RA Setiguchi J., Sekowaka A., Seror S.J., Serro P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamkoobi A., Tanaka T., Terpestra P., Tognoni A.,
RA Toledo V., Uchlyama S., Vandemol M., Vannier F., Vaesaroit A.,
RA Vliet A., Wambut R., Wedler E., Wedler H., Weitzmeyer T.,
RA Wintere P., Wipac A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zumbstein A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RL Nucleur 390;249-256 (1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: BELONGS TO THE ENA TRANSPORTER FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC -----
DR EMBL, 299107, CAB12540.1, -.
DR PIR, H69798; H69798.
DR Subtilisin, BG12867; Yerk.
DR Interpro, IPR000620; DUF6.
DR Pfam, PF00892; DUF6; 2.
KW Hypothetical protein; Transport; Transmembrane; Complete proteome.
FT TRANSMEM 27 47 POTENTIAL.
FT TRANSMEM 56 76 POTENTIAL.
FT TRANSMEM 90 110 POTENTIAL.
FT TRANSMEM 119 139 POTENTIAL.
FT TRANSMEM 147 167 POTENTIAL.
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 206 226 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT TRANSMEM 270 290 POTENTIAL.
FT TRANSMEM 294 314 POTENTIAL.
SQ SEQUENCE 330 AA; 35758 MW; 7C6C65F1EDB276B5 CRC64;
Query Match 91.7%; Score 33; DB 1; Length 330;
Beet Local Similarity 83.3%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB	LDMSYSTV	244
0y	1	LDMSYSTV 6
Db	239	LDMSYSTV 244
RESULT 3		
FAD1_SCHPO	STANDARD;	PRT; 265 AA.
ID_074841:		
DT 30-MAY-2000	(Rel. 39, Created)	
DT 30-MAY-2000	(Rel. 39, Last sequence update)	
DT 28-FEB-2003	(Rel. 41, Last annotation update)	
De	Probable FAD synthetase (EC 2.7.7.2) (FAD adenyllyltransferase) (FAD pyrophosphorylase) (Flavin adenine dinucleotide synthetase).	
GN	SPCC1235.04C	
OS	Schizosaccharomyces pombe (fission yeast).	
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;	
OC	Schizosaccharomycetaceae; Schizosaccharomycetaceae;	
OX	Schizosaccharomycetes.	
NCBI	NCBI_TaxID=4896;	
LN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=972;	
RC	MEDLINE=21848401; PubMed=11859360;	
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,	
RA	Aguires J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,	
RA	Brooke K., Brown D., Brown S., Chillingworth T., Churcher C.M.,	
RA	Collins M., Connor R., Cronin A., Davis P., Feltham T., Fraser A.,	
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,	
RA	Hirolyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,	
RA	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,	
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,	
RA	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,	
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,	
RA	Skellern J., Simmonds M., Squares R., Squares S., Stevens K.,	
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,	
RA	Woodward J., Voickert G., Aert R., Robben J., Grymptre B.,	
RA	Welfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,	
RA	Gabel C., Fuchs M., Fritze C., Holzer E., Moesli D., Hilbert H.,	
RA	Borzym K., Langer I., Beck A., Lehrich H., Reinhardt R., Pohl T.M.,	
RA	Eger P., Zimmermann W., Medler H., Wambutt R., Punnett B.,	
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Motier S.,	
RA	Gallibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,	
RA	Lucas M., Roche M., Gallard C., Tallada V.A., Garzon A., Thode G.,	
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,	
RA	Domiguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,	
RA	Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,	
RA	Shpakovski G.V., Ussery D., Barrett B.G., Nuree P.;	
RL	"The genome sequence of Schizosaccharomyces pombe.";	
RL	Nature 415:871-880(2002).	
CC	-1- FUNCTION: ADENYLATES FMN TO FAD (BY SIMILARITY).	
CC	-1- CATALYTIC ACTIVITY: ATP + FMN = diphosphate + FAD.	
CC	-1- SIMILARITY: BELONGS TO THE PAPS REDUCTASE FAMILY. FAD1 SUBFAMILY.	
CC	-----	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
CC	EMBL; AL031764; CAA21108.1; -	
DR	PIR; T40878; T40878.	
DR	GeneDB; Sperm; SPCC1235.04C; -	
DR	InterPro; IPR002500; PAPS_reduct.	
DR	Pfam; PF01507; PAPS_reduct; 1.	
DR	Transferrase; Nucleotidyltransferase; FAD; FMN.	
DR	SEQUENCE 265 AA; 30608 MW; BC6C62B6F4A5F3 CRC64;	
Query March	88.9%;	Score 32; DB 1; Length 265;
Best Local	Similarity 100.0%;	Pred. NO. 62;
Matches	5; Conservative 0;	Mismatches 0; Gaps 0;

QY 1 LDMSY 5
 DB 173 LDMSY 177

RESULT 4

YKAB_BACFI STANDARD; PRT; 445 AA.
 ID YKAB_BACFI
 AC P30268;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Probable aminotransferase in Kaca 3 region (EC 2.6.-.-) (ORF B).
 OS Bacillus firmus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxId=1399;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Quirk P.G., Krulwich T.A.;
 RL Submitted (DEC-1991) to the EMBL/Genbank/DBJ databases.
 CC -1- COFACTOR: Pyridoxal phosphate (Potential).
 CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
 CC aminotransferases.

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CC -----
 DR EMBL; L02548; AAA22560.1; -.
 DR PIR; S27492; S27492.
 DR HSP; P13995; 10J3.
 DR InterPro: IPR005814; AminoTrans_3.
 DR Pfam; PF00202; AminoTrans_3; 1.
 DR PROSITE; PS00600; AA_TRANSF_3; 1.
 KM Hypothetical protein; AminoTransferase; Transferase;
 KW Pyridoxal phosphate.
 FT BINDING 280
 FT SEQUENCE 445 AA; 48849 MM; 5C921199BC2E248C CRC64;

Query Match 88.9%; Score 32; DB 1; Length 445;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSYL 6
 DB 4 DMSYL 8

RESULT 5
 CLS_CLOPE STANDARD; PRT; 476 AA.
 ID CLS_CLOPE
 AC Q92NC6;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cardiolipin synthetase (EC 2.7.8.-) (Cardiolipin synthase) (CL
 DE synthase).
 GN CLS OR CLSD OR CPB1430.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 NCBI_TaxId=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCTC 8237 / ATCC 13124 / CN 1491 / Type A;
 RX MEDLINE=20049836; PubMed=10585141;
 RA Koyama M., Katayama S., Kaji M., Taniguchi Y., Matsushita O.,
 Minami J., Morita S., Okabe A.;

RT "A Clostridium perfringens hem gene cluster contains a cysG (B)
 RT homologue that is involved in cobalamin biosynthesis."
 RL Microbiol. Immunol. 43:947-957(1999).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=13 / Type A;
 RX MEDLINE=21664373; PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kohara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 CC -1- FUNCTION: Catalyzes the reversible phosphatidyl group transfer
 CC from one phosphatidylglycerol molecule to another to form
 CC cardiolipin (CL) (diphosphatidylglycerol) and glycerol (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: 2 Phosphatidylglycerol =
 CC diphosphatidylglycerol + glycerol.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY. CARDIOLIPIN
 CC SYNTHASE SUBFAMILY.
 CC -1- SIMILARITY: Contains 2 PLD phospholipase domains.

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CC -----
 DR EMBL; AB017186; BA74786.1; -.
 DR EMBL; AP003190; BAB81136.1; -.
 DR PIR; T43863; T43863.
 DR HAMAP; MF_00190; -; 1.
 DR InterPro: IPR001736; PLD.
 DR Pfam; PF00614; PLDC; 2.
 DR SMART; SM00155; PLDC; 2.
 DR PROSITE; PS50035; PLD; 2.
 KM Transferrase; Phospholipid biosynthesis; Transmembrane;
 KW Repeat; Complete proteome.
 FT TRANSMEM 2
 FT TRANSMEM 31
 FT DOMAIN 207
 FT DOMAIN 207
 FT ACT SITE 389
 FT ACT SITE 212
 FT ACT SITE 394
 FT ACT SITE 394
 FT CONFICT 469
 FT SEQUENCE 476 AA; 55040 MM; 8EC32FC113F0A9CB CRC64;

Query Match 88.9%; Score 32; DB 1; Length 476;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5
 DB 265 LDMSY 269

RESULT 6
 SBST_CAEEL STANDARD; PRT; 517 AA.
 ID SBST_CAEEL
 AC Q9NAD6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SRP-2003 (Rel. 42, Last annotation update)
 DE Putative seestrin.
 GN Y74C9A.5.
 OS Caenorhabditis elegans.
 OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 NCBI_TaxId=6239;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Du H., Woldmann P., Ames M.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP CONCEPTUAL TRANSLATION.
 RA Axelsson K., Baltoch A.;
 RL Unpublished observations (MAR-2001).
 CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).
 CC -1- SIMILARITY: Belongs to the sestrin family.
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC -----
 DR EMBL; AC024206; AAF36051.1; ALT_SEQ.
 DR Wormpep; Y74C9A.5; CE24663.
 DR InterPro; IPR006730; PA26.
 DR Pfam; PF04636; PA26; 1.
 KW Hypothetical protein; Nuclear protein.
 SQ Hypothetical protein; D7BC041916D0E205 CRC64;
 SQ
 Query March 88.9%; Score 32; DB 1; Length 517;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSYL 6
 Db 156 IDMSYM 161

RESULT 7
 ORC1_SCHPO STANDARD; PRT; 707 AA.
 AC P54789;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Origin recognition complex subunit 1.
 GN ORC1 OR ORP1 OR SPBC29A10.15.
 OS Schizosaccharomyces pombe (Fission Yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 OC NCBI_TaxID=4896;
 OX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96099401; PubMed=7502077;
 RA Gavin K.A., Hidaka M., Stillman B.D.;
 RT "Conserved initiator proteins in eukaryotes.";
 RL Science 270:1667-1671(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=96109289; PubMed=8618924;
 RA Muzi-Falconi M., Kelly T.J.;
 RT "Orp1, a member of the Cdc18/Cdc6 family of S-phase regulators, is
 RT homologous to a component of the origin recognition complex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:12475-12479(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Brooks J., Peat N., Hayles J., Basham D., Bowman S.,
 RA Sgouros K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quay M.A., Rabbittowitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Stevens S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grympey B.,
 RA Wajsbjerg I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wandut R., Furnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Gallibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas R., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Carructi L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shipakoveki G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RN Nature 415:871-880(2002).
 RN [4]
 RP SUBUNIT.
 RX MEDLINE=20006240; PubMed=10535928;
 RA Moon K.Y., Kong D., Lee J.K., Raychaudhuri S., Hurwitz J.;
 RT "Identification and reconstitution of the origin recognition complex
 RT from Schizosaccharomyces pombe.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:12367-12372(1999).
 CC -1- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT
 CC BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL
 CC REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO
 CC THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION.
 CC -1- SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY DURING THE CELL
 CC CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE ORC1 FAMILY.
 CC -----
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 CC -----
 DR EMBL; U40378; AAC49141.1; -;
 DR EMBL; U43392; AAB38247.1; -;
 DR EMBL; U38522; AAC49129.1; -;
 DR EMBL; AL034463; CAA22443.1; -;
 DR PIR; T40070; T40070.
 DR GENDB Spombe; SPBC29A10.15; -;
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR000637; AT_hook.
 DR InterPro; IPR001025; BAH.
 DR Pfam; PF00004; AAA; 1.
 DR Pfam; PF02178; AT_hook; 1.
 DR Pfam; PF01426; BAH; 1.
 DR SMART; SM00382; AAA; 1.
 DR SMART; SM00384; AT_hook; 1.
 DR SMART; SM00439; BAH; 1.
 KW DNA replication; Nuclear protein; DNA-binding; ATP-binding.
 FT NP BIND 368 375 ATP (POTENTIAL).
 SQ SEQUENCE 707 AA; 80514 MW; D056018159A40A44 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSY 5
 |||||

CC -1- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the
CC nonreducing end of alpha-1,4-glucan.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N) =
CC UDP + {(1,4)-alpha-D-glucosyl} (N+1).
CC -1- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,
CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.
CC -1- PATHWAY: Glycogen biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
CC FAMILY.
CC -----
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CC -----
DR EMBL, J04501; AAA88046.1; -
DR EMBL, Z33622; CAAB8316.1; -
DR EMBL, Z33623; CAAB8316.1; JOINED.
DR EMBL, Z33609; CAAB8316.1; JOINED.
DR EMBL, Z33624; CAAB8316.1; JOINED.
DR EMBL, Z33625; CAAB8316.1; JOINED.
DR EMBL, Z33626; CAAB8316.1; JOINED.
DR EMBL, Z33610; CAAB8316.1; JOINED.
DR EMBL, Z33627; CAAB8316.1; JOINED.
DR EMBL, Z33628; CAAB8316.1; JOINED.
DR EMBL, Z33629; CAAB8316.1; JOINED.
DR EMBL, Z33630; CAAB8316.1; JOINED.
DR EMBL, Z33631; CAAB8316.1; JOINED.
DR EMBL, Z33633; CAAB8316.1; JOINED.
DR EMBL, U32573; AAB60385.1; -
DR PIR, A32156; AAB60385.1; -
DR Genew; HGNC:4706; GYS1.
DR GK, P13807; -
DR MIM, 138570; -
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Allosteric enzyme; Phosphorylation; Disease mutation;
KW Diabetes mellitus; Polymorphism.
FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
FT MOD_RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 641 641 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 645 645 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 649 649 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 653 653 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 658 658 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 710 710 PHOSPHORYLATION (BY SIMILARITY).
FT VARIANT 130 130 K -> E (IN dbSNP:5456).
FT VARIANT 283 283 N -> S (IN dbSNP:5461).
FT VARIANT 359 359 E -> G (IN dbSNP:5465).
FT VARIANT 416 416 M -> V (IN dbSNP:5447).
FT VARIANT 464 464 G -> S (IN dbSNP:5473).
FT VARIANT 619 619 E -> Q (IN dbSNP:5450).
FT VARIANT 691 691 P -> A (IN dbSNP:5453).
FT CONFLICT 136 136 /FTID=VAR_014731.
FT CONFLICT 462 462 T -> I (IN REF. 1 AND 3).
FT CONFLICT 608 608 MISSING (IN REF. 3).
FT CONFLICT 706 706 A -> D (IN REF. 3).
SQ SEQUENCE 737 AA; 83785 MW; 0B321BFBDB0BD7F CRC64;
Query Match 88.9%; Score 32; DB 1; Length 737;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSYL 6
Db 596 LDWKYL 601
RESULT 10
GYS1_MACMU STANDARD; PRT; 737 AA.
AC QBMJ26;
DT 28-FEB-2003 (Rel. 41, Last created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Glycogen (starch) synthase, muscle (EC 2.4.1.11).
GN GYS1 OR GYS.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Skeletal muscle;
RA Ottmeyer H.K., Marciani K.R., Hansen B.C.;
RT "Monkey skeletal muscle glycogen synthase sequence."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the
CC nonreducing end of alpha-1,4-glucan (By similarity).
CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N) =
CC UDP + {(1,4)-alpha-D-glucosyl} (N+1).
CC -1- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,
CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.
CC -1- PATHWAY: Glycogen biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
CC FAMILY.
CC -----
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CC -----
DR EMBL, AF529178; AAM93267.1; -
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Allosteric enzyme; Phosphorylation.
FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
FT MOD_RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 641 641 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 645 645 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 649 649 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 653 653 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 658 658 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 698 698 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 710 710 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 737 AA; 83786 MW; B8B0B3114C58F56C CRC64;
Query Match 88.9%; Score 32; DB 1; Length 737;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LDMSYL 6
Db 596 LDWKYL 601
RESULT 11
GYS3_MOUSE STANDARD; PRT; 737 AA.
ID GYS3_MOUSE
AC P54859;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glycogen [search] synthase, brain (EC 2.4.1.11).
GN GYS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=OPI Albinos; TISSUE=Brain;
RX MEDLINE=96385248; PubMed=8793107;
RA Pellegrini G., Rossier C., Magistretti P.J., Martin J.L.;
RT "Cloning, localization and induction of mouse brain glycogen
  synthase.";
RL Brain Res. Mol. Brain Res. 38:191-199(1996).
CC -1- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the
  nonreducing end of alpha-1,4-glucan.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =
  UDP + ((1,4)-alpha-D-glucosyl) (N+1).
CC -1- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,
  AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.
CC -1- PATHWAY: Glycogen biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
  FAMILY.
CC -----
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CC -----
DR EMBL; X94616; CAA64322.1; -.
DR MGD; MGI:107378; Gys3.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KM Allosteric enzyme; Phosphorylation.
FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
FT MOD RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 640 640 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 644 644 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 648 648 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 652 652 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 656 656 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 697 697 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 710 710 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 737 AA; 83824 MW; 891A0614C8F6C085 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 737;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDMSYL 6
DB 595 LDMKYL 600

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RP SEQUENCE FROM N.A.
RA Seldin M.F., Xue Z., Rochelle J.M., DeBry R., Surwit R.;
RT "Mouse glycogen synthase gene.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the
  nonreducing end of alpha-1,4-glucan (By similarity).
CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =
  UDP + ((1,4)-alpha-D-glucosyl) (N+1).
CC -1- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,
  AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE (BY SIMILARITY).
CC -1- PATHWAY: Glycogen biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
  FAMILY.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U53218; AAD09457.1; -.
DR MGD; MGI:101805; Gys1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KM Allosteric enzyme; Phosphorylation.
FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
FT MOD RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 641 641 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 645 645 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 649 649 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 653 653 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 657 657 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 698 698 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 738 AA; 83955 MW; 6C2C8B5D5004F1D1 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 738;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDMSYL 6
DB 596 LDMKYL 601

```

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RESULT 13
MSG DICI
AC P54637;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Myosin II heavy chain.
GN MYOJ.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Metazoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=AX3.
RX MEDLINE=96215148; PubMed=8636147;
RA Hammer J.A. III, Jung G.;
RT "The sequence of the dictyostelium myo J heavy chain gene predicts a
  novel, dimeric, unconventional myosin with a heavy chain molecular
  mass of 258 kDa.";
RL J. Biol. Chem. 271:7120-7127(1996).
RN (2)
RP SEQUENCE OF 1-1021 FROM N.A.
RX MEDLINE=97039016; PubMed=8884597;
RA Peterson M.D., Urzoleo A.S., Titus M.A.;
RT "Dictyostelium discoideum myoJ: a member of a broadly defined myosin
  V class or a class XI unconventional myosin?";

```

RL J. Muscle Res. Cell Motil. 17:411-424(1996).
 RN (3)
 RP SEQUENCE OF 182-298 FROM N.A.
 RX MEDLINE=95023928; PubMed=7937787;
 RA Titus M.A., Kuspa A., Loomis W.F.;
 RT "Discovery of myosin genes by physical mapping in Dictyostelium";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9446-9450(1994).
 CC -1- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN AND HAS ATPASE
 CC ACTIVITY THAT IS ACTIVATED BY ACTIN.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.
 CC -1- SIMILARITY: Contains 1 dilute domain.
 CC -1- SIMILARITY: Contains 3 IQ domains.
 CC -----
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 CC -----
 DR EMBL; U42409; AAA85186.1; -;
 DR EMBL; L35322; AAA79858.1; -;
 DR PIR; T18278; T18278.
 DR HSBP; P08799; IMND.
 DR DictyDb; DD01095; myoJ.
 DR InterPro; IPR002710; DIL.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR001609; myosin_head.
 DR InterPro; IPR004009; Myosin_N.
 DR Pfam; PF01843; DIL; 1.
 DR Pfam; PF00612; IQ; 6.
 DR Pfam; PF00063; myosin_head; 2.
 DR Pfam; PF02736; Myosin_N; 1.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR ProDom; PD003376; DIL; 1.
 DR ProDom; PD000355; myosin_head; 1.
 DR SMART; SM00015; IQ; 3.
 DR SMART; SM00242; MYSC; 1.
 DR PROSITE; PS50096; IQ; 3.
 KW Myosin; ATP-binding; Actin-binding; Calmodulin-binding; Repeat;
 KW Coiled coil.
 FT DOMAIN 1 809 MYOSIN HEAD-LIKE.
 FT DOMAIN 824 851 IQ 1.
 FT DOMAIN 872 901 IQ 2.
 FT DOMAIN 943 972 IQ 3.
 FT DOMAIN 973 1812 COILED COIL (POTENTIAL).
 FT DOMAIN 2060 2220 DILUTE.
 FT NP_BIND 174 181 ATP (POTENTIAL).
 FT DOMAIN 669 749 ACTIN-BINDING.
 FT CONFLICT 191 191 L -> F (IN REF. 2).
 FT CONFLICT 284 284 A -> T (IN REF. 2).
 FT CONFLICT 291 291 G -> R (IN REF. 2).
 FT CONFLICT 332 347 NKGCFEIEGVSDSEH -> IEMNELKVTYRMS (IN
 FT REF. 2).
 FT CONFLICT 550 550 N -> K (IN REF. 2).
 FT CONFLICT 865 866 HH -> QQ (IN REF. 2).
 SQ SEQUENCE 2245 AA; 258478 MW; 615SEFIDLAB4SBE CRC64;
 Query Match 88.9%; Score 32; DB 1; Length 2245;
 Best Local Similarity 66.7%; Pred. No. 5e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSYL 6
 DB 530 IDMSYI 535
 RESULT 14
 RM49 CABEL STANDARD; PRT; 223 AA.
 AC Q21939;

DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Potential mitochondrial 60S ribosomal protein L49 (MRP-L49).
 GN R1D1.9.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Steward C.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE L49EM FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL; Z75547; CAA99906.1; -;
 DR PIR; T24188; T24188.
 DR WormPep; R1D1.9; CRO6314.
 DR Pfam; PF05046; Img2; 1.
 KW Hypothetical protein; Ribosomal protein; Mitochondrion.
 SQ SEQUENCE 223 AA; 25862 MW; 2A8DC95CB13CB3F CRC64;
 Query Match 86.1%; Score 31; DB 1; Length 223;
 Best Local Similarity 66.7%; Pred. No. 78;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSYL 6
 DB 90 IDMSYV 95
 RESULT 15
 O46A_DROME STANDARD; PRT; 385 AA.
 ID O46A_DROME
 AC P81919; Q9V5X9; Q9V5H3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Odorant receptor 46a.
 GN OR46A OR OR46F.1 OR DOR46F.1 OR AN9 OR CG17849.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99389723; PubMed=10458908;
 RA Gao Q., Chess A.;
 RT "Identification of candidate Drosophila olfactory receptors from
 RT genomic DNA sequence";
 RL Genomics 60:31-39(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutcliffe G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Pfeiffer G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Baou A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Fessler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Foster A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Houtin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kesterson J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Labko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mepheson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclet J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Renner K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Klamor I., Simpson M., Skupski M.P., Smith T.,
 RA Szyrkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weincock G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gbabe R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP REVISIONS.
 RP STRAIN=Berkeley;
 RC MEDLINE=22426069; PubMed=12537572;
 RX Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Beccencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.R.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [4]
 RP IDENTIFICATION, AND TISSUE SPECIFICITY.
 RX MEDLINE=99166868; PubMed=10669338;
 RA Clyne P.J., Watt C.G., Freeman M.R., Leessing D., Kim J., Carlson J.R.;
 RT "A novel family of divergent seven-transmembrane proteins: candidate
 RT odorant receptors in *Drosophila*.";
 RL Neuron 22:327-338(1999).
 CC -1- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF 17 OLFACTORY RECEPTOR
 CC NEURONS IN THE MAXILLARY PALP.
 CC -1- SIMILARITY: BELONGS TO FAMILY DR-OR OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; AE003830; AAF58834.2; -
 DR FLYBase; FBgn026388; Or46a.
 DR InterPro; IPR004117; Tcm_6.
 DR Pfam; PF02949; 7tm_6; 1.
 KW Transmembrane; G-protein coupled receptor; Olfaction; Glycoprotein;

KW Multigene family.
 FT DOMAIN 1 37
 FT TRANSMEM 38 58
 FT DOMAIN 59 65
 FT TRANSMEM 66 86
 FT DOMAIN 87 127
 FT TRANSMEM 128 148
 FT DOMAIN 149 170
 FT TRANSMEM 171 191
 FT DOMAIN 192 255
 FT TRANSMEM 256 276
 FT DOMAIN 277 287
 FT TRANSMEM 288 308
 FT DOMAIN 309 354
 FT TRANSMEM 355 375
 FT DOMAIN 376 385
 SQ SEQUENCE 385 AA; 44483 MW; BB062862B7A59310 CRC64;
 Query Match 86.1%; Score 31; DB 1; Length 385;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSTL 6
 DB 148 LDMSTL 153
 Search completed: February 18, 2004, 14:28:13
 Job time : 4.55263 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds

(Without alignments)
79,423 Million cell updates/sec

Title: US-09-643-260-14

Sequence: 1 LDMSFL 6

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	91.4	404	1 YCFD_HABIN	P44663 haemophilus
2	31	88.6	135	1 VAL2_CLVK	P14976 cassava lat
3	31	88.6	135	1 VAL2_CLVN	P14968 cassava lat
4	31	88.6	135	1 VAL2_TYLCV	P27262 tomato yell
5	31	88.6	204	1 HIS2_YERPE	Q82FY1 yerbina pe
6	31	88.6	240	1 LEC5_VATWA	P81371 vatatea ma
7	31	88.6	355	1 CXAS_RAT	P28234 ratius norv
8	31	88.6	356	1 CXAS_CANPA	P33725 canis fami
9	31	88.6	357	1 CXAS_HUMAN	P01231 mus musculu
10	31	88.6	357	1 CXAS_MOUSE	P18860 gallus gall
11	31	88.6	368	1 CXAS_CHICK	P18860 gallus gall
12	31	88.6	382	1 LYS1_CANAL	P43065 candida alb
13	31	88.6	383	1 P2C4_SCHPO	O14166 schizosacch
14	31	88.6	399	1 CXAS_CHICK	P36391 gallus gall
15	31	88.6	400	1 NUCM_PROMI	Q37619 proteobeca
16	31	88.6	405	1 CXAS_BOVIN	P41987 bos taurus
17	31	88.6	415	1 CXAS_RAT	P29414 ratius norv
18	31	88.6	416	1 CXAS_MOUSE	Q64448 mus musculu
19	31	88.6	432	1 CXAS_HUMAN	P48185 homo sapien
20	31	88.6	434	1 CXAS_HUMAN	Q9Y688 homo sapien
21	31	88.6	439	1 CXAS_MOUSE	P28236 mus musculu
22	31	88.6	439	1 CXAS_SHEEP	P55917 ovis aries
23	31	88.6	510	1 CXS6_CHICK	P29415 gallus gall
24	31	88.6	1363	1 ILPR_BRLA	O02466 brachiolesto
25	31	88.6	98	1 YDAS_ECOLI	P26063 escherichia
26	31	88.6	225	1 TRPF_CANAL	P43073 candida alb
27	31	88.6	225	1 MKKS_HUMAN	Q9HPI1 homo sapien
28	31	88.6	654	1 CBP1_YEAST	P07252 saccharomyc
29	31	88.6	709	1 KRPI_SCHPO	Q09175 schizosacch
30	31	88.6	745	1 IKKA_HUMAN	O15111 h inhibitor
31	31	88.6	745	1 IKKA_MOUSE	O60680 m inhibitor
32	31	88.6	751	1 TALA_POVHA	P03075 hamster pol
33	31	88.6	756	1 IKKB_HUMAN	O14920 homo sapien

34	30	85.7	757	1 IKKB_MOUSE	O88351 mus musculu
35	30	85.7	757	1 IKKB_RAT	Q98378 ratius norv
36	30	85.7	3746	1 ACVS_PENCH	P19787 pentacillium
37	30	85.7	3791	1 ACVT_PENCH	P26046 pentacillium
38	29	82.9	139	1 YOR2_ADEG1	P20744 avian adeno
39	29	82.9	179	1 Y256_SUI50	Q98055 mycoplasma
40	29	82.9	228	1 Y268_MYCGE	P47510 mycoplasma
41	29	82.9	233	1 CR29_ENTHI	P19476 entamoeba h
42	29	82.9	284	1 YK62_SULTO	Q96706 sulfolobus
43	29	82.9	328	1 NIK3_AZOB	P45672 azospirillum
44	29	82.9	330	1 YETK_BACSU	O31540 bacillus su
45	29	82.9	344	1 METE_THERVO	Q97914 thermoplasma

ALIGNMENTS

RESULT 1
YCFD_HABIN STANDARD, PRT, 404 AA.
AC P44663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein H10396.
GN H10396.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellales; Haemophilus.
OX NCBI_TaxId=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fetschmann R.D., Adams M.D., White O., Clayton R.A., Kirtness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Heddlom E., Cotton M.D.,
RA Utecherback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RT Science 269:496-512(1995).
RL [2]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=20137488; PubMed=10675023;
RA Langen H., Takece B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
RT Electrophoresis 21:411-429(2000).
CC -1- SIMILARITY: STRONG, TO E.COLI YCFD.
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CC
CC EMBL, U32723; AAC22055.1; -
CC PIR, A64151; A64151.
CC TIGR, H10396; -
CC InterPro: IPR003347; TP JmjC.
CC SMART: SM00558; JmjC, 1.
CC Complete proteome.
SQ SBQUNCE 404 AA; 46419 MW, A3FP26064D3FB84C CRC64;
Query Match 91.4%; Score 32; DB 1; Length 404;
Best Local Similarity 83.3%; Pred. No. 70;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSPFL 6
|||||
Db 366 LDMNAFL 371

RESULT 2

VAL2_CLVW STANDARD; PRT; 135 AA.
AC P14976;
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL2 protein (15.2 kDa protein).
GN AC2.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.

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CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro: IPR000942; Gemin1.AL2.
DR Pfam; PF01440; Gemin1.AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemin1.AL2; 1.
SQ SEQUENCE 135 AA; 15159 MW; 75D24A8CD636848 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. NO. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSFL 6
|||||
Db 128 DMSFL 132

RESULT 3

VAL2_CLVW STANDARD; PRT; 135 AA.
AC P14968;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL2 protein (15.2 kDa protein).
GN AC2.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
RL Nucleic Acids Res. 18:197-198(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.

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DR EMBL; X17095; CAA34952.1; -.
DR PIR; S07593; S07593.
DR InterPro; IPR000942; Gemin1.AL2.
DR Pfam; PF01440; Gemin1.AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemin1.AL2; 1.
SQ SEQUENCE 135 AA; 15178 MW; 2825C2P42E5E1F49 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. NO. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSFL 6
|||||
Db 128 DMSFL 132

RESULT 4

VAL2_TYLCV STANDARD; PRT; 135 AA.
AC P27262;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL2 protein (C2 protein).
GN C2.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92024070; PubMed=1926771;
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component.";
RL Virology 185:151-161(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.

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CC EMBL; X15656; CAA33689.1; -.
DR PIR; C40779; OOCVCA.
DR InterPro; IPR000942; Gemin1.AL2.
DR Pfam; PF01440; Gemin1.AL2; 1.
DR PRINTS; PR00230; GEMCOATAL2.
DR ProDom; PD001117; Gemin1.AL2; 1.
SQ SEQUENCE 135 AA; 15611 MW; F111C8C2F7E9DD32 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. NO. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSFL 6
|||||
Db 128 DMSFL 132

RESULT 5

HIS2_YERPE STANDARD; PRT; 204 AA.
ID HIS2_YERPE
AC Q8ZFT1;

DT 28-FEB-2003 (Rel. 41, Last Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histidine biosynthesis bifunctional protein hsisB [includes:
 DE Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (PRA-CH);
 DE Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH)].
 GN HSI1 OR HSI2 OR YPO1542 OR Y2628.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SRRATN-CC-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=1156360;
 RA Parikh H.J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
 RA Penrice M.B., Sebailia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Felwell T., Hamlin N., Holroyd S., Jørgen K., Kariyasek A.V.,
 RA Leather S., Moulton J., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
 RA "Genome sequence of Yersinia pestis, the causative agent of plague,"
 RT Nature 413:523-527(2001).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=KIMS / Biovar Medvevalis;
 RX MEDLINE=21137863; PubMed=212430;
 RA Deng W., Burland V., Plunkett G. II, Boutin A., Mayhew G.F., Liles P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Milles M.L., Watson J.S., Blattner F.R.,
 RA Perry R.D.,
 RT "Genome sequence of Yersinia pestis KIM,"
 RL J. Bacteriol. 184:4601-4611(2002).
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-ATP + H(2)O = 1-(5-
 CC -1- phosphoribosyl)-AMP + diphosphate.
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-AMP + H(2)O = 1-(5-
 CC -1- phosphoribosyl)-5-(1-(5-phosphoribosyl)-imidazole-4-carboxamide.
 CC -1- PATHWAY: Histidine biosynthesis; second step.
 CC -1- PATHWAY: Histidine biosynthesis; third step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE PRA-CH
 CC FAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE PRA-PH
 CC FAMILY.
 CC -----
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 DR EMBL: AJ141419; CA90365.1; -
 DR EMBL: AE013864; AA06182.1; -
 DR PIR: ABO188; ABO188.
 DR HAMAP: MF 01019; -; 1.
 DR InterPro: IPR002496; PRA-CH.
 DR InterPro: IPR002497; PRA-PH.
 DR Pfam: PF01502; PRA-CH; 1.
 DR Pfam: PF01503; PRA-PH; 1.
 DR ProDom: PD002610; PRA-CH; 1.
 DR ProDom: PD002611; PRA-PH/CH; 1.
 KM Histidine biosynthesis; Multifunctional enzyme; Hydrolase;
 KW Complete proteome.
 FT DOMAIN 1 114 PHOSPHORIBOSYL-AMP CYCLOHYDROLASE.
 FT DOMAIN 115 204 PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE.
 SQ SEQUENCE 204 AA; 22807 MW; BF3328DF1C0A8C79 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 DMSFL 6
 Db 111 DMSFL 115
 RESULT 6
 LECS VATWA STANDARD; PRT; 240 AA.
 ID LECS VATWA
 AC P81371;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Seed lectin (VWL).
 OS Vatairea macrocarpa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid 1; Fabales; Fabaceae; Papilionoideae; Dalbergiaceae; Vatairea.
 OX NCBI_TaxID=77050;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed.
 RX MEDLINE=98218569; PubMed=9559667;
 RA Calvee J.U., Santos C.F., Mann K., Grangeiro T.B., Nantz M.,
 RA Urbake C., Sousa-Cavada B.,
 RT "Amino acid sequence, glycan structure, and proteolytic processing of
 the lectin of Vatairea macrocarpa seeds,"
 RL FEBS Lett. 425:286-292(1998).
 CC -1- FUNCTION: LECTIN THAT BINDS GALACTOSE.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- TISSUE SPECIFICITY: Seed.
 CC -1- PTM: PARTIALLY N-GLYCOSYLATED AT POSITIONS 111 AND 183 WITH
 CC THE HEPTASACCHARIDE (BETA-XYLOSYL-1,2) (ALPHA-MANNOSYL-1,6) (ALPHA-
 CC MANNOSE-1,3) (BETA-MANNOSYL-1,4-GALNAc-BETA-1,4-GALNAc-BETA-1,4
 CC [ALPHA-FUCOSYL-1,3]GLCNAC. A SMALL PROPORTION OF ALPHA CHAINS ARE
 CC PROTEOLYTICALLY CLEAVED AT 114-115 INTO GAMMA AND BETA CHAINS.
 CC THIS IS PROBABLY DEPENDENT ON THE DEGLYCOSYLATION OF N-111.
 CC -1- MISCELLANEOUS: BINDS ONE MANGANESE (OR OTHER TRANSITION METAL) ION
 CC AND ONE CALCIUM ION. THE METAL IONS ARE ESSENTIAL FOR THE
 CC SACHARIDE-BINDING AND CELL-AGGLUTININATING ACTIVITIES (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE LEGUMINOUS LECTIN FAMILY.
 DR HSSP: P19588; 1LUL.
 DR GlycoSuiteDB; P81371; -
 DR InterPro: IPR000985; Lectin_legA.
 DR InterPro: IPR001220; Lectin_legB.
 DR Pfam: PF00138; Lectin_legA; 1.
 DR Pfam: PF00139; Lectin_legB; 1.
 DR ProDom: PD000671; Lectin_legA; 1.
 DR ProDom: PD000711; Lectin_legB; 1.
 DR ProSite: PS00307; LECTIN LEGUME BETA; 1.
 DR ProSite: PS00308; LECTIN LEGUME ALPHA; 1.
 KW Lectin; Calcium; Manganese; Glycoprotein.
 FT CHAIN 1 240
 FT CHAIN 1 114 SEED LECTIN ALPHA CHAIN.
 FT CHAIN 115 239 SEED LECTIN BETA CHAIN.
 FT METAL 123 123 MANGANESE (BY SIMILARITY).
 FT METAL 125 125 MANGANESE AND CALCIUM (BY SIMILARITY).
 FT METAL 129 129 CALCIUM (BY SIMILARITY).
 FT METAL 132 132 MANGANESE AND CALCIUM (BY SIMILARITY).
 FT METAL 137 137 MANGANESE (BY SIMILARITY).
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 183 183 I -> V.
 FT VARIANT 117 117 M -> K.
 FT VARIANT 148 148 G -> A.
 FT VARIANT 154 154 E -> Q.
 FT VARIANT 168 168
 FT UNSURE 239 240
 SQ SEQUENCE 240 AA; 26197 MW; C17DF6B2568C65C1 CRC64;

Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DMSF 5
|||||
Db 224 DMSF 228

RESULT 7
CXAS_RAT STANDARD; PRT; 355 AA.

ID CXAS_RAT
AC P28234;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gap junction alpha-5 protein (Connexin 40) (Cx40).
GN GJA5 OR CXN-40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=92112940; PubMed=1370487;
RA Haefliger J.-A., Bruzone R., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Paul D.L.;
RT "Four novel members of the connexin family of gap junction proteins.
RT Molecular cloning, expression, and chromosome mapping."
RT J. Biol. Chem. 267:2057-2064(1992).
RL [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=93021055; PubMed=1328644;
RA Beyer E.C., Reed K.E., Westphale E.M., Kanter H.L., Larson D.M.;
RT "Molecular cloning and expression of rat connexin40, a gap junction
RT protein expressed in vascular smooth muscle."
RT J. Membr. Biol. 127:69-76(1992).
RL [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=9806770; PubMed=9403066;
RA Seul K.H., Taddei P.N., Beyer E.C.;
RT "Mouse connexin40: gene structure and promoter analysis."
RT Genomics 46:120-126(1997).
RL -1- FUNCTION: One gap junction consists of a cluster of closely packed
pairs of transmembrane channels, the connexons, through which
materials of low mw diffuse from one cell to a neighboring cell.
CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in lung.
CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
SUBFAMILY.

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DR EMBL: M76535; AAA41000.1; -
DR EMBL: M83092; AAA41194.1; -
DR EMBL: AF021806; AAC55502.1; -
DR EMBL: AF022136; AAC55503.1; -
DR PIR: A42053; A42053.
DR InterPro: IPR000500; Connexin.
DR Pfam: PF00029; connexin.1.
DR PRINTS: PR00206; CONNEXIN.
DR SMART: SM00037; CNX; 1.
DR PROSITE: PS00407; CONNEXINS_1; 1.
DR PROSITE: PS00408; CONNEXINS_2; 1.
DR Gap junction, Transmembrane.
FT INIT_MET 0 0 BY SIMILARITY.

FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 40 POTENTIAL.
FT DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 76 98 POTENTIAL.
FT DOMAIN 99 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 177 POTENTIAL.
FT DOMAIN 178 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 227 POTENTIAL.
FT DOMAIN 228 355 POTENTIAL.
SQ SEQUENCE 355 AA; 40102 MW; 4F8594386800B9 CRC64;

Query Match Score 31; DB 1; Length 355;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSF 6
|||||
Db 2 DMSF 6

RESULT 8
CXAS_CANPA STANDARD; PRT; 356 AA.

ID CXAS_CANPA
AC P33725;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gap junction alpha-5 protein (Connexin 40) (Cx40).
GN GJA5
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92136511; PubMed=1310450;
RA Kanter H.L., Safitz J.E., Beyer E.C.;
RT "Cardiac myocytes express multiple gap junction proteins."
RT Circ. Res. 70:438-444(1992).
RL -1- FUNCTION: One gap junction consists of a cluster of closely packed
pairs of transmembrane channels, the connexons, through which
materials of low mw diffuse from one cell to a neighboring cell.
CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
SUBFAMILY.

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DR EMBL: M81347; AAA30838.1; -
DR PIR: A49024; A49024.
DR InterPro: IPR000500; Connexin.
DR Pfam: PF00029; connexin.1.
DR PRINTS: PR00206; CONNEXIN.
DR SMART: SM00037; CNX; 1.
DR PROSITE: PS00407; CONNEXINS_1; 1.
DR PROSITE: PS00408; CONNEXINS_2; 1.
DR Gap junction, Transmembrane.
FT INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 40 POTENTIAL.
FT DOMAIN 41 76 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 77 99 POTENTIAL.
FT DOMAIN 100 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 177 POTENTIAL.
FT DOMAIN 178 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 227 POTENTIAL.

FT DOMAIN 228 356 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 356 AA; 39801 MW; C8431D56CF9E78BE CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 356;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DMSFL 6
 DB 2 DMSFL 6

RESULT 9
 ID CXAS_HUMAN STANDARD; PRT; 357 AA.
 AC P36382;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Gap junction alpha-5 protein (Connexin 40) (Cx40).
 GN Cx45.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95055780; PubMed=7966354;
 RA Kanter H.L., Saffitz J.E., Beyer E.C.;
 RT "Molecular cloning of two human cardiac gap junction proteins,
 RT connexin40 and connexin45.";
 RL J. Mol. Cell. Cardiol. 26:861-868 (1994).
 [2]
 RP REVISIONS.
 RA Beyer E.C., Christensen E.A.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RA Lin H.H., Jin N., Kiang D.T.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RA Heefliger J.-A., Goy J.J., Maebler G.;
 RT "Spontaneous cases of dilated cardiomyopathies associated with
 RT arrionentricular conduction defects are not linked to mutation within
 RT the connexins 40 and 43 genes.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heif F.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Sengupta M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein W.J., Udell T.B., Tomshylyk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bogak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Holton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallie D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: One gap junction consists of a cluster of closely packed
 CC pairs of transmembrane channels, the connexons, through which

CC materials of low mw diffuse from one cell to a neighboring cell.
 CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
 CC SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U03486; AAA60457.2; -;
 CC EMBL: L34954; AAA91833.1; -;
 CC EMBL: AF151979; MAD37801.1; -;
 CC EMBL: BC013313; AAH13313.1; -;
 CC DR Genew; HGNC:4279; GJA5.
 CC MIM: 121013; -;
 CC DR GO; GO:0015285; F:connexon channel activity; TAS.
 CC DR GO; GO:0007043; P:intercellular junction assembly; TAS.
 CC DR GO; GO:0006936; P:muscle contraction; TAS.
 CC DR InterPro; IPR000500; Connexin.
 CC Pfam; PF00029; connexin; 1.
 CC DR PRINTS; PR00206; CONNEXIN.
 CC DR SMART; SM00037; CNX; 1.
 CC DR PROSITE; PS00407; CONNEXINS_1; 1.
 CC DR PROSITE; PS00408; CONNEXINS_2; 1.
 CC KW Gap junction; Transmembrane.
 CC FT INIT MET 0 0
 CC FT DOMAIN 1 22 BY SIMILARITY.
 CC FT TRANSMEM 23 40 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 76 98 POTENTIAL.
 CC FT DOMAIN 99 163 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 164 183 POTENTIAL.
 CC FT DOMAIN 184 205 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 206 228 POTENTIAL.
 CC FT DOMAIN 229 357 CYTOPLASMIC (POTENTIAL).
 CC SQ SEQUENCE 357 AA; 40249 MW; 63FP9AA3CAED760 CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 357;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DMSFL 6
 DB 2 DMSFL 6

RESULT 10
 ID CXAS_MOUSE STANDARD; PRT; 357 AA.
 AC Q01231;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gap junction alpha-5 protein (Connexin 40) (Cx40).
 GN GJA5 OR CXN-40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6;
 RX MEDLINE=92299686; PubMed=1318884;
 RA Hempmann J., Suchyna T., Lichtenberg-Frate H., Jungbluth S.,
 RA Dahl E., Schwarz J., Nicholson B.J., Willecke K.;
 RT "Molecular cloning and functional expression of mouse connexin40, a
 RT second gap junction gene preferentially expressed in lung.";
 RL J. Cell Biol. 117:1299-1310 (1992).

CC -1- FUNCTION: One gap junction consists of a cluster of closely packed
 CC pairs of transmembrane channels, the connexons, through which
 CC materials of low mw diffuse from one cell to a neighboring cell.
 CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Kidney, heart and skin, but most abundant
 CC in lung.
 CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
 CC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: X61675; CAA43850.1; -.
 CC PIR: S23111; S23111.
 CC MGD: MGI:95716; Gja5.
 CC InterPro: IPR000500; Connexin.
 CC Pfam: PF00029; connexin.1.
 CC PRINTS: PR00206; CONNEXIN.
 CC SMART: SM00037; CNX.1.
 CC PROSITE: PS00407; CONNEXINS_1; 1.
 CC PROSITE: PS00408; CONNEXINS_2; 1.
 CC Gap junction; Transmembrane.
 CC INIT MET 0 0
 CC BY SIMILARITY.
 CC FT DOMAIN 23 22 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSSEM 23 40 POTENTIAL.
 CC FT DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSSEM 76 98 POTENTIAL.
 CC FT DOMAIN 99 155 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSSEM 156 178 POTENTIAL.
 CC FT DOMAIN 179 205 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSSEM 206 228 POTENTIAL.
 CC FT DOMAIN 229 357 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSSEM 357 40282 MW; 7823CDAS7A9CTC90 CRC64;
 CC SEQUENCE 357 AA; 40282 MW; 7823CDAS7A9CTC90 CRC64;
 CC
 CC Query Match 88.6%; Score 31; DB 1; Length 357;
 CC Best Local Similarity 100.0%; Pred. No. 94;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 2 DMSFL 6
 CC DB 2 DMSFL 6
 CC
 CC RESULT 11
 CC ID CA5_CHICK STANDARD; PRT; 368 AA.
 CC AC P18860;
 CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
 CC DT 01-NOV-1990 (Rel. 16, Last annotation update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Gap junction alpha-5 protein (Connexin 42) (Cx42).
 CC OS Gallus gallus (Chicken).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC CC Gallus.
 CC NCBI_TaxId=9031;
 CC RN NCB1_TaxId=9031;
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=90354434; PubMed=2167316;
 CC RA Beyer E.C.;
 CC RT "Molecular cloning and developmental expression of two chick embryo
 CC gap junction proteins."
 CC J. Biol. Chem. 265:14439-14443(1990).
 CC -1- FUNCTION: One gap junction consists of a cluster of closely packed
 CC pairs of transmembrane channels, the connexons, through which
 CC materials of low mw diffuse from one cell to a neighboring cell.
 CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Mostly in heart, and in the whole embryo,
 CC liver, stomach, and pectoral muscle.
 CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
 CC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: M35043; AAA48716.1; -.
 CC PIR: B37819; B37819.
 CC InterPro: IPR000500; Connexin.
 CC Pfam: PF00029; connexin.1.
 CC PRINTS: PR00206; CONNEXIN.
 CC SMART: SM00037; CNX.1.
 CC PROSITE: PS00407; CONNEXINS_1; 1.
 CC PROSITE: PS00408; CONNEXINS_2; 1.
 CC Gap junction; Transmembrane.
 CC INIT MET 0 0
 CC BY SIMILARITY.
 CC FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSSEM 23 45 POTENTIAL.
 CC FT DOMAIN 46 75 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSSEM 76 98 POTENTIAL.
 CC FT DOMAIN 99 159 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSSEM 160 182 POTENTIAL.
 CC FT DOMAIN 183 210 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSSEM 211 233 POTENTIAL.
 CC FT DOMAIN 234 368 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSSEM 368 41613 MW; 853A042PFS1DACB CRC64;
 CC SEQUENCE 368 AA; 41613 MW; 853A042PFS1DACB CRC64;
 CC
 CC Query Match 88.6%; Score 31; DB 1; Length 368;
 CC Best Local Similarity 100.0%; Pred. No. 97;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 2 DMSFL 6
 CC DB 2 DMSFL 6
 CC
 CC RESULT 12
 CC ID LYS1_CANAL STANDARD; PRT; 382 AA.
 CC AC P43065;
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
 CC DT 01-NOV-1995 (Rel. 32, Last annotation update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Saccharomyces dehydrogenase [NAD+, L-lysine forming] (EC 1.5.1.7)
 CC DE (Lysine--2-oxoglutarate reductase) (SDH).
 CC OS Saccharomyces cerevisiae.
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC CC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 CC CC NCBI_TaxId=5476;
 CC RN NCB1_TaxId=5476;
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=95012722; PubMed=7927784;
 CC RA Garrard R.C., Schmidt T.M., Bhattacharjee J.K.;
 CC RT "Molecular and functional analysis of the LYS1 gene of Candida
 CC albicans."
 CC Infect. Immun. 62:5027-5031(1994).
 CC -1- CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine + NAD(+) +
 CC + H(2)O = L-lysine + 2-oxoglutarate + NADH.
 CC -1- PATHWAY: Lysine biosynthesis; alpha-aminoacidic acid pathway;
 CC eighth (last) step.
 CC -1- SUBUNIT: Monomer (by similarity).
 CC -1- SIMILARITY: TO OTHER FUNGAL SACCHAROPINE DEHYDROGENASE.
 CC -----
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DR EMBL, U13233; AAA21362.1; -
 DR InterPro: IPR004002; Aladh_PNT.
 DR Pfam: PF01262; Aladh_PNT_C; 1.
 DR Pfam: PF05222; Aladh_PNT_N; 1.
 KM Lysine biosynthesis; Oxidoreductase; NAD.
 FT ACT SITE 217 BY SIMILARITY
 SQ SEQUENCE 382 AA; 42394 MW; A3620191DF04888F CRC64;

Query Match 88.6%; Score 31; DB 1; Length 382;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DMSF 5
 DB 151 DMSF 155

RESULT 13
 P2C4_SCHPO STANDARD; PRT; 383 AA.
 AC 014156; Q9UR02;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein phosphatase 2C homolog 4 (EC 3.1.3.16) (PP2C-4).
 GN PTC4 OR SPAC4A8.03C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 NC NCB1_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., SUBUNIT, SUBCELLULAR LOCATION, AND FUNCTION.
 RC STRAIN=972;
 RX MEDLINE=99365157; PubMed=10436019;
 RA Gaiter F., Ruseell P.;
 RT "vacuole fusion regulated by protein phosphatase 2C in fission
 RL yeast." Mol. Biol. Cell 10:2647-2654(1999).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21648401; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Baaham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Mount S., Mungall K., Murphy L., Niblett D., Odeil C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowtsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkert G., Aert R., Robben J., Grynoprez B.,
 RA Wellens I., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wandt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Drenth S., Gloux S., Lelubre V., Mottler S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucan M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
 RA Cernetti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Useery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: HAS A ROLE IN THE REGULATION OF VACUOLE FUSION.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- CORFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND, VACUOLAR.
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
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DR EMBL, AF140285; AAD27651.1; -
 DR EMBL, Z98762; CAB58554.1; -
 DR PIR, T38772; T38772.
 DR GenedB Spombe; SPAC4A8.03C; -
 DR InterPro: IPR001932; PP2C-like.
 DR InterPro: IPR000222; PP2C.
 DR Pfam: PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C_SIG; 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KM Hydrolyase; Magnesium; Manganese; Membrane; Multigene family.
 FT METAL 92
 FT METAL 308
 FT METAL 347
 FT METAL 347
 SQ SEQUENCE 383 AA; 43569 MW; 88B0CC2BD4E49BF CRC64;

Query Match 88.6%; Score 31; DB 1; Length 383;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSF 6
 DB 299 DMSF 303

RESULT 14
 CXAB_CHICK STANDARD; PRT; 399 AA.
 AC P36381; O92144;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gap junction alpha-8 protein (Connexin 45.6) (CX45.6).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCB1_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=lens;
 RX MEDLINE=94325667; PubMed=8049527;
 RA Jiang J.X., White T.W., Goodenough D.A., Paul D.L.;
 RT "Molecular cloning and functional characterization of chick lens
 RT fiber connexin 45.6." Mol. Biol. Cell 5:363-373(1994).
 RL [2]
 RN SEQUENCE OF 1-235 FROM N.A.
 RP TISSUE=lens fibers;
 RC TISSUE=lens fibers;
 RX MEDLINE=96437509; PubMed=8840185;
 RA Sawada K., Agata K., Eguchi G.;
 RT "Characterization of terminally differentiated cell state by
 RT categorizing cDNA clones derived from chicken lens fibers.";
 RL Int. J. Dev. Biol. 40:531-535(1996).

```

CC -1- FUNCTION: One gap junction consists of a cluster of closely packed
CC pairs of transmembrane channels, the connexons, through which
CC materials of low mw diffuse from one cell to a neighboring cell.
CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; L24799; AAA57134.1; -
DR EMBL; D26333; BAA05381.1; -
DR PIR; I50219; I50219.
DR InterPro; IPR000500; Connexin.
DR InterPro; IPR002266; Connexin50.
DR Pfam; PF03509; Connexin50; 1.
DR Pfam; PF00029; connexin; 1.
DR PRINTS; PRO0206; CONNEXIN.
DR SMART; SM00037; CNX; 1.
DR PROSITE; PS00407; CONNEXINS_1; 1.
DR PROSITE; PS00408; CONNEXINS_2; 1.
KM Gap junction; Transmembrane.
FT INIT MET 0 0 BY SIMILARITY.
FT DOMAIN 1 19 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 20 42 POTENTIAL.
FT DOMAIN 43 73 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 74 96 POTENTIAL.
FT DOMAIN 97 151 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 152 174 POTENTIAL.
FT DOMAIN 175 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 229 POTENTIAL.
FT DOMAIN 230 399 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 145 146 EG -> DL (IN REF. 2).
FT CONFLICT 187 188 WP -> D (IN REF. 2).
FT CONFLICT 233 235 IRR -> SEL (IN REF. 2).
SQ SEQUENCE 399 AA; 45485 MW; 4197392ADB6CB5CA CRC64;

Query Match 88.6%; Score 31; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSFL 6
DB 2 DMSFL 6

RESULT 15
NUCM_PROT1 STANDARD; PRT; 400 AA.
AC Q37619;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 49 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.5.3) (NADH dehydrogenase subunit 7).
GN NAD7.
OS Prototheca wickerhamii.
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Prototheca.
OC NCBI_TaxID=3111;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=263-11;
RX MEDLINE=94180393; PubMed=8133522;
RA Wolff G., Planke I., Lang B.F., Kueck U., Burger G.;
RT "Complete sequence of the mitochondrial DNA of the chlorophyte alga

```

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RT Prototheca wickerhamii. Gene content and genome organization.";
RL J. Mol. Biol. 237:75-86(1994).
CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE. COMPONENT OF THE IRON-SULFUR (IP) FRAGMENT OF
CC THE ENZYME.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 49 kDa SUBUNIT FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U02970; AAD12640.1; -
DR PIR; T11921; T11921.
DR InterPro; IPR001135; Oxidored.49kDa.
DR Pfam; PF00346; complex1_49kd; 1.
DR PROSITE; PS00535; COMPLEX1_49K; 1.
KM Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 400 AA; 45810 MW; 7227458F8E80BC9D2 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSF 5
DB 221 LDMSF 225

Search completed: February 18, 2004, 14:28:12
Job time : 4.55263 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35

Sequence: 1 LDMSFL 6

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PTCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/PTCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US09D_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppa/US10D_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	10 US-09-847-940B-14	Sequence 14, Appl
2	35	100.0	6	11 US-09-847-946A-14	Sequence 14, Appl
3	33	94.3	218	12 US-10-032-189-107	Sequence 107, Appl
4	33	94.3	218	12 US-09-863-776-50	Sequence 50, Appl
5	33	94.3	218	12 US-09-861-151A-91	Sequence 91, Appl
6	33	94.3	827	12 US-10-347-470A-26	Sequence 26, Appl
7	32	91.4	6	10 US-09-847-940B-15	Sequence 15, Appl
8	32	91.4	6	11 US-09-847-946A-15	Sequence 15, Appl
9	32	91.4	56	10 US-09-764-877-1782	Sequence 1782, Ap
10	32	91.4	56	12 US-10-242-515-1782	Sequence 1782, Ap
11	32	91.4	743	12 US-10-104-047-2340	Sequence 2340, Ap
12	31	88.6	124	9 US-09-925-302-460	Sequence 460, Appl
13	31	88.6	157	10 US-09-738-626-4783	Sequence 4783, Ap
14	31	88.6	184	15 US-10-078-770-86	Sequence 86, Appl
15	31	88.6	238	15 US-10-078-770-96	Sequence 96, Appl

16	31	88.6	264	12 US-10-097-111-300	Sequence 300, Appl
17	31	88.6	305	15 US-10-078-770-90	Sequence 90, Appl
18	31	88.6	317	12 US-10-032-189-32	Sequence 32, Appl
19	31	88.6	358	12 US-10-438-537-4	Sequence 4, Appl1
20	31	88.6	358	12 US-10-295-027-1228	Sequence 1228, Ap
21	31	88.6	413	12 US-10-032-189-106	Sequence 106, Appl
22	31	88.6	416	12 US-10-032-189-105	Sequence 105, Appl
23	31	88.6	417	12 US-10-032-189-104	Sequence 104, Appl
24	31	88.6	433	12 US-09-863-776-48	Sequence 48, Appl
25	31	88.6	435	12 US-10-032-189-102	Sequence 102, Appl
26	31	88.6	435	12 US-10-032-189-103	Sequence 103, Appl
27	31	88.6	515	12 US-10-108-260A-3041	Sequence 3041, Ap
28	31	88.6	1025	12 US-10-345-072-7	Sequence 7, Appl1
29	31	88.6	1025	15 US-10-195-144-7	Sequence 7, Appl1
30	31	88.6	1285	12 US-10-369-493-12354	Sequence 12354, A
31	30	85.7	6	10 US-09-847-940B-2	Sequence 2, Appl1
32	30	85.7	6	11 US-09-847-946A-2	Sequence 2, Appl1
33	30	85.7	6	11 US-09-847-946A-33	Sequence 33, Appl1
34	30	85.7	7	11 US-09-847-946A-37	Sequence 37, Appl1
35	30	85.7	8	11 US-09-847-946A-30	Sequence 30, Appl1
36	30	85.7	8	11 US-09-847-946A-38	Sequence 38, Appl1
37	30	85.7	9	11 US-09-847-946A-29	Sequence 29, Appl1
38	30	85.7	9	11 US-09-847-946A-32	Sequence 32, Appl1
39	30	85.7	9	11 US-09-847-946A-35	Sequence 35, Appl1
40	30	85.7	9	11 US-09-847-946A-36	Sequence 36, Appl1
41	30	85.7	10	11 US-09-847-946A-31	Sequence 31, Appl1
42	30	85.7	10	11 US-09-847-946A-34	Sequence 34, Appl1
43	30	85.7	11	11 US-09-847-946A-28	Sequence 28, Appl1
44	30	85.7	11	11 US-09-847-946A-132	Sequence 132, Appl
45	30	85.7	11	11 US-09-847-946A-140	Sequence 140, Appl

ALIGNMENTS

RESULT 1
US-09-847-940B-14
Sequence 14, Application US/09847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PFI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-14
Query Match 100.0%; Score 35; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0;
QY 1 LDMSFL 6
Db 1 LDMSFL 6
RESULT 2
US-09-847-946A-14
Sequence 14, Application US/09847946A
Patent No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J

APPLICANT: Ghosh, Sanjay
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PFI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NBD peptide
US-09-847-946A-14

Query Match 100.0%; Score 35; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
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Db 1 LDMSFL 6

RESULT 3
US-10-032-189-107
Sequence 107, Application US/10032189
Publication No. US20030170630A1

GENERAL INFORMATION:

APPLICANT: Alsebrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zethusen, Bryan D
APPLICANT: Paturajan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Shinkels, Richard A
APPLICANT: Grose, William M
APPLICANT: Szekeres, Edward S
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Caeman, Stacie J
APPLICANT: Boldog, Ferenc L
APPLICANT: Gorman, Linda
APPLICANT: Gangoli, Esha A
APPLICANT: Fernandes, Elma R
APPLICANT: Rieger, Daniel K
APPLICANT: Edinger, Shlomit R
APPLICANT: Gunther, Erik
APPLICANT: Millet, Isabelle
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: 60/274,192
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/277,826
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/282,981
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/309,247
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/311,754
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 107
LENGTH: 218
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Connexin
US-10-032-189-107

Query Match 94.3%; Score 33; DB 12; Length 218;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
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Db 1 LDMSFL 6

RESULT 4
US-09-863-776-50
Sequence 50, Application US/09863776
Publication No. US20030198953A1

GENERAL INFORMATION:

APPLICANT: Spytek, Kimberly A
APPLICANT: Majumder, Kumud
APPLICANT: Tchernev, Velizar T
APPLICANT: Mishra, Vishnu
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spaderna, Steven K
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Li, Li
APPLICANT: Taupier, Raymond J
APPLICANT: Gangoli, Esha
TITLE OF INVENTION: No. US20030198953A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-020
CURRENT APPLICATION NUMBER: US/09/863,776
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 09/540,763
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/206,679
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/206,688
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/206,829
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/207,748
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 60/207,798
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 60/208,263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 60/208,831
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/209,451

PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/210,060
PRIOR FILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: 60/219,507
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 60/221,337
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/221,927
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 60/263,135
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,688
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/263,694
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 218
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Connexin
US-09-863-776-50

Query Match 94.3%; Score 33; DB 12; Length 218;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
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Db 1 MDMSFL 6

RESULT 5
US-09-981-151A-91
Sequence 91, Application US/09981151A
Publication No. US20030212256A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit R
APPLICANT: Gerlach, Valerie
APPLICANT: Macdougall, John R
APPLICANT: Malyanekar, Muriel M
APPLICANT: Smithson, Glenda
APPLICANT: Miller, Isabelle
APPLICANT: Peyman, John A
APPLICANT: Stone, David J
APPLICANT: Gunther, Erik
APPLICANT: Rilleman, Karen
APPLICANT: Shlomek, Richard A
APPLICANT: Padigaru, Muralidhara
APPLICANT: Guo, Xiaojie
APPLICANT: Patturajan, Meera
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Burgess, Catherine E
APPLICANT: Zerhusen, Bryan D
APPLICANT: Kekuda, Ramesh
APPLICANT: Spytek, Kimberly A
APPLICANT: Gangoli, Esha A
APPLICANT: Fernandes, Elma R
APPLICANT: Gorman, Linda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-168
CURRENT APPLICATION NUMBER: US/09/981,151A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/241,040
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/241,058
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/241,063
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/241,243

PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/242,152
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/242,482
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,611
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,612
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,880
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,881
PRIOR FILING DATE: 2000-10-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 91
LENGTH: 218
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Connexin
US-09-981-151A-91

Query Match 94.3%; Score 33; DB 12; Length 218;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
:|||||
Db 1 MDMSFL 6

RESULT 6
US-10-347-470A-26
Sequence 26, Application US/10347470A
Publication No. US20040002054A1
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Hwang, Ho Yon
TITLE OF INVENTION: SOY NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 01997/542003
CURRENT APPLICATION NUMBER: US/10/347,470A
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: US 60/349,630
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/390,930
PRIOR FILING DATE: 2002-06-24
SOFTWARE: FastSeq for Windows Version 4.0
NUMBER OF SEQ ID NOS: 81
SEQ ID NO 26
LENGTH: 827
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-10-347-470A-26

Query Match 94.3%; Score 33; DB 12; Length 827;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
:|||||
Db 370 LDMSFL 375

RESULT 7
US-09-847-940B-15
Sequence 15, Application US/09847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar

;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-117CP
;; CURRENT APPLICATION NUMBER: US/09/847,940B
;; CURRENT FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: 09/643,260
;; PRIOR FILING DATE: 2000-08-22
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 15
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-15

Query Match 91.4%; Score 32; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 LDMSPL 6
Db 1 LDMSYL 6

RESULT 8
US-09-847-946A-15
;; Sequence 15, Application US/09847946A
;; Publication No. US20030054999A1
;; GENERAL INFORMATION:
;; APPLICANT: May, Michael J
;; APPLICANT: Ghosh, Sankar
;; APPLICANT: Findeis, Mark A
;; APPLICANT: Phillips, Kathryn
;; APPLICANT: Hannig, Gerhard
;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;; FILE REFERENCE: PPI-119
;; CURRENT APPLICATION NUMBER: US/09/847,946A
;; CURRENT FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: 60/201,261
;; PRIOR FILING DATE: 2000-05-02
;; PRIOR APPLICATION NUMBER: 09/643,260
;; PRIOR FILING DATE: 2000-08-22
;; NUMBER OF SEQ ID NOS: 160
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 15
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-15

Query Match 91.4%; Score 32; DB 11; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 LDMSPL 6
Db 1 LDMSYL 6

RESULT 9
US-09-764-877-1782
;; Sequence 1782, Application US/09764877
;; Patent No. US20020147140A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC005
;; CURRENT APPLICATION NUMBER: US/09/764,877
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - refer to PALM or file wrapper

;; NUMBER OF SEQ ID NOS: 4031
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1782
;; LENGTH: 56
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (51)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (56)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1782

Query Match 91.4%; Score 32; DB 10; Length 56;
Best Local Similarity 83.3%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 LDMSPL 6
Db 27 LDMSYL 32

RESULT 10
US-10-242-515-1782
;; Sequence 1782, Application US/10242515
;; Publication No. US20040009488A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC005C1
;; CURRENT APPLICATION NUMBER: US/10/242,515
;; CURRENT FILING DATE: 2002-09-13
;; PRIOR APPLICATION NUMBER: 09/764,877
;; PRIOR FILING DATE: 2001-01-17
;; PRIOR APPLICATION NUMBER: 60/179,065
;; PRIOR FILING DATE: 2000-01-31
;; PRIOR APPLICATION NUMBER: 60/180,628
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: 60/214,886
;; PRIOR FILING DATE: 2000-06-28
;; PRIOR APPLICATION NUMBER: 60/217,487
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/225,758
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/220,963
;; PRIOR FILING DATE: 2000-07-26
;; PRIOR APPLICATION NUMBER: 60/217,496
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/225,447
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/218,290
;; PRIOR FILING DATE: 2000-07-14
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 4031
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1782
;; LENGTH: 56
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (51)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (56)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-515-1782

Query Match 91.4%; Score 32; DB 12; Length 56;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSFL 6
Db 27 LDMSFL 32

RESULT 11
US-10-104-047-2340
; Sequence 2340, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2340
; LENGTH: 743
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2340

Query Match 91.4%; Score 32; DB 12; Length 743;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
Db 98 VDMSFL 103

RESULT 12
US-09-925-302-460
; Sequence 460, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 460
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (119)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-460

Query Match 88.6%; Score 31; DB 9; Length 124;
Best Local Similarity 100.0%; Pred. No. 5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DMSFL 6
Db 50 DMSFL 54

RESULT 13
US-09-738-626-4783
; Sequence 4783, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAMA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4783
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4783

Query Match 88.6%; Score 31; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 5
Db 72 LDMSFL 76

RESULT 14
US-10-078-770-86
; Sequence 86, Application US/10078770
; Publication No. US20030003471A1
; GENERAL INFORMATION:
; APPLICANT: Farnodu, Omojayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: CDNAS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/10/078,770
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01

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; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 86
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (98)
; NAME/KEY: UNSURE
; LOCATION: (104)..(105)
; NAME/KEY: UNSURE
; LOCATION: (115)
; NAME/KEY: UNSURE
; LOCATION: (117)
; NAME/KEY: UNSURE
; LOCATION: (123)
; NAME/KEY: UNSURE
; LOCATION: (126)..(127)
; NAME/KEY: UNSURE
; LOCATION: (136)
; NAME/KEY: UNSURE
; LOCATION: (159)
; NAME/KEY: UNSURE
; LOCATION: (174)..(175)
; US-10-078-770-86
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Query Match      88.6%; Score 31; DB 15; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDMSF 5
         |||||
Db      18 LDMSF 22
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RESULT 15
US-10-078-770-96
; Sequence 96, Application US/10078770
; Publication No. US20030003471A1
; GENERAL INFORMATION:
; APPLICANT: Farnodu, OmoIayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: CDMS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/10/078,770
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 96
; LENGTH: 238
; TYPE: PRT
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; ORGANISM: Zea mays
US-10-078-770-96
Query Match      88.6%; Score 31; DB 15; Length 238;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDMSF 5
         |||||
Db      26 LDMSF 30
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Search completed: February 18, 2004, 15:42:00
Job time : 17.7529 secs
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35

Sequence: 1 LDMSFL 6

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*

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6: /cgn2_6/ptodata/1/1aa/backflist1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	91.4	829	4 US-09-252-991A-27150	Sequence 27150, A
2	31	88.6	86	4 US-09-107-532A-7054	Sequence 7054, Ap
3	31	88.6	277	1 US-08-118-270-68	Sequence 68, Appl
4	31	88.6	277	5 PCT-US93-08528-68	Sequence 68, Appl
5	31	88.6	382	2 US-08-360-606B-30	Sequence 30, Appl
6	30	85.7	177	4 US-09-328-352-5063	Sequence 5063, Ap
7	30	85.7	365	4 US-09-328-352-7147	Sequence 7147, Ap
8	30	85.7	397	4 US-09-107-532A-4918	Sequence 4918, Ap
9	30	85.7	413	4 US-09-328-352-7815	Sequence 7815, Ap
10	30	85.7	745	2 US-08-887-518-3	Sequence 3, Appl
11	30	85.7	745	2 US-09-023-321-3	Sequence 3, Appl
12	30	85.7	745	2 US-08-890-853-4	Sequence 4, Appl
13	30	85.7	745	2 US-09-032-475-3	Sequence 3, Appl
14	30	85.7	745	2 US-09-099-125A-4	Sequence 4, Appl
15	30	85.7	745	2 US-09-099-124A-4	Sequence 4, Appl
16	30	85.7	745	3 US-09-032-476-4	Sequence 4, Appl
17	30	85.7	745	3 US-08-890-854-4	Sequence 4, Appl
18	30	85.7	745	3 US-09-023-324-4	Sequence 4, Appl
19	30	85.7	745	3 US-09-168-629-2	Sequence 2, Appl
20	30	85.7	745	3 US-08-910-820-10	Sequence 10, Appl
21	30	85.7	745	3 US-08-810-131A-2	Sequence 2, Appl
22	30	85.7	745	4 US-09-109-986-4	Sequence 4, Appl
23	30	85.7	745	4 US-09-844-908-10	Sequence 10, Appl
24	30	85.7	745	4 US-09-868-758-3	Sequence 3, Appl
25	30	85.7	756	2 US-08-887-518-4	Sequence 4, Appl
26	30	85.7	756	2 US-09-023-321-4	Sequence 2, Appl
27	30	85.7	756	2 US-08-890-853-2	Sequence 2, Appl

28	30	85.7	756	2 US-09-032-475-4	Sequence 4, Appl
29	30	85.7	756	2 US-09-099-125A-2	Sequence 2, Appl
30	30	85.7	756	2 US-09-099-124A-2	Sequence 2, Appl
31	30	85.7	756	3 US-09-032-476-2	Sequence 2, Appl
32	30	85.7	756	3 US-08-890-854-2	Sequence 2, Appl
33	30	85.7	756	3 US-09-023-324-2	Sequence 2, Appl
34	30	85.7	756	3 US-09-168-629-15	Sequence 15, Appl
35	30	85.7	756	3 US-08-910-820-9	Sequence 9, Appl
36	30	85.7	756	4 US-09-109-986-2	Sequence 2, Appl
37	30	85.7	756	4 US-09-844-908-9	Sequence 9, Appl
38	30	85.7	756	4 US-09-868-758-4	Sequence 4, Appl
39	30	85.7	768	2 US-08-222-617A-5	Sequence 5, Appl
40	30	85.7	996	4 US-09-417-197-123	Sequence 123, App
41	30	85.7	997	4 US-09-417-197-121	Sequence 121, App
42	30	85.7	3666	2 US-08-222-617A-12	Sequence 12, Appl
43	30	85.7	3727	2 US-08-222-617A-27	Sequence 27, Appl
44	30	85.7	3778	2 US-08-222-617A-2	Sequence 2, Appl
45	29	82.9	70	3 US-09-242-050-4	Sequence 4, Appl

ALIGNMENTS

```

RESULT 1
US-09-252-991A-27150
; Sequence 27150, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfeld et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR APPLICATION NUMBER: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27150
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27150

Query Match      91.4%; Score 32; DB 4; Length 829;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSFL 6
Db      486 LDMSYL 491

RESULT 2
US-09-107-532A-7054
; Sequence 7054, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDING ADDRESSES:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC

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OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107.532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arietello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7054:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...86
SEQUENCE DESCRIPTION: SEQ ID NO: 7054:
US-09-107-532A-7054

Query Match 88.6%; Score 31; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWSF 5
DB 42 DWSF 46

RESULT 3
US-08-118-270-68
Sequence 68, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-68

Query Match 88.6%; Score 31; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
DB 81 DWSFL 85

RESULT 4
PCT-US93-08528-68
Sequence 68, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-68

Query Match 88.6%; Score 31; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
DB 81 DWSFL 85

RESULT 5
US-08-360-606B-30
Sequence 30, Application US/08360606B
Patent No. 5919617
GENERAL INFORMATION:
APPLICANT: Jnanendra K. Bhattacharjee
APPLICANT: Richard C. Garrad
APPLICANT: Paul L. Skatrud
APPLICANT: Robert P. Peery
TITLE OF INVENTION: Methods and Reagents for
TITLE OF INVENTION: Detecting Fungal Pathogens in a
TITLE OF INVENTION: Biological Sample
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive Suite 3200
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,606B
FILING DATE: December 21, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berghoff, Paul H.
REGISTRATION NUMBER: 30,243
REFERENCE/DOCKET NUMBER: 94,319
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: yes
HYPOTHETICAL: yes
ORIGINAL SOURCE:
ORGANISM: Candida albicans
US-08-360-606B-30

Query Match 88.6%; Score 31, DB 2, Length 382;
Best Local Similarity 100.0%; Pred. No. 4,3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSF 5
DB 151 LDMSF 155

RESULT 6
US-09-328-352-5063
Sequence 5063, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNIT FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5063
LENGTH: 177
TYPE: PRT

ORGANISM: Acinetobacter baumannii
US-09-328-352-5063

Query Match 85.7%; Score 30; DB 4, Length 177;
Best Local Similarity 66.7%; Pred. No. 2,9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 137 IDMTFL 142

RESULT 7
US-09-328-352-7147
Sequence 7147, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNIT FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7147
LENGTH: 365
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-7147

Query Match 85.7%; Score 30; DB 4, Length 365;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 23 LDMSFL 28

RESULT 8
US-09-107-532A-4918
Sequence 4918, Application US/09107532A
Patent No. 6563275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucetle-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4918:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...397
SEQUENCE DESCRIPTION: SEQ ID NO: 4918:
US-09-107-532A-4918

Query Match 85.7%; Score 30; DB 4; Length 397;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
: : : :
Db 233 IDMTFL 238

RESULT 9
US-09-328-352-7815
Sequence 7815, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7815
LENGTH: 413
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-7815

Query Match 85.7%; Score 30; DB 4; Length 413;
Best Local Similarity 66.7%; Pred. No. 6.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
: : : :
Db 183 IDMTFL 188

RESULT 10
US-08-887-518-3
Sequence 3, Application US/08887518
Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
: : : :
Db 738 LDMSWL 743

RESULT 11
US-09-023-321-3
Sequence 3, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
Db 738 LDMSWL 743

RESULT 12

US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V.
; APPLICANT: Moronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890.853
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-890-853-4

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
Db 738 LDMSWL 743

RESULT 13

US-09-032-475-3
; Sequence 3, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Mu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO

STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
Db 738 LDMSWL 743

RESULT 14

US-09-099-125A-4
; Sequence 4, Application US/09099125A
; Patent No. 5916760
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V.
; APPLICANT: Moronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,125A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:

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Job time : 7.06579 secs.

TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
Db 738 LDMSWL 743

RESULT 15
US-09-099-124A-4
Sequence 4, Application US/09099124A
Patent No. 5839302
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,124A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-124A-4

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
Db 738 LDMSWL 743

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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
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35.929 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDMSAL 6

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptcdatc/1/1aa/6A.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	93.9	502	4	US-09-635-872A-13
2	31	93.9	502	4	US-09-636-077A-13
3	30	90.9	118	4	US-08-311-731A-240
4	30	90.9	516	4	US-09-277-262-2
5	30	90.9	735	4	US-09-252-991A-32240
6	30	90.9	1891	2	US-08-804-227C-12
7	30	90.9	1891	2	US-08-804-198-6
8	29	87.9	201	1	US-07-929-580B-5
9	29	87.9	223	1	US-07-708-885B-3
10	29	87.9	223	1	US-07-714-386-3
11	29	87.9	223	1	US-07-708-888A-3
12	29	87.9	268	4	US-09-252-991A-30879
13	29	87.9	297	4	US-09-172-952-10
14	29	87.9	345	3	US-08-858-003-14
15	29	87.9	345	3	US-08-166-166-34
16	29	87.9	345	3	US-08-997-467-34
17	29	87.9	352	4	US-09-198-452A-702
18	29	87.9	464	4	US-09-252-991A-29305
19	29	87.9	480	4	US-09-252-991A-17687
20	29	87.9	529	4	US-09-252-991A-29757
21	29	87.9	703	4	US-09-252-991A-17865
22	29	87.9	1580	2	US-08-804-227C-11
23	29	87.9	1580	2	US-08-804-198-5
24	29	87.9	3729	2	US-08-804-227C-4
25	28	84.8	208	4	US-08-631-607-3
26	28	84.8	208	4	US-09-098-358B-3
27	28	84.8	536	4	US-09-252-991A-31124

28	28	84.8	1151	4	US-09-252-991A-23596	Sequence 23596, A
29	28	84.8	1843	3	US-09-413-814-50	Sequence 50, Appl
30	28	84.8	2595	3	US-09-036-987A-2	Sequence 2, Appl
31	28	84.8	2595	3	US-09-370-700-2	Sequence 2, Appl
32	28	84.8	2595	3	US-09-603-207-2	Sequence 2, Appl
33	28	84.8	3248	1	US-08-353-700-1	Sequence 1, Appl
34	28	84.8	3248	5	PCT-US95-16216-1	Sequence 1, Appl
35	27	81.8	29	3	US-09-082-279B-1276	Sequence 1276, Ap
36	27	81.8	29	4	US-09-315-304B-1276	Sequence 1276, Ap
37	27	81.8	29	4	US-09-834-784-1276	Sequence 1276, Ap
38	27	81.8	35	3	US-09-082-279B-1427	Sequence 1427, Ap
39	27	81.8	35	4	US-09-315-304B-1427	Sequence 1427, Ap
40	27	81.8	35	4	US-09-834-784-1427	Sequence 1427, Ap
41	27	81.8	45	3	US-09-040-285A-9	Sequence 9, Appl
42	27	81.8	80	3	US-09-040-285A-3	Sequence 3, Appl
43	27	81.8	111	4	US-09-107-532A-5707	Sequence 5707, Ap
44	27	81.8	209	3	US-09-040-285A-8	Sequence 8, Appl
45	27	81.8	229	3	US-09-040-285A-7	Sequence 7, Appl

ALIGNMENTS

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RESULT 1
US-09-635-872A-13
; Sequence 13, Application US/09635872A
; Patent No. 6534300
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASE:
; FILE REFERENCE: 195613US0
; CURRENT APPLICATION NUMBER: US/09/635, 872A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153, 831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-635-872A-13

Query Match          93.9%; Score 31; DB 4; Length 502;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
Db      372 LDMSAM 377

RESULT 2
US-09-636-077A-13
; Sequence 13, Application US/09636077A
; Patent No. 653785
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
; FILE REFERENCE: 195612US0
; CURRENT APPLICATION NUMBER: US/09/636, 077A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153, 831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-636-077A-13

Query Match          93.9%; Score 31; DB 4; Length 502;

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Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 372 LDMSAM 377

RESULT 3

US-08-311-731A-240
Sequence 240, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 240:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Mycobacterium leprae
US-08-311-731A-240

Query Match 90.9%; Score 30; DB 4; Length 118;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 93 LDMSAV 98

RESULT 4

US-09-277-262-2
Sequence 2, Application US/09277262
Patent No. 6395482
GENERAL INFORMATION:
APPLICANT: KAREYIORGOU, Maria
APPLICANT: GOGOS, JOSEPH A
TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
FILE REFERENCE: 600-1-223 CIP

CURRENT APPLICATION NUMBER: US/09/277,262
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/229,530
EARLIER FILING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 516
TYPE: PRT
ORGANISM: Homo sapiens
US-09-277-262-2

Query Match 90.9%; Score 30; DB 4; Length 516;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 231 LDMSL 236

RESULT 5

US-09-252-991A-32240
Sequence 32240, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. RUBENFIELD et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,116
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32240
LENGTH: 735
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32240

Query Match 90.9%; Score 30; DB 4; Length 735;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 379 VDMSAL 384

RESULT 6

US-08-804-227C-12
Sequence 12, Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: DEHOFF, BRADLEY S.
APPLICANT: KUHSTOSS, STUART A.
APPLICANT: ROSECK, PAUL R., Jr.
APPLICANT: SUTTON, KIMBERLY L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1891 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-227C-12

Query Match 90.9%; Score 30; DB 2; Length 1891;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMWAL 6
DB 904 LDMWAL 909

RESULT 7
US-08-804-198-6
Sequence 6, Application US/08804198
Patent No. 5945320
GENERAL INFORMATION:
APPLICANT: Burgett, Stanley G.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rao, Negaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Roelbeck, Paul R., Jr.
TITLE OF INVENTION: PLATENOIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1891 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-198-6

Query Match 90.9%; Score 30; DB 2; Length 1891;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMWAL 6
DB 904 LDMWAL 909

RESULT 8
US-07-929-580B-5
Sequence 5, Application US/07929580B
Patent No. 5426181
GENERAL INFORMATION:
APPLICANT: Lee, Tae Ho
APPLICANT: Lee, Gene W.
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-14,
TITLE OF INVENTION: DNA Coding Therefor and Uses Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Broadway and Nelmark
STREET: 419 Seventh Street, NW
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/929,580B
FILING DATE: 19920814
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/640,492
FILING DATE: 14-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Guy Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: LEE25/VILCEK-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-929-580B-5

Query Match 87.9%; Score 29; DB 1; Length 201;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMWAL 6
DB 180 LDMWAL 185

RESULT 9
US-07-708-885B-3
Sequence 3, Application US/07708885B
Patent No. 5245017
GENERAL INFORMATION:
APPLICANT: Maswoswe, Sibusiswe M.
APPLICANT: Brigman, Joseph V.
APPLICANT: Toch, Carol A.
APPLICANT: Thomas, Peter
TITLE OF INVENTION: Method for Isolating
TITLE OF INVENTION: CEA-Binding Protein

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720kb storage
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/708,8858
FILING DATE: 19910531
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: C-reactive protein
PUBLICATION INFORMATION:
AUTHORS: Lei, Ke-Jian
AUTHORS: Liu, Teresa
AUTHORS: Zou, Gerald
AUTHORS: Soravia, Emilia
AUTHORS: Liu, Teh-Yung
AUTHORS: Goldman, Neil D.
TITLE: Genomic Sequence for Human
JOURNAL: J. of Biological Chemistry
VOLUME: 260
ISSUE: 24
PAGES: 13377-83
DATE: 25 OCT 1985
US-07-708-885B-3

Query Match 87.9%; Score 29; DB 1; Length 223;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSAL 6
DB 202 LDWQAL 207

RESULT 10
US-07-714-386-3
Sequence 3, Application US/07114386
Patent No. 5278290
GENERAL INFORMATION:
APPLICANT: Thomas, Peter
APPLICANT: Toth, Carol A.
APPLICANT: Maswowe, Sibusisiwe M.
APPLICANT: Brigman, Joseph V.
TITLE OF INVENTION: Binding Protein for
NUMBER OF SEQUENCES: 4
NUMBER OF INVENTION: CEA and Uses Thereof
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720kb storage
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/708,8858
FILING DATE: 19910531
PRIOR APPLICATION DATA:

MEDIUM TYPE: Diskette, 3.5 inch, 720kb storage
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/714,386
FILING DATE: 19910531
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: C-reactive protein
PUBLICATION INFORMATION:
AUTHORS: Lei, Ke-Jian
AUTHORS: Liu, Teresa
AUTHORS: Zou, Gerald
AUTHORS: Soravia, Emilia
AUTHORS: Liu, Teh-Yung
AUTHORS: Goldman, Neil D.
TITLE: Genomic Sequence for Human
JOURNAL: J. of Biological Chemistry
VOLUME: 260
ISSUE: 24
PAGES: 13377-83
DATE: 25 OCT 1985
US-07-714-386-3

Query Match 87.9%; Score 29; DB 1; Length 223;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSAL 6
DB 202 LDWQAL 207

RESULT 11
US-07-708-888A-3
Sequence 3, Application US/07708888A
Patent No. 5281697
GENERAL INFORMATION:
APPLICANT: Toth, Carol A.
APPLICANT: Thomas, Peter
APPLICANT: Maswowe, Sibusisiwe M.
APPLICANT: Brigman, Joseph V.
TITLE OF INVENTION: CEA-Binding Protein
NUMBER OF SEQUENCES: 4
NUMBER OF INVENTION: and Uses Thereof
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720kb storage
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/708,888A
FILING DATE: 19910531
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; APPLICATION NUMBER:
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 223 amino acids
;   TYPE: AMINO ACID
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
;   NAME/KEY: C-reactive protein
;   ORGANISM: Pseudomonas aeruginosa
;   AUTHORS: Lei, Ke-Jian
;   AUTHORS: Liu, Teresa
;   AUTHORS: Zou, Gerald
;   AUTHORS: Soravia, Emilia
;   AUTHORS: Liu, Teh-Yung
;   AUTHORS: Goldman, Neil D.
;   TITLE: Genomic Sequence for Human
;   TITLE: C-reactive Protein
;   JOURNAL: Journal of Biological
;   VOLUME: 260
;   ISSUE: 24
;   PAGES: 13377-83
;   DATE: 25 OCT 1985
; US-07-708-888A-3
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Query Match      87.9%: Score 29; DB 1; Length 223;
Best Local Similarity 83.3%: Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 LDMSA 6
        |||||
Db      202 LDMSA 207
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RESULT 12
US-09-252-991A-30879
; Sequence 30879, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenfield et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;   FILE REFERENCE: 107196.136
;   CURRENT APPLICATION NUMBER: US/09/252,991A
;   CURRENT FILING DATE: 1999-02-18
;   PRIOR APPLICATION NUMBER: US 60/074,788
;   PRIOR FILING DATE: 1998-02-18
;   PRIOR APPLICATION NUMBER: US 60/094,190
;   PRIOR FILING DATE: 1998-07-27
;   NUMBER OF SEQ ID NOS: 33142
;   SEQ ID NO 30879
;   LENGTH: 268
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-30879
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Query Match      87.9%: Score 29; DB 4; Length 268;
Best Local Similarity 100.0%: Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDMSA 5
        |||||
Db      135 LDMSA 139
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RESULT 13
US-09-172-952-30
; Sequence 30, Application US/09172952
; Patent No. 6368793
```

```

; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; APPLICANT: Datois, Veronique
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/172,952
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Y14R-Bc
; US-09-172-952-30
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```

Query Match      87.9%: Score 29; DB 4; Length 297;
Best Local Similarity 100.0%: Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 LDMSA 5
        |||||
Db      59 LDMSA 63
```

```

RESULT 14
US-08-858-003-34
; Sequence 34, Application US/08858003
; Patent No. 6060234
; GENERAL INFORMATION:
;   APPLICANT: Katz, Leonard
;   APPLICANT: Scaesi, Diane L.
;   APPLICANT: Summers Jr., Richard G.
;   APPLICANT: Ruan, Xiaozan
;   APPLICANT: Pereda-Lopez, Ana
;   APPLICANT: Kakavas, Stephan J.
;   TITLE OF INVENTION: NOVEL POLYPEPTIDE DERIVATIVES
;   TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
;   NUMBER OF SEQUENCES: 34
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Abbott Laboratories
;   STREET: 100 Abbott Park Rd.
;   CITY: Abbott Park
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60064-3500
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSeq Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/858,003
;   FILING DATE: 16-MAY-1979
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Diane Casuto
;   REGISTRATION NUMBER: P-40,943
;   REFERENCE/DOCKET NUMBER: 4952.US.P2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (847)-938-3137
;   TELEFAX: (847)-938-2623
;   TELEX:
;   INFORMATION FOR SEQ ID NO: 34:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 345 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: NO. 6060234e
; US-08-858-003-34
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Query Match 87.9%; Score 29; DB 3; Length 345;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDM\$AL 6
DB 43 LDM\$VL 48

RESULT 15

US-09-078-166-34

; Sequence 34, Application US/09078166

; Patent No. 6063561

; GENERAL INFORMATION:

; APPLICANT: Katz, Leonard

; APPLICANT: Staszi, Diane L.

; APPLICANT: Summers Jr., Richard G.

; APPLICANT: Ruam, Xiaohu

; APPLICANT: Pereda-Lopez, Ana

; APPLICANT: Kakava, Stephan J.

; TITLE OF INVENTION: NOVEL POLYPEPTIDE DERIVATIVES

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Rd.

; CITY: Abbott Park

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: PasteSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/078,166

; FILING DATE: 16-MAY-1979

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Dianne Casulo

; REGISTRATION NUMBER: P-40,943

; REFERENCE/DOCKET NUMBER: 4952.US.P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (847)-938-3137

; TELEFAX: (847)-938-2623

; TELEX:

; INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 345 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6063561e

; US-09-078-166-34

Query Match 87.9%; Score 29; DB 3; Length 345;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDM\$AL 6
DB 43 LDM\$VL 48

Search completed: February 18, 2004, 14:41:50
Job time : 8.06579 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3664 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	94.4	241	16 Q98D63	Q98D63 rhizobium 1
2	34	94.4	281	16 Q8NVL6	Q8NVL6 staphylococ
3	34	94.4	282	16 Q932C8	Q932C8 staphylococ
4	34	94.4	282	16 Q065S1	Q065S1 mycobacteri
5	33	91.7	195	11 Q8BR0	Q8BR0 mus musculu
6	33	91.7	237	11 Q9JMP2	Q9JMP2 mus musculu
7	33	91.7	263	11 Q9CRS3	Q9CRS3 mus musculu
8	33	91.7	392	11 Q99KPS	Q99KPS mus musculu
9	32	88.9	66	16 Q8CKO2	Q8CKO2 yerinella pe
10	32	88.9	93	12 Q70791	Q70791 rice yellow
11	32	88.9	107	2 Q684S5	Q684S5 ancylobacte
12	32	88.9	138	2 Q8GBK5	Q8GBK5 uncultured
13	32	88.9	138	2 Q8GBK0	Q8GBK0 uncultured
14	32	88.9	138	2 Q8GBJ4	Q8GBJ4 uncultured
15	32	88.9	153	16 Q8XBY6	Q8XBY6 escherichia
16	32	88.9	168	16 Q91265	Q91265 pseudomona

17	32	88.9	179	11 Q8BZU5	Q8BZU5 mus musculu
18	32	88.9	193	12 Q99FU7	Q99FU7 human echov
19	32	88.9	195	5 Q18653	Q18653 caenorhabd1
20	32	88.9	230	10 Q945X8	Q945X8 theobroma c
21	32	88.9	244	10 Q945Y3	Q945Y3 theobroma c
22	32	88.9	248	4 Q96T10	Q96T10 homo sapien
23	32	88.9	250	10 Q945X9	Q945X9 theobroma c
24	32	88.9	251	16 Q9K863	Q9K863 bacillus ha
25	32	88.9	255	10 Q945Y4	Q945Y4 theobroma c
26	32	88.9	255	10 Q945Z3	Q945Z3 theobroma c
27	32	88.9	255	10 Q945Y5	Q945Y5 theobroma c
28	32	88.9	259	16 Q826N5	Q826N5 salmone
29	32	88.9	271	17 Q978V7	Q978V7 thermoplas
30	32	88.9	278	6 Q9XTA8	Q9XTA8 oryctolagus
31	32	88.9	302	16 Q8X8Q1	Q8X8Q1 escherichia
32	32	88.9	312	10 Q9AYF3	Q9AYF3 oryza sativ
33	32	88.9	315	13 Q91838	Q91838 coturnix co
34	32	88.9	349	5 Q17692	Q17692 caenorhabd1
35	32	88.9	379	16 Q82935	Q82935 salmone
36	32	88.9	382	2 Q68661	Q68661 actinobacil
37	32	88.9	382	10 Q8H2C3	Q8H2C3 persea amer
38	32	88.9	383	16 Q8FKN0	Q8FKN0 escherichia
39	32	88.9	386	16 Q84474	Q84474 chlamydia t
40	32	88.9	391	16 P95247	P95247 mycobacteri
41	32	88.9	407	2 Q55047	Q55047 shigella so
42	32	88.9	414	2 Q950Y1	Q950Y1 pleistomonas
43	32	88.9	414	2 Q9F738	Q9F738 shigella so
44	32	88.9	414	11 Q9CXT6	Q9CXT6 mus musculu
45	32	88.9	415	16 Q8VJK7	Q8VJK7 mycobacteri

ALIGNMENTS

RESULT 1

Q98D63 PRELIMINARY, PRT; 241 AA.

AC Q98D63, 01-OCT-2001 (TREMBLrel. 18, Created)

DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Putative hydrolase, ripening-related protein-like.

GN MUR4841.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OX NCBI_Taxid=381;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MAFF303099;

RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Matanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.,

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium

RT Mesorhizobium loti."

RL DNA Res. 7:331-338(2000).

DR EMBL; AP003005; BAB51408.1; -

DR InterPro; IPR006402; HAD-SF-1A-v3.

DR InterPro; IPR005834; Hydrolase.

DR Pfam; PF00702; Hydrolase; 1.

DR TIGRPFAM; TIGR01509; HAD-SF-1A-v3; 1.

KW Hydrolase; Complete proteome.

SQ SEQUENCE 241 AA; 27332 MW; 6AB5B55907CC27A CRC64;

Query Match 94.4%; Score 34; DB 16; Length 241;

Best Local Similarity 83.3%; Pred. No. 1.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 90 LDYSWL 95

RESULT 2

Q8NVL6 PRELIMINARY; PRT; 281 AA.
 ID Q8NVL6
 AC Q8NVL6
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Hypothetical protein MW1944.
 GN MW1944.
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 acquired MRSA.";
 RL Lancet 358:1819-1827 (2002).
 DR EMBL; AP004828; BAB5809.1.-.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 281 AA; 33223 MW; 824E3760C698B42 CRC64;

Query Match 94.4%; Score 34; DB 16; Length 281;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
 DB 132 LDYSWL 137

RESULT 3

Q932C8 PRELIMINARY; PRT; 282 AA.
 ID Q932C8
 AC Q932C8
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein SAV0804.
 GN SAV0804.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Ilan J.-O., Ito T.,
 RA Karamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-U Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hatori M., Ogatawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240 (2001).
 DR EMBL; AP003360; BAB5696.1.-.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 282 AA; 33281 MW; 3529EEF85F1B1A6 CRC64;

Query Match 94.4%; Score 34; DB 16; Length 282;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
 DB 132 LDYSWL 137

RESULT 4
 ID 006551 PRELIMINARY; PRT; 282 AA.
 AC 006551;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical 30.9 kDa protein (O-methyltransferase, putative).
 GN OMT OR RV1153C OR MTC165.20C OR MT1187.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RX MEDLINE=98255987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Baeham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornby T., Jaffe K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolony J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikala A.,
 RA Bhat W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z95584; CAB09012.1.-.
 DR EMBL; AR006966; AKK4544.1.-.
 DR TIGR; MT1187.-.
 DR Tuberculist; RV1153C.-.
 DR InterPro; IPR003455; DUF142.
 DR Pfam; PF02409; Omt N; 1.
 KW Hypothetical protein; Transferase; Methyltransferase;
 KW Complete proteome.
 SQ SEQUENCE 282 AA; 30887 MW; 41760C508774154A CRC64;

Query Match 94.4%; Score 34; DB 16; Length 282;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
 DB 142 LDYSWL 147

RESULT 5

Q8BRRO PRELIMINARY; PRT; 195 AA.
 ID Q8BRRO
 AC Q8BRRO;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA the FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK045045; BAC32196.1; -
KM Hypothetical protein.
SQ SEQUENCE 195 AA; 22669 MW; 6C33550846800762 CRC64;

Query Match 91.7%; Score 33; DB 11; Length 195;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
Db 58 VDYSWL 63

RESULT 6
O9JMF2 PRELIMINARY; PRT; 237 AA.
AC O9JMF2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Unknown protein (Fragment).
GN 3322402L07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20145471; PubMed=10679242;
RA Inoue S., Sano H., Ohta M.;
RT "Growth suppression of Escherichia coli by induction of expression of
RT mammalian genes with transmembrane or Arpase domains."
RL Biochem. Biophys. Res. Commun. 268:553-561(2000).
DR EMBL; AB030195; BAA92758.1; -
DR MGI; MGI:1921273; 3322402L07RIK.
FT NON TER 1
SQ SEQUENCE 237 AA; 26633 MW; B0928A9C7A41D377 CRC64;

Query Match 91.7%; Score 33; DB 11; Length 237;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
Db 167 VDYSWL 172

RESULT 7
O9CRS3 PRELIMINARY; PRT; 263 AA.
AC O9CRS3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE 17 days embryo head cDNA, RIKEN full-length enriched library,
DE clone:3322402L07 product:hypothetical protein, full insert sequence
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;

RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arikawa T., Bono H., Carlini P., Fukuda S., Fukunishi Y., Furuno M.,
RA Haneagaki T., Hara A., Hayatsu N., Hiramoto K., Hirata T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Ozaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Yamamoto M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA the FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636;
RA Carlini P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159;
RA Carlini P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carlini P.,
RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami Y., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachihi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
DR EMBL; AK014383; BAB29312.2; -
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 263 AA; 30215 MW; 692304F88AD341AF CRC64;

Query Match 91.7%; Score 33; DB 11; Length 263;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
Db 126 VDYSWL 131

RESULT 8

099KPS
ID 099KPS PRELIMINARY; PRT; 392 AA.
AC 099KPS;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to cyclin 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straubeberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004071; AA04071.1; -
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 3.
DR SMART; SM00320; WD40; 2.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Cyclin; Repeat; WD repeat.
SQ SEQUENCE 392 AA; 44527 MW; 4B2E5CBAJA22075A CRC64;

Query Match 91.7%; Score 33; DB 11; Length 392;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
DB 384 VDYSWL 389

RESULT 9
08CKO2 PRELIMINARY; PRT; 66 AA.
ID 08CKO2;
AC 08CKO2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical.
GN Y3132.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Bivovar Mediaeval18;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Niles M.L., Mason J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AE013914; AAM86682.1; -
KW Hypothetical protein.
SQ SEQUENCE 66 AA; 7780 MW; EE5586B890246D88 CRC64;

Query Match 88.9%; Score 32; DB 16; Length 66;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYSWL 6
DB 46 DYSWL 50

RESULT 10
ID 070791 PRELIMINARY; PRT; 93 AA.
AC 070791;

DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical protein.
GN 6
OS Rice yellow stunt virus.
OC Viruses; ssRNA negative-strand viruses; Nonnegavirales;
OC Rhabdoviridae; Nucleorhabdovirus.
OX NCBI_TaxID=59380;
RN [1]
RP SEQUENCE FROM N.A.
RA Pang R., Luo Z., Zhao H.;
RT "Novel structure of the rice yellow stunt virus genome: a plant
RT rhabdovirus encodes seven genes."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011257; BAA25159.1; -
KW Hypothetical protein.
SQ SEQUENCE 93 AA; 10543 MW; A10CC3BD41F8305 CRC64;

Query Match 88.9%; Score 32; DB 12; Length 93;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
DB 63 IDYSWI 68

RESULT 11
068455 PRELIMINARY; PRT; 107 AA.
ID 068455;
AC 068455;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Halocid dehalogenase (Fragment).
OS Ancylobacter aquaticus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Ancylobacter.
OX NCBI_TaxID=100;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CN13.
RA Fortin N., Fulthorpe R.R., Allen D.G., Greer C.W.;
RT "Molecular analysis of bacterial isolates and total community DNA from
RT kraft pulp mill effluent treatment systems."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF043240; AAC08952.1; -
DR HSP; Q60099; 1A06.
DR InterPro; IPR005833; Hlg_nase/hydrolase.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00413; HADHALOGNASE.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 107 AA; 12177 MW; 2B777D4354B5D0C8 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 107;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
DB 6 LDYSWL 11

RESULT 12
ID 08GBK5 PRELIMINARY; PRT; 138 AA.
AC 08GBK5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

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DE Putative halocarboxylic acid dehalogenase (Fragment).
GN DEHII.
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RA Marchael J.R., Weightman A.J.;
RT "Relating the cultivable gene pool with the metagenome pool in activated
RT sludge.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ511306; CAD54096.1; -.
FT NON_TER 1
FT NON_TER 138
SQ SEQUENCE 138 AA; 15508 MW; A10B803019693F53 CRC64;

Query Match
Best Local Similarity 88.9%; Score 32; DB 2; Length 138;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 6 LDYSWL 11

RESULT 13
Q8GBKO PRELIMINARY; PRT; 138 AA.
AC Q8GBKO;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative halocarboxylic acid dehalogenase (Fragment).
GN DEHII.
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RA Marchael J.R., Weightman A.J.;
RT "Relating the cultivable gene pool with the metagenome pool in activated
RT sludge.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ511311; CAD54101.1; -.
FT NON_TER 1
FT NON_TER 138
SQ SEQUENCE 138 AA; 15643 MW; 3F31CE5C83979082 CRC64;

Query Match
Best Local Similarity 88.9%; Score 32; DB 2; Length 138;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 6 LDYSWL 11

RESULT 14
Q8GBJ4 PRELIMINARY; PRT; 138 AA.
AC Q8GBJ4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative halocarboxylic acid dehalogenase (Fragment).
GN DEHII.
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RA Marchael J.R., Weightman A.J.;
RT "Relating the cultivable gene pool with the metagenome pool in activated

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RT sludge.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ511319; CAD54109.1; -.
FT NON_TER 1
FT NON_TER 138
SQ SEQUENCE 138 AA; 15525 MW; 9C48CD30E1C42F40 CRC64;

Query Match
Best Local Similarity 88.9%; Score 32; DB 2; Length 138;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 6 LDYSWL 11

RESULT 15
Q8XBY6 PRELIMINARY; PRT; 153 AA.
AC Q8XBY6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein z0706.
GN z0706 OR EC30606.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grothbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potomousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Okubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shingawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
DR EMBL; AE005236; AAG54901.1; -.
DR EMBL; AP002552; BAB34029.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 153 AA; 17334 MW; 1AD056E0EAA29C65 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 16; Length 153;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5
Db 83 LDYSW 87

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Search completed: February 18, 2004, 14:35:52
 Job time : 19.3684 secs


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FT TRANSNM 171 193 4 (POTENTIAL).
FT DOMAIN 194 217 EXTRACELLULAR (POTENTIAL).
FT TRANSNM 218 239 5 (POTENTIAL).
FT DOMAIN 240 258 CYTOPLASMIC (POTENTIAL).
FT TRANSNM 259 280 6 (POTENTIAL).
FT DOMAIN 281 299 EXTRACELLULAR (POTENTIAL).
FT TRANSNM 300 320 7 (POTENTIAL).
FT DOMAIN 321 404 CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 202 BY SIMILARITY.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 404 AA; 45323 MW; EP187ECGDF2DC6C1 CRC64;

Query Match 91.7%; Score 33; DB 1; Length 404;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
DB 115 LDYTWL 120

RESULT 2
VLVS BPAPS STANDARD; PRT; 94 AA.
AC Q9T17;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative lysate protein S (P11).
GN 11.
OS Bacteriophage APSE-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=106199;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99420383; PubMed=10489345;
RA van der Wijk F., Dulleman A.M., Verbeek M., van den Heuvel J.F.J.M.;
RT "Isolation and characterization of APSE-1, a bacteriophage infecting
the secondary endosymbiont of acyrtosiphon pisum.";
RL Virology 262:104-113 (1999).
CC -1- PUNCTATION: ESSENTIAL FOR LYSIS OF THE BACTERIAL CELL WALL BY
DISRUPTING THE CELL MEMBRANE, THEREBY GIVING HYDROLYTIC ENZYMES
ACCESS TO THE CELL WALL (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LAMBDA PHAGE S PROTEIN FAMILY.
CC -----
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CC -----
CC EMBL; AF157835; AAF03954.1; -
DR InterPro; IPR006481; Holin_lambda.
DR Pfam; PF05106; Phage_holin_3; 1.
DR TIGRFAMs; TIGR01594; holin_lambda; 1.
KW Phage lysate protein.
SQ SEQUENCE 94 AA; 10589 MW; C3BE1A3181150120 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYSWL 6
DB 66 DYSWL 70

RESULT 3
HAD2_PSESP STANDARD; PRT; 229 AA.
ID_HAD2_PSESP

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AC P24070;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 2-haloalkanoic acid dehalogenase II (EC 3.8.1.2) (L-2-haloacid
dehalogenase II) (Halocarboxylic acid halidehydrolase II) (DEHII).
OS Pseudomonas sp. (strain CBS3).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139597; PubMed=1995594;
RA Schneider B., Mueller R., Frank R., Lingens F.;
RT "Complete nucleotide sequences and comparison of the structural genes
of two 2-haloalkanoic acid dehalogenases from Pseudomonas sp. strain
CBS3.";
RL J. Bacteriol. 173:1530-1535 (1991).
CC -1- CATALYTIC ACTIVITY: (S)-2-haloacid + H(2)O = (R)-2-hydroxyacid +
halide
CC -1- SIMILARITY: BELONGS TO THE 2-HALOALKANOIC ACID DEHALOGENASE
FAMILY.
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CC -----
CC EMBL; M62909; AAA25833.1; -
DR PIR; B38452; B38452.
DR HSSP; Q53464; 12RN.
DR InterPro; IPR006328; HAD_II.
DR InterPro; IPR006388; HAD_SF_IA_V2.
DR InterPro; IPR005833; Hlgase/hydrlase.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00413; HADHALOGENASE.
DR TIGRFAMs; TIGR01493; HAD_SF-IA-V2; 1.
DR TIGRFAMs; TIGR01428; HAD_type_II; 1.
KW Hydrolase.
FT ACT SITE
SQ SEQUENCE 229 AA; 25712 MW; A77AA63C97DD40AB CRC64;

Query Match 88.9%; Score 32; DB 1; Length 229;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
DB 45 LDYSWL 50

RESULT 4
HAD_XANNU STANDARD; PRT; 253 AA.
ID_HAD_XANNU
AC Q60099; Q56757;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 2-haloalkanoic acid dehalogenase (EC 3.8.1.2) (L-2-haloacid
dehalogenase) (Halocarboxylic acid halidehydrolase).
GN DHB.
OS Xanthobacter autotrophicus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Xanthobacter.
OX NCBI_TaxID=280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.
RX STRAIN=GJ10;
RX MEDLINE=92078101; PubMed=1744048;
RA van der Ploeg J., van Hall G., Janssen D.B.;

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RT "Characterization of the haloacid dehalogenase from Xanthobacter
 RT autotrophicus GJ10 and sequencing of the dh1b gene.";
 RL J. Bacteriol. 173:7925-7933(1991).
 RN [2]
 RP SEQUENCE OF 1-122 FROM N.A.
 RC STRAIN=GJ10;
 RX MEDLINE=9606306; PubMed=7580000;
 RA van der Ploeg J., Janssen D.B.;
 RT "Sequence analysis of the upstream region of dh1b, the gene encoding
 RT haloalkanoic acid dehalogenase of Xanthobacter autotrophicus GJ10.";
 RL Biodegradation 6:257-263(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) AND REVISION TO 84.
 RC STRAIN=GJ10;
 RX MEDLINE=98070500; PubMed=9407083;
 RA Ridder I.S., Rozeboom H.J., Kalk K.H., Janssen D.B., Dijkster B.W.;
 RT "Three-dimensional structure of L-2-haloacid dehalogenase from
 RT Xanthobacter autotrophicus GJ10 complexed with the substrate-analogue
 RT formate.";
 RL J. Biol. Chem. 272:33015-33022(1997).
 CC -1- FUNCTION: CATALYZES THE HYDROLYTIC DEHALOGENATION OF SMALL L-2-
 CC HALOALKANOIC ACIDS TO YIELD THE CORRESPONDING D-2-HYDROXYALKANOIC
 CC ACIDS. ACTIVE WITH 2-HALOGENATED CARBOXYLIC ACIDS AND CONVERTS
 CC ONLY THE L-ISOMER OF 2-CHLOROPROPIONIC ACID WITH INVERSION OF
 CC CONFIGURATION TO PRODUCE D-LACTATE. OPTIMAL ACTIVITY IS BETWEEN PH
 CC 9-10. AND MAXIMAL ACTIVITY SEEN AT PH 9.5.
 CC -1- CATALYTIC ACTIVITY: (S)-2-haloacid + H(2)O = (R)-2-hydroxyacid +
 CC halide.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: BELONGS TO THE 2-HALOALKANOIC ACID DEHALOGENASE
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL: M81691; AAA27590.1; -;
 CC EMBL: X86084; CAA60039.1; -;
 CC PIR: S52840; S52840.
 CC DR PDB: 1A06; 28-JAN-98.
 CC DR PDB: 1Q05; 29-NOV-99.
 CC DR PDB: 1Q06; 20-DEC-00.
 CC DR PDB: 1Q07; 20-DEC-00.
 CC DR InterPro: IPR006328; HAD_II.
 CC DR InterPro: IPR006388; HAD_SF_IA_V2.
 CC DR InterPro: IPR005833; H1gnase_hydrlase.
 CC DR Pfam: PF00702; Hydrolase; 1.
 CC DR PRINTS: PR00413; HADHALOGENASE.
 CC DR TIGRAME: TIGR01493; HAD-SF-IA-V2; 1.
 CC DR TIGRAME: TIGR01428; HAD_type_II; 1.
 CC KW Hydrolyase; 3D-structure.
 CC FT ACT_SITE 8
 CC FT CONFICT 84 84 D -> G (IN REF. 1 AND 2).
 CC FT STRAND 4 7
 CC FT STRAND 10 10
 CC FT TURN 11 13
 CC FT STRAND 14 14
 CC FT HELIX 16 19
 CC FT HELIX 20 26
 CC FT TURN 28 29
 CC FT HELIX 31 52
 CC FT TURN 33 53
 CC FT HELIX 38 58
 CC FT TURN 58 72
 CC FT TURN 73 74
 CC FT HELIX 79 86
 CC FT HELIX 87 91
 CC FT STRAND 94 94
 CC FT TURN 96 97

FT HELIX 98 105
 FT TURN 106 107
 FT STRAND 109 114
 FT HELIX 118 127
 FT TURN 128 129
 FT HELIX 131 133
 FT STRAND 136 139
 FT HELIX 140 143
 FT TURN 144 144
 FT TURN 147 148
 FT HELIX 150 160
 FT HELIX 150 160
 FT STRAND 167 171
 FT HELIX 174 183
 FT TURN 184 184
 FT STRAND 186 190
 FT HELIX 195 203
 FT TURN 209 217
 FT TURN 222 223
 FT STRAND 229 231
 FT HELIX 234 236
 FT HELIX 237 243
 SQ SEQUENCE 253 AA; 27469 MW; E2AB9DEBD37A5716 CRC64;
 QY 1 IDYSWL 6
 Db 43 LKYSWL 48
 Query Match 88.9%; Score 32; DB 1; Length 253;
 Best Local Similarity 83.3%; Pred. No. 34;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 RESULT 5
 SSAT_SALTY
 ID SSAT_SALTY STANDARD; PRT; 259 AA.
 AC P96068;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Secretion system apparatus protein ssat.
 GN SSAT OR STM1421.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 CX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2.
 RX MEDLINE=97285756; PubMed=9140973;
 RA Henzel M., Shea J.E., Raupach B., Monack D., Falkow S., Gleason C.,
 RA Kubo T., Holden D.W.;
 RT "Functional analysis of ssat and the ssat/U operon, 13 genes encoding
 RT components of the type III secretion apparatus of Salmonella
 RT pathogenicity island 2.";
 RL Mol. Microbiol. 24:155-167(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=2154948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvanev E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 CC -1- FUNCTION: PART OF A TYPE III SECRETION SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- SIMILARITY: BELONGS TO THE FLIR/MOPS/SPAR FAMILY.
 CC -----
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DR EMBL; X99944; CAA68201.1; -
 DR EMBL; AE008761; AAL20345.1; -
 DR SIVGene; SG10717; ssat.
 DR InterPro; IPR002010; Bac_export_1.
 DR InterPro; IPR006304; Spar_Yacet.
 DR Pfam; PF01311; Bac_export_1; 1.
 DR PRINTS; PR00953; TYPE31MRPROT.
 DR TIGRFam; TIGR01401; flir_1like_III; 1.
 KM Transprot; Protein transport; Transmembrane; Complete proteome.
 FT TRANSMEM 9
 FT TRANSMEM 29 POTENTIAL.
 FT TRANSMEM 35 55 POTENTIAL.
 FT TRANSMEM 78 98 POTENTIAL.
 FT TRANSMEM 127 147 POTENTIAL.
 FT TRANSMEM 185 205 POTENTIAL.
 FT TRANSMEM 214 234 POTENTIAL.
 SQ SEQUENCE 259 AA; 29218 MW; 8E5F0734991373DD CRC64;

Query Match 88.9%; Score 32; DB 1; Length 259;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYSWL 6
 Db 67 DYSWL 71

RESULT 6
 ABGR_ECOLI STANDARD; PRT; 302 AA.
 ID ABGR_ECOLI
 AC P77744;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative transcriptional regulator abgr.
 GN ABGR OR B1339.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RA MEDLINE=9742617; PubMed=9278503;
 RA Blatner F.R., Plunkett G. II, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kittpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shaoh Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA MEDLINE=97251357; PubMed=9097039;
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 RA Kaezi H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
 RA Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;
 RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map."
 RL DNA Res. 3:363-377(1996).
 RN [3]
 RP CHARACTERIZATION.
 RC STRAIN=BN101;
 RX MEDLINE=99047572; PubMed=9829935;

RA Hussein M.J., Green J.M., Nichols B.P.;
 RT "Characterization of mutations that allow p-aminobenzoyle-glutamate
 RT utilization by Escherichia coli."
 RL J. Bacteriol. 180:6260-6268(1998).
 CC -1- FUNCTION: COULD BE THE REGULATOR OF THE ABG OPERON
 CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.

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DR EMBL; AE000232; AAC74421.1; -
 DR EMBL; D90772; BAA14941.1; -
 DR EMBL; D90773; BAA14944.1; -
 DR PIR; F64883; F64883.
 DR EcoGene; EG13353; abgr.
 DR InterPro; IPR000847; HTH_LYER.
 DR InterPro; IPR005119; LysR_LYER.
 DR Pfam; PF00126; HTH_1; 1.
 DR Pfam; PF03466; LysR_substrate; 1.
 DR PRINTS; PR00039; HTH_LYER.
 DR PROSITE; PS00044; HTH_LYER_FAMILY; 1.
 KM Transcription regulation; DNA-binding; Complete proteome.
 FT DNA_BIND 22 41
 FT SEQUENCE 302 AA; 34058 MW; 57C83FA6D8ABA66 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 302;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSW 5
 Db 191 LDYSW 195

RESULT 7
 IRF1_CHICK STANDARD; PRT; 313 AA.
 ID IRF1_CHICK
 AC Q90876;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Interferon regulatory factor 1 (IRF-1).
 GN IRF1.
 OS Gallus gallus (Chicken).
 OC Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95241453; PubMed=7536924;
 RA Jungwirth C., Rebber M., Ozato K., Degen H.J., Schultze U.,
 RA David I.B.;
 RT "Chicken interferon consensus sequence-binding protein (ICSBP) and
 RT interferon regulatory factor (IRF) 1 genes reveal evolutionary
 RT conservation in the IRF gene family."
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3105-3109(1995).
 CC -1- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF
 CC TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON
 CC CONSENSUS SEQUENCE (ICS) AND ACTIVATES THOSE GENES (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: Belongs to the IRF family.
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 DR EMBL; L39766; AAA62160.1; -.
 DR HSRP; P15314; IIR1.
 DR InterPro; IPR001346; IIR.
 DR Pfam; PF00605; IIR; 1.
 DR PRINTS; PR00267; INTERNEGCT.
 DR PRODOM; PD002355; IIR; 1.
 DR SMART; SM00348; IIR; 1.
 DR PROSITE; PS00601; IIR; 1.
 DR Transcription regulation; DNA-binding; Activator; Nuclear protein.
 FT DNA BIND 7 109
 SQ SEQUENCE 313 AA; 36009 MW; 0895FA736FA7463 CRC64;

 Query Match 88.9%; Score 32; DB 1; Length 313;
 Best Local Similarity 83.3%; Pred. No. 43;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Oy 1 LDYSWL 6
 |||
 Db 295 LDYSWL 300

 RESULT 8
 AAT_RHLP STANDARD; PRT; 400 AA.
 AC 086459;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (ASPART).
 GN ASPC OR AATV.
 OS Rhizobium leguminosarum (biovar phaseol1).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OX NCBI_TaxID=385;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=8002;
 RA Allway D;
 RT "Sequence of an aspartate aminotransferase from Rhizobium
 RL leguminosarum."
 CC Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-separate + 2-oxoglutarate = oxaloacetate +
 CC L-glutamate.
 CC -1- SIMILARITY: BELONGS TO CLASS-1 OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.

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 DR EMBL; AJ006709; CA07198.1; -.
 DR HSRP; O56232; IBKG.
 DR InterPro; IPR001176; ACC_synthase.
 DR InterPro; IPR004839; Aminotransf1/2.
 DR Pfam; PF00155; aminotran 1.2; 1.
 DR PRINTS; PR00753; ACCSYNTHASE.
 DR PROSITE; PS00105; AA_TRANSFR_CLASS_1; 1.
 DR Transferrase; Aminotransferase; Pyridoxal phosphate.
 FT BINDING 239 239
 SQ SEQUENCE 400 AA; 43752 MW; 1375BE0A72934304 CRC64;

 Query Match 88.9%; Score 32; DB 1; Length 400;

Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Oy 1 LDYSW 5
 |||
 Db 87 LDYSW 91

 RESULT 9
 VGLG_RABV STANDARD; PRT; 524 AA.
 ID VGLG_RABV
 AC 008089;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Spike glycoprotein precursor.
 GN G.
 OS Rabies virus (strain Vukovo-32).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Lyssavirus.
 OX NCBI_TaxID=45418;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95070778; PubMed=7979981;
 RA Fodor I., Grabko V.I., Khozinaki V.V., Selimov M.A.;
 RT "Nucleotide and deduced amino acid sequences of the glycoprotein gene
 of rabies virus vaccine strain Vukovo-32."
 Arch. Virol. 135:459-459(1994).
 CC -1- FUNCTION: THIS PROTEIN FORMS SPIKES ON THE SURFACE OF THE VIRION.
 CC IT IS RESPONSIBLE BOTH FOR THE BINDING OF THE VIRUS TO SUSCEPTIBLE
 CC HOST CELLS AND FOR INDUCING THE UPTAKE OF THE VIRUS BY THE CELL.
 CC THE INTERACTION BETWEEN THE INTERNAL COMPONENTS OF THE VIRION AND
 CC THE PORTION OF THE GLYCOPROTEIN EXPOSED ON THE CYTOPLASMIC FACE OF
 CC THE PLASMA MEMBRANE PROBABLY DIRECTS ENVELOPMENT AND VIRUS
 CC BUDDING.
 CC -1- SUBUNIT: Homotrimer.

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 DR EMBL; X71879; CA50713.1; -.
 DR PIR; S33419; S33419.
 DR InterPro; IPR01903; Rhabd_glycop.
 DR Pfam; PF00974; Rhabdo_glycop.1.
 KM Transmembrane; Envelope protein; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 524
 FT TRANSMEM 20 524
 FT CARBOHYD 56 476
 FT CARBOHYD 56 476
 FT CARBOHYD 266 266
 FT CARBOHYD 338 338
 FT CARBOHYD 484 484
 SQ SEQUENCE 524 AA; 58692 MW; 6DB36E50406CC16D CRC64;

 Query Match 88.9%; Score 32; DB 1; Length 524;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Oy 2 DYSWL 6
 |||
 Db 137 DYSWL 141

 RESULT 10
 XYNA_CALSR STANDARD; PRT; 684 AA.
 ID XYNA_CALSR
 AC P40944;
 DT 01-FEB-1995 (Rel. 31, Created)

DT	01-FEB-1995	(Rel. 31, Last sequence update)
DT	28-FEB-2003	(Rel. 41, Last annotation update)
DE	Endo-1,4-beta-xylanase A precursor (EC 3.2.1.6) (Xylanase A)	
DE	(1,4-beta-D-xylan xylanohydrolase A).	
GN	XVNA.	
OS	Caldicellulosilyceptor sp. (strain Rtb8.4).	
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;	
CC	Caldicellulosilyceptor.	
OX	NCBI_TaxID=282387	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=97077616; PubMed=8920183;	
RA	"Dwivedi P.P., Gibbs M.D., Saul D.J., Bergquist P.L.,"	
RT	"Cloning, sequencing and overexpression in Escherichia coli of a	
RT	xylanase gene, xvna from the thermophilic bacterium Rtb8.4 genus	
RL	Caldicellulosilyceptor."	
APPL	Microbiol. Biotechnol. 45:86-93(1996).	
CC	-1 PATHWAY: Xylan degradation.	
CC	-1 LINKAGES IN XYLANS.	
CC	-1 SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL HYDROLASSES).	
CC	-----	
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CC	-----	
DR	EMBL; L18965; AAB4204.1; .	
DR	PIR; S41788; S41788.	
DR	HSSP; P10478; XYZ.	
DR	InterPro; IPR003305; CMM_CengC.	
DR	InterPro; IPR001000; Glyco_hydro_10.	
DR	Pfam; PF02018; CBM_4_2.	
DR	Pfam; PF00331; Glyco_hydro_10; 1.	
DR	SMART; SM00633; Glyco_10; 1.	
DR	PROSITE; PS00591; GLYCOSYL_HYDROL_F10; 1.	
KW	Xylan degradation; Hydrolase; Glycosylase; Signal; Repeat.	
FT	SIGNAL 1 34	
FT	CHAIN 35 684	
FT	ACT_SITE 490 490	
FT	ACT_SITE 598 598	
SO	SEQUENCE 684 AA; 78353 MW; 0AE575FAFB4BA5E6 CRC64;	
Qy	2 DYSWL 6	
DB	650 DYSWL 654	
Query Match	88.9%; Score 32; DB 1; Length 684;	
Best Local Similarity	100.0%; Pred. No. 99;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
RESULT 11		
ID_FCT_ERWCH STANDARD; PRT; 735 AA.		
AC Q47162;		
DT 01-NOV-1997 (Rel. 35, Created)		
DT 01-NOV-1997 (Rel. 35, Last sequence update)		
DT 01-NOV-1997 (Rel. 35, Last annotation update)		
DE FerriChrysoabactin receptor precursor.		
GN FCT.		
OS Brynina chrysanthemi.		
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
CC Enterobacteriaceae; Pectobacterium.		
OX NCBI_TaxID=556;		
RN [1]		
RP SEQUENCE FROM N.A.		
RA STRAIN=3937;		
RX MEDLINE=96165286; PubMed=8576065;		

RA	Savage C., Franza T., Expert D.;		
Rt	"Analysis of the Exwinda chrysaethemi ferrichrysobactin receptor		
Rt	gene: resemblance to the Escherichia coli fepA-fes bidirectional		
RL	promoter region and homology with hydroxamate receptors.";		
J.	Bacteriol. 178:1227-1231(1996).		
CC	-1- FUNCTION: INVOLVED IN THE INITIAL STEP OF IRON UPTAKE BY BINDING		
CC	CHRYSOBACTIN, AN IRON CHELATING SIDROPHORE THAT ALLOWS THE		
CC	BACTERIA TO EXTRACT IRON FROM THE ENVIRONMENT".		
CC	-1- SUBCELLULAR LOCATION: Outer membrane.		
CC	-1- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.		
CC	-----		
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CC	-----		
DR	EMBL; X87967; CAAG1205.1; --		
DR	PIR; S57486; S57486.		
DR	HSSP; P06971; 2PCP.		
DR	InterPro; IPR00531; TonB_boxC.		
DR	Pfam; PF00593; TonB_dep_Rec; 1.		
DR	PROSITE; PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG.		
DR	PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.		
KW	Signal; Receptor; Transmembrane; Outer membrane; Iron transport;		
KW	Transport; TonB box.		
FT	SIGNAL	1	38
FT	CHAIN	39	735
FT	SITE	45	52
FT	SITE	718	735
FT	DOMAIN	39	45
FT	TRANSMEM	46	54
FT	DOMAIN	55	82
FT	TRANSMEM	83	91
FT	DOMAIN	92	107
FT	TRANSMEM	108	116
FT	DOMAIN	117	124
FT	TRANSMEM	125	133
FT	DOMAIN	134	169
FT	TRANSMEM	170	178
FT	DOMAIN	179	179
FT	TRANSMEM	180	188
FT	DOMAIN	189	194
FT	TRANSMEM	195	203
FT	DOMAIN	204	222
FT	TRANSMEM	223	231
FT	DOMAIN	232	261
FT	TRANSMEM	262	270
FT	DOMAIN	271	286
FT	TRANSMEM	287	295
FT	DOMAIN	296	312
FT	TRANSMEM	313	321
FT	DOMAIN	322	328
FT	TRANSMEM	329	337
FT	DOMAIN	338	343
FT	TRANSMEM	344	352
FT	DOMAIN	353	378
FT	TRANSMEM	379	387
FT	DOMAIN	388	392
FT	TRANSMEM	393	401
FT	DOMAIN	402	403
FT	TRANSMEM	404	412
FT	DOMAIN	413	424
FT	TRANSMEM	425	433
FT	DOMAIN	434	448
FT	TRANSMEM	449	457
FT	DOMAIN	458	461
FT	TRANSMEM	462	470
FT	DOMAIN	471	495
FT	TRANSMEM	496	504
FT	DOMAIN	505	509
FT	PERICHRYSOBACTIN RECEPTOR.		
FT	TONB BOX.		
FT	TONB C-TERMINAL BOX.		
FT	PERIPLASMIC (POTENTIAL) .		
FT	POTENTIAL.		
FT	EXTRACELLULAR (POTENTIAL) .		
FT	POTENTIAL.		
FT	PERIPLASMIC (POTENTIAL) .		
FT	POTENTIAL.		
FT	EXTRACELLULAR (POTENTIAL) .		
FT	POTENTIAL.		
FT	PERIPLASMIC (POTENTIAL) .		
FT	POTENTIAL.		
FT	EXTRACELLULAR (POTENTIAL) .		
FT	POTENTIAL.		
FT	PERIPLASMIC (POTENTIAL) .		
FT	POTENTIAL.		
FT	EXTRACELLULAR (POTENTIAL) .		
FT	POTENTIAL.		
FT	PERIPLASMIC (POTENTIAL) .		
FT	POTENTIAL.		
FT	EXTRACELLULAR (POTENTIAL) .		
FT	POTENTIAL.		
FT	PERIPLASMIC (POTENTIAL) .		
FT	POTENTIAL.		
FT	EXTRACELLULAR (POTENTIAL) .		
FT	POTENTIAL.		
FT	PERIPLASMIC (POTENTIAL) .		
FT	POTENTIAL.		
FT	EXTRACELLULAR (POTENTIAL) .		
FT	POTENTIAL.		
FT	PERIPLASMIC (POTENTIAL) .		
FT	POTENTIAL.		
FT	EXTRACELLULAR (POTENTIAL) .		
FT	POTENTIAL.		
FT	PERIPLASMIC (POTENTIAL) .		
FT	POTENTIAL.		
FT	EXTRACELLULAR (POTENTIAL) .		
FT	POTENTIAL.		
FT	PERIPLASMIC (POTENTIAL) .		
FT	POTENTIAL.		
FT	EXTRACELLULAR (POTENTIAL) .		
FT	POTENTIAL.		
FT	PERIPLASMIC (POTENTIAL) .		
FT	POTENTIAL.		
FT	EXTRACELLULAR (POTENTIAL) .		
FT	POTENTIAL.		
FT	PERIPLASMIC (POTENTIAL) .		
FT	POTENTIAL.		
FT			

FT TRANSMEM 510 518 POTENTIAL.
 FT DOMAIN 519 538 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 539 547 POTENTIAL.
 FT DOMAIN 548 552 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 553 561 POTENTIAL.
 FT DOMAIN 562 568 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 569 577 POTENTIAL.
 FT DOMAIN 578 599 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 600 608 POTENTIAL.
 FT DOMAIN 609 649 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 650 658 POTENTIAL.
 FT DOMAIN 659 674 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 675 683 POTENTIAL.
 FT DOMAIN 684 695 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 696 704 POTENTIAL.
 FT DOMAIN 705 706 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 707 715 POTENTIAL.
 FT DOMAIN 716 726 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 727 735 POTENTIAL.
 SQ SEQUENCE 735 AA; 81055 MW; 3C37073B4538DC3C CRC64;

Query Match 88.9%; Score 32; DB 1; Length 735;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 DB 399 LDYSWL 404

RESULT 12

ID GUNB_CALSA STANDARD; PRT; 1039 AA.
 AC P10474;

DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endoglucanase/exoglucanase B precursor [Includes: Endoglucanase
 DE (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
 DE (Cellulohydrolyase); Exoglucanase (EC 3.2.1.91) (Exocellulohydrolyase)]
 DE (1,4-beta-cellulohydrolyase)].
 GN CELB.
 OS Caldocellum saccharolyticum (Caldicellulosigrupor saccharolyticus).
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
 OC Caldicellulosigrupor.
 OK NCBI_TaxId=44001;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89098398; PubMed=2789517;
 RA Saul D.J., Williams L.C., Love D.R., Chanley I.W., Bergquist P.I.;
 RT "Nucleotide sequence of a gene from Caldocellum saccharolyticum
 RT encoding for exocellulase and endocellulase activity."
 RL Nucleic Acids Res. 17:439-439(1989).
 CC -1- FUNCTION: THIS PROTEIN IS MADE UP OF TWO DOMAINS: THE N-TERMINAL
 CC DOMAIN HAS EXOGLUCANASE ACTIVITY WHILE THE C-TERMINAL DOMAIN IS
 CC AN ENDOGLUCANASE
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
 CC in cellulose and cellobiose, releasing cellobiose from the non-
 CC reducing ends of the chains.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO CELLULOSE FAMILY
 CC P (FAMILY 10 OF GLYCOSYL HYDROLASES).
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CELLULOSE FAMILY
 CC A (FAMILY 5 OF GLYCOSYL HYDROLASES).
 CC -----
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CC EMBL: X13602; CA31936.1; -
 DR PIR; S02711; S02711.
 DR HSSP; Q06851; INBC.
 DR InterPro; IPR001956; CBD 3.
 DR InterPro; IPR001000; Glyco_hydro_10.
 DR InterPro; IPR001547; Glyco_hydro_5.
 DR Pfam; PF00942; CBM 3.1.
 DR Pfam; PF00150; cellulase; 1.
 DR Pfam; PF00331; Glyco_hydro_10; 1.
 DR PRINTS; PR00134; GLHYDRASE10.
 DR PRODOM; PD001947; CBD 3.1.
 DR SMART; SM00633; Glyco_10; 1.
 DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; 1.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
 KW Cellulose degradation; Hydrolyase; Glycosidase; Repeat;
 KW Multifunctional enzyme; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 1039 ENDOGLUCANASE/EXOGLUCANASE B
 FT DOMAIN 376 416 THR/PRO-RICH, TANDM REPEATS OF T-P.
 FT DOMAIN 417 570 CELLULOSE-BINDING (BY SIMILARITY).
 FT DOMAIN 571 618 THR/PRO-RICH, TANDM REPEATS OF T-P.
 FT ACT SITE 177 177 PROTON DONOR (POTENTIAL).
 FT ACT SITE 285 285 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 792 792 BY SIMILARITY.
 SQ SEQUENCE 1039 AA; 117641 MW; 0E0378171594DDE CRC64;

Query Match 88.9%; Score 32; DB 1; Length 1039;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
 DB 339 DYSWL 343

RESULT 13

ID YE15_HAEIN STANDARD; PRT; 200 AA.
 AC P44187;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein H11415.
 GN H11415.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OK NCBI_TaxId=727;
 RN 11
 RP SEQUENCE FROM N.A.
 RX STRAIN=RD / KM20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kinkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shetty R., Liu L.-T., Glodek A., Kelley J.M.,
 RA Wetman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,
 RA Utecherback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Georgagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd."
 RL Science 269:496-512(1995).
 CC -1- SIMILARITY: SOME, TO MYCOBACTERIOPHAGES D29 AND L5 GP10.
 CC -----
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 CC EMBL; U32821; AAC23066.1; -.
 DR PIR; H64028; H64028.
 DR HSSP; P23951; 2BAA.
 DR TIGR; H11415; -.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 200 AA; 22895 MW; 42199FDNA4859FBB CRC64;
 Query Match 86.1%; Score 31; DB 1; Length 200;
 Best Local Similarity 83.3%; Pred. No. 42;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LDYSWL 6
 Db 61 LNYSWL 66
 RESULT 14
 UL78_HCMVA STANDARD; PRT; 431 AA.
 ID UL78_HCMVA
 AC P16751;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein UL78.
 GN UL78.
 OS Human cytomegalovirus (strain AD169).
 OC Viruses; dsDNA viruses, not RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 NC NCBI_TaxID=10360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90269039; PubMed=2161319;
 RA Chae M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
 RA Hosenell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
 RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
 RT "Analysis of the protein-coding content of the sequence of human
 RT cytomegalovirus strain AD169.";
 RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

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 CC EMBL; X17403; CA35351.1; -.
 DR PIR; S09841; S09841.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; UNKNOWN_1.
 KM Hypothetical protein; Transmembrane.
 FT TRANSMEM 42 62 POTENTIAL.
 FT TRANSMEM 74 94 POTENTIAL.
 FT TRANSMEM 111 131 POTENTIAL.
 FT TRANSMEM 153 173 POTENTIAL.
 FT TRANSMEM 202 222 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 FT TRANSMEM 279 299 POTENTIAL.
 FT CARBOHYD 105 105 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 431 AA; 47357 MW; 34668FE7F908C657 CRC64;
 Query Match 86.1%; Score 31; DB 1; Length 431;
 Best Local Similarity 83.3%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 LDYSWL 6
 Db 180 LDYRWL 185

RESULT 15
 IKKA HUMAN STANDARD; PRT; 745 AA.
 ID IKKA HUMAN
 AC O1511; O14666; O13132; O92467;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (IC 2.7.1.-)
 DE (I kappa-B kinase alpha) (IKBA) (IKK-alpha) (IKAPPAB kinase)
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
 DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFIKBA).
 GN CHUK OR IKKA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RC TISSUE=T-cell;
 RX MEDLINE=97386461; PubMed=9244310;
 RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Roche M.;
 RT "Identification and characterization of an IkappaB kinase.";
 RL Cell 90:373-383(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=97394468; PubMed=9252186;
 RA Didonato J.A., Hayakawa M., Rochwart D.M., Zandi E., Karin M.;
 RT "A cytokine-responsive IkappaB kinase that activates the transcription
 RT factor NF-kappaB.";
 RL Nature 388:548-554(1997).
 RN [3]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
 RP SER-176.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=98008813; PubMed=9346484;
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
 RT NF-kappaB activation.";
 RL Science 278:860-866(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=95032998; PubMed=9813230;
 RA Hu M.C.-T., Wang Y.-P.;
 RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 RT embryonic tissues but localized to different human chromosomes.";
 RL Gene 222:31-40(1998).
 RN [5]
 RP SEQUENCE OF 32-745 FROM N.A.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connolly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1995).
 RN [6]
 RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
 RP AND SER-180.
 RX MEDLINE=98188283; PubMed=9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
 RT Ser-176.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 RN [7]
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RX MEDLINE=99413720; PubMed=10485710; Pfeiffer S.R., Pfeiffer L.M.,
 RA Ozes O.N., Mayo L.D., Guetin J.A., Pfeiffer S.R., Pfeiffer L.M.,
 RA Donner D.B.;
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt
 RT serine-threonine kinase.";

RL Nature 401:82-85(1999).
 RN [8]
 RP IKKA-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhase M., Hayekawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of Ikkappa kinase activity through
 RL IKKbeta subunit phosphorylation.";
 RL Science 284:305-313(1999).
 RN [9]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein
 RL kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [10]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RL inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 RN [11]
 RP SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKKB AND IKKG.
 RX MEDLINE=21968797; PubMed=11971985;
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 RT "Regulation of SRC-3 (pCTP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
 RL activity by I kappa B kinase.";
 RL Mol. Cell. Biol. 22:3549-3561(2002).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-GAMMA/IKK-
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
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 CC -----
 DR EMBL, AF012890; AAC51662.1; -;
 DR EMBL, AF009225; AAC51671.1; -;
 DR EMBL, AF080157; AAD08996.1; -;
 DR EMBL, U22512; AAC50713.1; -;
 DR HSSP, Q63450; 1A06.
 DR GeneW, HGNC:1974; CHUK.
 DR MIM, 600664; -;
 DR GO, GO:0005737; C:cytoplasm; TAS.
 DR GO, GO:0006384; F:ikappaB kinase activity; TAS.
 DR GO, GO:0007345; F:embryogenesis and morphogenesis; TAS.
 DR GO, GO:0007252; P:I-kappaB phosphorylation; TAS.
 DR GO, GO:0006955; P:immune response; TAS.
 DR InterPro, IPR000719; Prot_kinase.
 DR InterPro, IPR002290; Ser_thr_kinase.
 DR InterPro, IPR001245; Tyr_kinase; I.
 DR Pfam, PF00069; kinase; I.

DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW transferase; Serine/threonine-protein kinase; ATP-binding;
 KW phosphorylation.
 FT DOMAIN 15 302
 FT 455 476
 FT 738 743
 FT NP_BIND 21 29
 FT BINDING 44 44
 FT ACT_SITE 144 144
 FT MOD_RES 23 23
 FT MOD_RES 176 176
 FT MUTAGEN 23 23
 FT MUTAGEN 44 44
 FT MUTAGEN 44 44
 FT MUTAGEN 176 176
 FT MUTAGEN 176 176
 FT MUTAGEN 176 176
 FT MUTAGEN 179 179
 FT MUTAGEN 180 180
 FT CONFLICT 543 543
 FT CONFLICT 604 604
 FT CONFLICT 679 680
 FT CONFLICT 684 684
 FT CONFLICT 686 687
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
 Query Match 86.1%; Score 31; DB 1; Length 745;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSL 6
 DB 738 LDYSL 743
 Search completed: February 18, 2004, 14:28:10
 Job time : 4.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	94.7	282	2 B70555	probable omt prote
2	33	91.7	404	2 JC5784	adrenomedullin rec
3	32	88.9	122	2 S52840	haloalkanoic acid
4	32	88.9	153	2 P90704	hypothetical prote
5	32	88.9	153	2 A85555	hypothetical prote
6	32	88.9	168	2 A83390	probable sigma-70
7	32	88.9	195	2 T29815	hypothetical prote
8	32	88.9	229	2 B38452	2-haloacid dehalog
9	32	88.9	251	2 B84016	hypothetical prote
10	32	88.9	259	2 AG0696	probable type III
11	32	88.9	302	2 C90869	probable transcrip
12	32	88.9	302	2 F85749	probable transcrip
13	32	88.9	302	2 F64883	probable transcrip
14	32	88.9	349	2 T15422	hypothetical prote
15	32	88.9	379	2 AH0542	conserved hypotet
16	32	88.9	386	2 H71511	probable 2-compone
17	32	88.9	391	2 A70663	hypothetical PEP prote
18	32	88.9	414	2 T44513	hypothetical prote
19	32	88.9	440	2 T32190	hypothetical prote
20	32	88.9	524	2 S33419	glycoprotein G - r
21	32	88.9	684	2 S41788	anti-1,4-beta-xyla
22	32	88.9	694	2 A95251	antigen, cell wall
23	32	88.9	700	2 P98115	conserved hypotet
24	32	88.9	704	2 T30910	xylanase (BC 3.2.1
25	32	88.9	735	2 T34531	hypothetical prote
26	32	88.9	705	2 S57486	ferrichryobactin
27	32	88.9	872	2 B75073	ATP-dependent RNA
28	32	88.9	915	2 A43802	cellulase (BC 3.2.
29	32	88.9	1039	2 S02711	cellulase (BC 3.2.

30	32	88.9	1209	2 T16663	hypothetical prote
31	32	88.9	1232	2 D64413	cobalamn biosynth
32	32	88.9	1319	2 S75705	hypothetical prote
33	32	88.9	1779	2 T31085	xylanase - Caldice
34	31	86.1	200	2 H64028	hypothetical prote
35	31	86.1	234	2 A93543	phosphoglycolate p
36	31	86.1	262	2 T20203	hypothetical prote
37	31	86.1	431	2 S09841	hypothetical prote
38	31	86.1	618	2 D71055	probable indolepyr
39	31	86.1	745	2 T49101	conserved helix-10
40	31	86.1	837	2 H82970	hypothetical prote
41	31	86.1	1010	2 D72203	hypothetical prote
42	30	83.3	61	2 D82732	hypothetical prote
43	30	83.3	144	2 A10698	probable pathogen
44	30	83.3	154	2 F90195	conserved hypotet
45	30	83.3	225	2 S38672	ywbB protein - Bac

ALIGNMENTS

RESULT 1
B70555
probable omt protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: B70555
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, J.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.
Mature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295887; PMID:9634230
A:Accession: B70555
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-282 <COL>
A:Cross-references: GB:Z95584; GB:AL123456; NID:G3261774; PID:CA809012.1; PID:6317129;
A:Experimental source: strain H37RV
C:Genes: omt
A:Gene: omt

Query Match 94.4%; Score 34; DB 2; Length 282;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 142 LDYSWL 147

RESULT 2
JC5784
adrenomedullin receptor - human
C:Species: Homo sapiens (man)
C:Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C:Accession: JC5784
R:Haenze, U.; Dietrich, K.; Doetsch, J.; Raecher, W.
Biochem. Biophys. Res. Commun. 240, 183-188, 1997
A>Title: Molecular cloning of a novel human receptor gene with homology to the rat adre
A:Reference number: JC5784; MUID:98042541; PMID:9367907
A:Accession: JC5784
A:Molecule type: mRNA
A:Residues: 1-404 <HAE>
A:Cross-references: GB:Y13583; NID:G2652933; PID:CAA73910.1; PID:G2652934
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; receptor; transmembrane protein
F:58-79/Domain: transmembrane #status predicted <TM1>
F:91-113/Domain: transmembrane #status predicted <TM2>
F:128-149/Domain: transmembrane #status predicted <TM3>
F:171-199/Domain: transmembrane #status predicted <TM4>
F:218-239/Domain: transmembrane #status predicted <TM5>

F:260-280/Domain: transmembrane #status predicted <TM6>
F:301-320/Domain: transmembrane #status predicted <TM>
F:28,37/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.7%; Score 33; DB 2; Length 404;
Best Local Similarity 83.3%; Pred. No. 82;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
| | | | |
Db 115 LDYTWL 120

RESULT 3

S52840

haloalkanoic acid dehalogenase - Xanthobacter autotrophicus (fragment)

C/Species: Xanthobacter autotrophicus

C/Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 11-Jan-2000

C/Accession: S52840

R:Van der Ploeg, J.; Janssen, D.B.

submitted to the EMBL Data Library, April 1995

A/Description: Sequence analysis of the upstream region of dhb, the gene encoding halo

A/Reference number: S52838

A/Accession: S52840

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-122 <VAN>

A/Cross-references: EMBL:X66084; NID:G763396; PIDN:CA60039.1; PID:G763399

C/superfamily: Alkaligenes eutrophus phosphoglycolate phosphatase

Query Match 88.9%; Score 32; DB 2; Length 122;
Best Local Similarity 83.3%; Pred. No. 36;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
| | | | |
Db 43 LDYSWL 48

RESULT 4

P90704

hypothetical protein EC60606 [imported] - Escherichia coli (strain O157:H7, substrain R1

C/Species: Escherichia coli

C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C/Accession: P90704

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hartfort, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene

A/Reference number: A9629; MUID:21156231; PMID:11258796

A/Accession: P90704

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-153 <NAV>

A/Cross-references: GB:BA000007; PIDN:BA034029.1; PID:G13360064; GSPDB:GN00154

A/Experimental source: strain O157:H7, substrain R1MD 050952

C/Genetics:

A/Gene: EC60606

Query Match 88.9%; Score 32; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 45;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 5
| | | | |
Db 83 LDYSWL 87

RESULT 5

AB5555

hypothetical protein Z0706 [imported] - Escherichia coli (strain O157:H7, substrain EDL9

C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C/Accession: AB5555
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lam, A.; Diallanita, E.; Potamoultis, K.; Apodect
Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: AB5480; MUID:21074935; PMID:11206551

A/Accession: AB5555

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-153 <STO>

A/Cross-references: GB:AB005174; NID:G12513450; PIDN:AA054901.1; GSPDB:GN00145; UNCP:Z

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A/Gene: Z0706

Query Match 88.9%; Score 32; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 45;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 5
| | | | |
Db 83 LDYSWL 87

RESULT 6

AB3390

probable sigma-70 factor, ECF subfamily PA2050 [imported] - Pseudomonas aeruginosa (str

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C/Accession: AB3390

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; I

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lin

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A/Reference number: AB2950; MUID:20437337; PMID:10984043

A/Accession: AB3390

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-168 <STO>

A/Cross-references: GB:AB004631; GB:AB004091; NID:G9948050; PIDN:AA05438.1; GSPDB:GN00

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA2050

Query Match 88.9%; Score 32; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 50;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
| | | | |
Db 18 DYSWL 22

RESULT 7

T29815

hypothetical protein C46A5.8 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T29815

R:Johnson, D.; Stellyes, L.

submitted to the EMBL Data Library, June 1996

A/Description: The sequence of C. elegans cosmid C46A5.

A/Reference number: Z20690

A/Accession: T29815

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-195 <JOH>

A/Cross-references: EMBL:U61948; PIDN:AB03148.1; GSPDB:GN00022; CESP:C46A5.8

A/Experimental source: strain Bristol N2; clone C46A5

C/Genetics:

A/Gene: CESP:C46A5.8

A/Map position: 4

A:introns: 93/3; 122/3

Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 195;
C:Species: *Pseudomonas* sp.
Matches 5; Conservative 100.0%; Pred. No. 59; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSL 6

DB 74 DYSL 78

RESULT 8

B38452

2-haloacid dehalogenase (EC 3.8.1.2) II - *Pseudomonas* sp.C:Species: *Pseudomonas* sp.
C:Date: 31-Jul-1991 #sequence_rev1sion 31-Jul-1991 #text_change 24-Nov-1999C:Accession: B38452
R:Schneider, B.; Mueller, R.; Frank, R.; Langens, F.

J. Bacteriol. 173, 1530-1535, 1991

A:Title: Complete nucleotide sequences and comparison of the structural genes of two 2-haloacid dehalogenases from *Pseudomonas* sp.
A:Reference number: A38452; MUID:91139597; PMID:1995594

A:Accession: B38452

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-229 <SCH>

A:Cross-references: GB:M62909; GB:M37619; NID:G151249; PIDN:AAA25833.1; PID:G151250

C:Superfamily: Alkaline phosphatase

C:Keywords: hydrolase

Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 229;
C:Species: *Bacillus halodurans*
Matches 5; Conservative 83.3%; Pred. No. 70; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSL 6

DB 45 LDYSL 50

RESULT 9

B84016

Hypothetical protein BH2930 [imported] - *Bacillus halodurans* (strain C-125)C:Species: *Bacillus halodurans*
C:Date: 01-Dec-2000 #sequence_rev1sion 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: B84016

R:Takami, H.; Nakagawa, K.; Takai, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: B84016

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-251 <STO>

A:Cross-references: GB:AP001517; GB:BA000004; NID:G10175500; PIDN:BA06649.1; GSPDB:GN00

C:Genetics:

A:Gene: BH2930

Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 251;
C:Species: *Bacillus halodurans*
Matches 5; Conservative 100.0%; Pred. No. 77; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSL 5

DB 153 LDYSL 157

RESULT 10

AG0696

probable type III secretion protein *seal* [imported] - *Salmonella enterica* subsp. *enterica*C:Species: *Salmonella enterica* subsp. *enterica* serovar TyphimuriumA:Note: this species has also been called *Salmonella typhimurium*

C:Date: 09-Nov-2001 #sequence_rev1sion 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AG0696

R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Cronin, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moyle, S.; O'Garra, P.

Nature 413, 848-852, 2001

A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* ser

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AG0696

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-259 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD01944.1; PID:G16502786; GSPDB:GN00176

C:Genetics:

A:Gene: *seal*

Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 259;
C:Species: *Escherichia coli*
Matches 5; Conservative 100.0%; Pred. No. 79; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSL 6

DB 67 DYSL 71

RESULT 11

C90869

probable transcription regulator *lysr*-type [imported] - *Escherichia coli* (strain O157:H7)C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_rev1sion 18-Jul-2001 #text_change 24-Aug-2001

C:Accession: C90869

R:Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.;

Gotoh, N.; Yasunaga, T.; Kihara, S.; Shibata, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen

A:Reference number: A96629; MUID:21156231; PMID:11258796

A:Accession: C90869

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-302 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA035346.1; PID:G13361388; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: *ECs1923*C:Superfamily: regulatory protein *lysr*

Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 302;
C:Species: *Escherichia coli*
Matches 5; Conservative 100.0%; Pred. No. 93; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSL 5

DB 191 LDYSL 195

RESULT 12

F85749

probable transcription regulator *lysr*-type *ydaK* [imported] - *Escherichia coli* (strain C-125)C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_rev1sion 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: F85749

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grobbeck, E.J.; Davis, N.W.; Lam, A.; Diallanta, E.; Potamoudis, K.; Apodaca

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: F85749

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-302 <STO>

A:Cross-references: GB:AB005174; NID:G12515416; PIDN:AG056458.1; GSPDB:GN00145; UNCP:22

A:Experimental source: strain O157:H7, substrain EDU933

C:Genetics:

A:Gene: *ydaK*

C:Superfamily: regulatory protein 1lv

Query Match 88.9%; Score 32; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSW 5
DB 191 LDYSW 195

RESULT 13

Probable transcritption regulator ydA - *Escherichia coli* (strain K-12)

C:Species: *Escherichia coli*

C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

C/Accession: F64883

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A.; Rose, D.J.; Mau, B.; Sano, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-302 <BLAT>

A:Cross-references: GB:AE000232; GB:U00096; NID:g1787600; PIND:AACT4421.1; PID:g1787601;

A:Experimental source: strain K-12, Substrain MG1655

C/Genetics:

A:Gene: ydA

C:Superfamily: regulatory protein 1lv

C:Keywords: DNA binding; transcription regulation

F:21-51/Region: regulatory protein 1lv motif

Query Match 88.9%; Score 32; DB 2; Length 302;

Best Local Similarity 100.0%; Pred. No. 93;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSW 5
DB 191 LDYSW 195

RESULT 14

T15422

hypothetical protein C06A8.6 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Jan-2000

C/Accession: T15422

R:Leimach, D.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid C06A8.

A:Reference number: Z18348

A/Accession: T15422

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-349 <LEI>

A:Cross-references: EMBL:U39849; NID:g1055041; PID:g1055044; PIND:AAA81047.1; CESP:C06A8

C/Genetics:

A:Gene: CESP:C06A8.6

A:Introns: 29/3; 202/3; 316/3

C:Superfamily: decorin, leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan

Query Match 88.9%; Score 32; DB 2; Length 349;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYSWL 6
DB 49 DYSWL 53

RESULT 15

AH0542

conserved hypothetical protein STY0359 (imported) - *Salmonella enterica* subsp. enteric

C:Species: *Salmonella enterica* subsp. enterica serovar Typh

A>Note: this species has also been called *Salmonella typhi*

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C/Accession: AH0542

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher;

th, T.; Connor, R.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar;

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K

A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* ser

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A/Accession: AH0542

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-379 <PAR>

A:Cross-references: GB:AL513382; PIND:CAD08784.1; PID:g16501600; GSPDB:GN00176

C/Genetics:

A:Gene: STY0359

C:Superfamily: Streptomyces coelicolor hypothetical protein SCR15.16c

Query Match 88.9%; Score 32; DB 2; Length 379;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYSWL 6
DB 275 DYSWL 279

Search completed: February 18, 2004, 14:38:48
Job time : 8.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgm2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgm2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgm2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgm2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgm2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgm2_6/prodata/1/1aa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	91.7	404	1	US-08-696-770-2
2	33	88.9	404	2	US-09-015-557-2
3	32	88.9	217	4	US-09-107-532A-4133
4	32	88.9	228	4	US-09-552-991A-24998
5	32	88.9	230	2	US-08-637-759B-457
6	32	88.9	230	3	US-08-871-355A-457
7	32	88.9	230	4	US-09-301-945-457
8	32	88.9	351	3	US-08-591-685-7
9	32	88.9	375	3	US-08-591-685-11
10	32	88.9	404	2	US-08-282-197C-62
11	32	88.9	438	2	US-08-282-197C-59
12	32	88.9	1426	3	US-09-136-574A-43
13	31	86.1	745	2	US-08-887-518-3
14	31	86.1	745	2	US-09-023-321-3
15	31	86.1	745	2	US-08-890-853-4
16	31	86.1	745	2	US-09-032-475-3
17	31	86.1	745	2	US-09-099-125A-4
18	31	86.1	745	2	US-09-099-124A-4
19	31	86.1	745	2	US-09-032-476-4
20	31	86.1	745	3	US-08-890-854-4
21	31	86.1	745	3	US-09-023-324-4
22	31	86.1	745	3	US-09-168-629-2
23	31	86.1	745	3	US-08-910-820-10
24	31	86.1	745	3	US-08-810-131A-2
25	31	86.1	745	4	US-09-109-986-4
26	31	86.1	745	4	US-09-844-908-10
27	31	86.1	745	4	US-09-668-758-3

28	31	86.1	756	2	US-08-887-518-4	Sequence 4, App11
29	31	86.1	756	2	US-09-023-321-4	Sequence 4, App11
30	31	86.1	756	2	US-08-890-853-2	Sequence 2, App11
31	31	86.1	756	2	US-09-032-475-4	Sequence 4, App11
32	31	86.1	756	2	US-09-099-125A-2	Sequence 2, App11
33	31	86.1	756	2	US-09-099-124A-2	Sequence 2, App11
34	31	86.1	756	3	US-09-032-476-2	Sequence 2, App11
35	31	86.1	756	3	US-08-890-854-2	Sequence 2, App11
36	31	86.1	756	3	US-09-023-324-2	Sequence 2, App11
37	31	86.1	756	3	US-09-168-629-15	Sequence 15, App1
38	31	86.1	756	3	US-08-910-820-9	Sequence 9, App11
39	31	86.1	756	4	US-09-109-986-2	Sequence 2, App11
40	31	86.1	756	4	US-09-844-908-9	Sequence 9, App11
41	31	86.1	756	4	US-09-868-758-4	Sequence 4, App11
42	31	86.1	996	4	US-09-417-197-123	Sequence 123, App
43	31	86.1	997	4	US-09-417-197-121	Sequence 121, App
44	31	86.1	1709	4	US-09-392-812A-6	Sequence 6, App1
45	30	83.3	112	4	US-09-328-352-7614	Sequence 7614, Ap

ALIGNMENTS

RESULT 1
US-08-696-770-2
; Sequence 2, Application US/08696770
; Patent No. 5763218
; GENERAL INFORMATION:
; APPLICANT: Fujii, Ryo
; APPLICANT: Hinuma, Shuji
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Pasteo Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,770
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: TAKS0001-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLBUCE TYPE: Peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:

US-08-696-770-2

Query Match 91.7%; Score 33; DB 1; Length 404;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 115 LDYTWL 120

RESULT 2

US-09-015-557-2
Sequence 2, Application US/09015557
Patent No. 5932702
GENERAL INFORMATION:
APPLICANT: Fujii, Ryo
APPLICANT: Hinuma, Shuji
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven
APPLICANT: Soppet, Daniel
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,557
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/696,770
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: TAK50001-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-09-015-557-2

Query Match 91.7%; Score 33; DB 2; Length 404;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 115 LDYTWL 120

RESULT 3

US-09-107-532A-4133

Sequence 4133, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4133:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...217
SEQUENCE DESCRIPTION: SEQ ID NO: 4133:
US-09-107-532A-4133

Query Match 88.9%; Score 32; DB 4; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5
Db 89 LDYSW 93

RESULT 4

US-09-252-991A-24998
Sequence 24998, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24998
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24998

Query Match 88.9%; Score 32; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
Db 78 DYSWL 82

RESULT 5
US-08-637-759B-457
; Sequence 457, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 457:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-457

Query Match 88.9%; Score 32; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
Db 67 DYSWL 71

RESULT 6

US-08-871-355A-457
; Sequence 457, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,355A
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 457:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-457

Query Match 88.9%; Score 32; DB 3; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
Db 67 DYSWL 71

RESULT 7
US-09-201-945-457
; Sequence 457, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; SOFTWARE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 457:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-201-945-457

Query Match 88.9%; Score 32; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
Db 67 DYSWL 71

RESULT 8
US-08-591-685-7
Sequence 7, Application US/08591685
Patent No. 6083733
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Thermostable xylanases
NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,685
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-685-7

Query Match 88.9%; Score 32; DB 3; Length 351;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
Db 317 DYSWL 321

RESULT 9
US-08-591-685-11
Sequence 11, Application US/08591685

Patent No. 6083733
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Thermostable xylanases
NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,685
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-685-11

Query Match 88.9%; Score 32; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
Db 328 DYSWL 332

RESULT 10
US-08-282-197C-62
Sequence 62, Application US/08282197C
Patent No. 5871730
GENERAL INFORMATION:
APPLICANT: Brzezinski, Ryszard
APPLICANT: Dery, Claude V
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0410000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-282-197C-62

Query Match 88.9%; Score 32; DB 2; Length 404;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
|||||

DB 328 DYSWL 332

RESULT 11

US-08-282-197C-59
; Sequence 59, Application US/08282197C
; Patent No. 5871730
; GENERAL INFORMATION:
; APPLICANT: Bizezinski, Ryszard
; APPLICANT: Dery, Claude V
; APPLICANT: Beaulieu, Carole
; TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Climbala, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0410000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: both

US-08-282-197C-59

Query Match 88.9%; Score 32; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
|||||

DB 339 DYSWL 343

RESULT 12

US-09-136-574A-43
; Sequence 43, Application US/09136574A
; Patent No. 6294366
; GENERAL INFORMATION:
; APPLICANT: Farrington, Graham K.
; APPLICANT: Anderson, Paige
; APPLICANT: Gibbs, Moreland
; APPLICANT: Bergquist, Peter
; APPLICANT: Daniels, Roy
; APPLICANT: Morgan, Hugh W.
; APPLICANT: Williams, Diane P.

TITLE OF INVENTION: Compositions and Methods for
Treating Cellulose Containing Fabrics Using Truncated
Cellulase Enzyme Compositions

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/932,571
FILING DATE: September 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 1997US001/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1426 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: No. 6294366e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-136-574A-43

Query Match 88.9%; Score 32; DB 3; Length 1426;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
|||||

DB 339 DYSWL 343

RESULT 13

US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
||:||||
DB 738 LDMSWL 743

RESULT 14
US-09-023-321-3
Sequence 3, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
||:||||

DB 738 LDMSWL 743

RESULT 15
US-08-890-853-4
Sequence 4, Application US/08890853
Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goedel, David V.
APPLICANT: Moronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
||:||||
DB 738 LDMSWL 743

Search completed: February 18, 2004, 14:41:49
Job time: 7.06579 secs

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OM protein - protein search, using ew model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDFSMTL 6

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
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3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/ECTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	91.4	452	4 US-09-252-991A-31360	Sequence 31360, A
2	31	88.6	21	1 US-08-798-897-13	Sequence 13, Appl
3	31	88.6	21	2 US-08-978-523-13	Sequence 13, Appl
4	31	88.6	23	2 US-08-337-646A-23	Sequence 23, Appl
5	31	88.6	23	3 US-08-927-326-23	Sequence 23, Appl
6	31	88.6	25	2 US-08-337-646A-29	Sequence 29, Appl
7	31	88.6	25	3 US-08-927-326-29	Sequence 29, Appl
8	31	88.6	154	3 US-08-077-848A-3	Sequence 3, Appl
9	31	88.6	154	3 US-09-211-640-3	Sequence 3, Appl
10	31	88.6	154	4 US-09-378-536-3	Sequence 3, Appl
11	31	88.6	154	4 US-09-687-260-3	Sequence 3, Appl
12	31	88.6	229	2 US-08-408-095-19	Sequence 19, Appl
13	31	88.6	232	2 US-08-408-095-17	Sequence 17, Appl
14	31	88.6	232	2 US-08-408-095-18	Sequence 18, Appl
15	31	88.6	236	1 US-08-112-208C-11	Sequence 11, Appl
16	31	88.6	236	1 US-08-248-819A-11	Sequence 11, Appl
17	31	88.6	236	1 US-08-607-269-21	Sequence 21, Appl
18	31	88.6	236	1 US-08-607-269-22	Sequence 21, Appl
19	31	88.6	236	2 US-08-337-646A-11	Sequence 11, Appl
20	31	88.6	236	2 US-08-856-531-11	Sequence 11, Appl
21	31	88.6	236	2 US-08-856-034-11	Sequence 11, Appl
22	31	88.6	236	3 US-09-127-048-9	Sequence 9, Appl
23	31	88.6	236	4 US-08-927-326-11	Sequence 11, Appl
24	31	88.6	236	4 US-09-379-820A-11	Sequence 11, Appl
25	31	88.6	236	5 PCT-US95-04600-21	Sequence 21, Appl
26	31	88.6	236	5 PCT-US95-04600-22	Sequence 22, Appl
27	31	88.6	239	1 US-08-333-565-51	Sequence 51, Appl

28	31	88.6	239	1 US-08-112-208C-10	Sequence 10, Appl
29	31	88.6	239	1 US-08-248-819A-10	Sequence 10, Appl
30	31	88.6	239	1 US-08-248-819A-12	Sequence 12, Appl
31	31	88.6	239	1 US-08-607-269-20	Sequence 20, Appl
32	31	88.6	239	1 US-08-471-058-12	Sequence 12, Appl
33	31	88.6	239	1 US-08-405-702A-12	Sequence 12, Appl
34	31	88.6	239	1 US-08-690-095-4	Sequence 4, Appl
35	31	88.6	239	2 US-08-465-485A-21	Sequence 21, Appl
36	31	88.6	239	2 US-08-661-479-51	Sequence 51, Appl
37	31	88.6	239	2 US-08-365-466A-15	Sequence 15, Appl
38	31	88.6	239	2 US-08-365-466A-17	Sequence 17, Appl
39	31	88.6	239	2 US-08-337-646A-10	Sequence 10, Appl
40	31	88.6	239	2 US-08-337-646A-12	Sequence 12, Appl
41	31	88.6	239	2 US-08-408-095-16	Sequence 16, Appl
42	31	88.6	239	2 US-08-856-531-10	Sequence 10, Appl
43	31	88.6	239	2 US-08-856-034-10	Sequence 10, Appl
44	31	88.6	239	3 US-08-471-057-12	Sequence 12, Appl
45	31	88.6	239	3 US-09-113-789-4	Sequence 4, Appl

ALIGNMENTS

```

RESULT 1
US-09-252-991A-31360
Sequence 31360, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31360
LENGTH: 452
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31360

Query Match      91.4% Score 32; DB 4; Length 452;
Best Local Similarity 83.3% Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDFSMTL 6
DB      410 LDFSMTL 415

RESULT 2
US-08-798-897-13
Sequence 13, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Gaestelila, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
STATE: Washington
CITY: Washington
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Edmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-798-897-13

Query Match 88.6%; Score 31; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 7 DFSWL 11

RESULT 3
US-08-978-523-13
Sequence 13, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Edmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-978-523-13

Query Match 88.6%; Score 31; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 7 DFSWL 11

RESULT 4
US-08-337-646A-23
Sequence 23, Application US/08337646A
Patent No. 5856171
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,646A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-337-646A-23

Query Match 88.6%; Score 31; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 16 DFSWL 20

RESULT 5
US-08-927-326-23
Sequence 23, Application US/08927326
Patent No. 6184202
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.

TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,646
FILING DATE: 10-NOV-1994
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-927-326-23

Query Match 88.6%; Score 31; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 16 DFSWL 20

RESULT 6
US-08-337-646A-29
Sequence 29, Application US/08337646A
Patent No. 5856171
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,646A

FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-337-646A-29

Query Match 88.6%; Score 31; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 16 DFSWL 20

RESULT 7
US-08-927-326-29
Sequence 29, Application US/08927326
Patent No. 6184202
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,646
FILING DATE: 10-NOV-1994
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-927-326-29

Query Match 88.6%; Score 31; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
|||
Db 16 DFSWL 20

RESULT 8
US-08-077-848A-3
Sequence 3, Application US/08077848A
Patent No. 5470955
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,848A
FILING DATE: 16-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: bcl-2a1pha
FEATURE:
NAME/KEY: Protein
LOCATION: 1..154
US-08-077-848A-3

Query Match 88.6%; Score 31; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
|||
Db 126 DFSWL 130

RESULT 9

US-09-211-640-3
Sequence 3, Application US/09211640
Patent No. 6020466
GENERAL INFORMATION:

APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,640
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441,375
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: bcl-2a1pha
FEATURE:
NAME/KEY: Protein
LOCATION: 1..154
US-09-211-640-3

Query Match 88.6%; Score 31; DB 3; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
|||
Db 126 DFSWL 130

RESULT 10
US-09-378-536-3
Sequence 3, Application US/09378536
Patent No. 6200763
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,536
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/077,848
FILING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: bcl-2alpha
FEATURE:
NAME/KEY: Protein
LOCATION: 1..154
US-09-378-536-3

Query Match 88.6%; Score 31; DB 3; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFWL 6
DB 126 DFWL 130

RESULT 11
US-09-687-260-3
Sequence 3, Application US/09687260
Patent No. 6528263
GENERAL INFORMATION:
APPLICANT: Craigs, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/687,260
FILING DATE: 12-OCT-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/378,536
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: PD-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: bcl-2alpha
FEATURE:
NAME/KEY: Protein
LOCATION: 1..154
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-687-260-3

Query Match 88.6%; Score 31; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFWL 6
DB 126 DFWL 130

RESULT 12
US-08-408-095-19
Sequence 19, Application US/08408095
Patent No. 5858678
GENERAL INFORMATION:
APPLICANT: Chinnadural, Govindasamy
TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,095
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
FILING DATE: (202)293-7060
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-408-095-19

Query Match 88.6%; Score 31; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFWL 6
DB 126 DFWL 130

Db 201 DFSWL 205

RESULT 13

US-08-408-095-17
Sequence 17, Application US/08408095
Patent No. 5858678

GENERAL INFORMATION:

APPLICANT: Chinnadurai, Govindaswamy
TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,095
FILING DATE: 21-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)293-7060

TELEFAX: (202)293-7860

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 232 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-408-095-17

Query Match 88.6%; Score 31; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6

Db 204 DFSWL 208

RESULT 14

US-08-408-095-18
Sequence 18, Application US/08408095
Patent No. 5858678

GENERAL INFORMATION:

APPLICANT: Chinnadurai, Govindaswamy
TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,095

FILING DATE: 21-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mack, Susan J.

REGISTRATION NUMBER: 30,951

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)293-7060

TELEFAX: (202)293-7860

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 232 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-408-095-18

Query Match 88.6%; Score 31; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6

Db 204 DFSWL 208

RESULT 15

US-08-112-208C-11
Sequence 11, Application US/08112208C
Patent No. 5691179

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/112,208C
FILING DATE: 26-AUG-1993

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15726A-000610

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 236 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-112-208C-11

Query Match 88.6%; Score 31; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6

Db 208 DFSWL 212

Wed Feb 18 17:21:03 2004

us-09-643-260-11.ra1

Page 7

Search completed: February 18, 2004, 14:41:49
Job time : 8.06579 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-10

Perfect score: 33

Sequence: 1 LDASWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	290	1	BLAI_XANMA
2	30	90.9	648	1	Y084_HUMAN
3	30	90.9	918	1	CARP_CORGL
4	30	90.9	919	1	CARP_CORCT
5	29	87.9	177	1	CYCL_PARD
6	29	87.9	245	1	HIS4_SHEON
7	29	87.9	277	1	THTI_CABEL
8	29	87.9	286	1	YDRC_ECOLI
9	29	87.9	289	1	THTR_CHICK
10	29	87.9	295	1	THTR_CHICK
11	29	87.9	296	1	RECO_ANASP
12	29	87.9	296	1	THTM_HUMAN
13	29	87.9	296	1	THTM_RAT
14	29	87.9	296	1	THTR_BOVIN
15	29	87.9	296	1	THTR_CHICK
16	29	87.9	296	1	THTR_HUMAN
17	29	87.9	299	1	RFBG_SALTY
18	29	87.9	359	1	RFBG_SALTY
19	29	87.9	360	1	MMT2_CABEL
20	29	87.9	424	1	Y826_METTH
21	29	87.9	430	1	PUCK_BACSU
22	29	87.9	459	1	NUAM_MOUSE
23	29	87.9	464	1	Y113_CABEL
24	29	87.9	477	1	RP54_ECOLI
25	29	87.9	477	1	RP54_KLEPN
26	29	87.9	477	1	RP54_SALTY
27	29	87.9	481	1	CHPS_EMENT
28	29	87.9	491	1	XYLE_ECOLI
29	29	87.9	509	1	TDT_HUMAN
30	29	87.9	510	1	G6PD_ASPNG
31	29	87.9	511	1	G6PD_EMENT
32	29	87.9	514	1	DKC1_HUMAN
33	29	87.9	520	1	TDT_BOVIN

34	29	87.9	854	1	DIS1_HUMAN
35	29	87.9	1034	1	BGLI_BACME
36	29	87.9	1043	1	RPO_NODAY
37	29	87.9	3770	1	ACVS_EMENT
38	29	87.9	225	1	ALKD_PSEPU
39	28	84.8	230	1	GPR4_BUCAP
40	28	84.8	325	1	IRF1_HUMAN
41	28	84.8	401	1	HIS2_SYNY3
42	28	84.8	494	1	DPOM_HUMAN
43	28	84.8	502	1	NU2C_MESVI
44	28	84.8	506	1	TDT_CHICK
45	28	84.8	508	1	NO60_DROME

ALIGNMENTS

RESULT 1
ID BLAI_XANMA STANDARD; PRT; 290 AA.
AC P52700;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Metallo-beta-lactamase Li precursor (Beta-lactamase, type II)
DS (EC 3.5.2.6) (Penicillinase).
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IID 1275;
RX MEDLINE=94289479; PubMed=8018721;
RA Walsh T.R., Hall L., Asseinder S.D., Nichols W.W., Cartwright S.J., Macgowan A.P., Bennett P.W.;
RT "Sequence analysis of the Li metallo-beta-lactamase from Xanthomonas maltophilia.";
RT Biochem. Biophys. Acta 1218:199-201(1994).
RN [2]
RP SEQUENCE OF 34-65.
RC STRAIN=IID 1275;
RX MEDLINE=86025393; PubMed=3931629;
RA Bicknell R., Emanuel E.L., Gagnon J., Waley S.G.;
RT "The production and molecular properties of the zinc beta-lactamase of Pseudomonas maltophilia IID 1275.";
RT Biochem. J. 229:791-797(1985).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX MEDLINE=99030465; PubMed=9611546;
RA Ullah J.H., Walsh T.R., Taylor I.A., Emery D.C., Verma C.S., Gambin S.J., Spencer J.;
RT "The crystal structure of the Li metallo-beta-lactamase from Stenotrophomonas maltophilia at 1.7 A resolution.";
RT J. Mol. Biol. 284:125-136(1998).
CC -1- FUNCTION: HAS A HIGH ACTIVITY AGAINST IMPENEM. UNSTABLE BELOW PH 8, UNLESS ZINC IS PRESENT.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-amino acid.
CC -1- COFACTOR: BINDS TWO ZINC IONS PER MOLECULE.
CC -1- ENZYME REGULATION: Inhibited by Hg(2+) or Cu(2+). Reduced enzymatic activity in presence of Co(2+), Ni(2+), Cd(2+), and Mn(2+).
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Periplasmic (potential).
CC -1- SIMILARITY: Belongs to the class-B beta-lactamase family.
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DR EMBL; X75074; CAA52968.1; -

DR PIR; S45349; S45349.

DR PDB; 1SML; 20-SEP-99.

DR InterPro; IPR001018; Beta_lactamase_B.

DR InterPro; IPR001279; Bactamase-like.

DR Pfam; PF00753; lactamase_B.1.

DR PROSITE; PS00743; BETA_LACTAMASE_B_1.1.

DR PROSITE; PS00744; BETA_LACTAMASE_B_2; FALSE NEG.

KW Hydrolase; Zinc; Antibiotic resistance; Periplasmic; Signal;

KW 3D-structure.

FT SIGNAL 1 21

FT PROPEP 22 33

FT CHAIN 34 290

FT DISULFID 239 267

FT METAL 105 105

FT METAL 107 107

FT METAL 109 109

FT METAL 181 181

FT METAL 205 205

FT METAL 217 217

FT CONFLICT 36 37

FT CONFLICT 40 40

FT CONFLICT 56 58

FT CONFLICT 63 63

FT HELIX 36 39

FT STRAND 41 41

FT STRAND 45 48

FT TURN 49 50

FT STRAND 51 53

FT STRAND 56 56

FT TURN 57 58

FT STRAND 59 59

FT TURN 62 66

FT STRAND 67 68

FT STRAND 69 73

FT STRAND 76 76

FT HELIX 78 80

FT HELIX 81 90

FT TURN 91 92

FT HELIX 95 97

FT STRAND 98 102

FT HELIX 108 111

FT TURN 112 113

FT HELIX 114 120

FT STRAND 124 127

FT HELIX 129 136

FT TURN 137 139

FT STRAND 142 142

FT TURN 143 145

FT STRAND 146 146

FT TURN 147 147

FT STRAND 158 159

FT TURN 162 163

FT STRAND 165 168

FT TURN 169 170

FT STRAND 171 177

FT TURN 210 211

FT TURN 218 219

FT TURN 221 222

FT HELIX 223 235

FT TURN 236 236

FT STRAND 241 243

FT HELIX 247 250

FT TURN 251 251

FT HELIX 254 259

FT TURN 260 263

POTENTIAL.

METALLO-BETA-LACTAMASE L1.

ZINC 1.

ZINC 1.

ZINC 2.

ZINC 1.

ZINC 2.

AS -> OR (IN REF. 2).

Q -> A (IN REF. 2).

TED -> ROH (IN REF. 2).

L -> H (IN REF. 2).

FT HELIX 267 287

SQ SEQUENCE 290 AA; 30801 MW; 0B34CAB54518BC1E CRC64;

Query Match

Best Local Similarity 83.3%; Score 30; DB 1; Length 290;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 34 VDASWL 39

RESULT 2

Y084 HUMAN STANDARD; PRT; 648 AA.

ID Y084 HUMAN

AC 014639;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypothetical protein KIAA0084 (HA2022) (Fragment).

GN KIAA0084.

OS Homo sapiens (Human).

OC Burkarya; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Bone marrow;

RX MEDLINE=95308325; PubMed=7788527;

RA Nagase T., Miyajima K.-I., Kawarabayashi Y., Kotani H., Sato S.,

RA Tabata S., Ishikawa K.-I., Kawarabayashi Y., Kotani H., Nomura N.,

RT Prediction of the coding sequences of unidentified human genes. III.

RT The coding sequences of 40 new genes (KIAA081-KIAA0120) deduced by

RT analysis of cDNA clones from human cell line KG-1."

RL DNA Res. 2:37-43(1995).

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CC -----

CC EMBL; D42043; BAA07644.1; -

KW Hypothetical protein.

KM NON TER 1

SQ SEQUENCE 648 AA; 70463 MW; 88F68A62D6C1CDA1 CRC64;

Query Match

Best Local Similarity 90.9%; Score 30; DB 1; Length 648;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 384 LDASWL 389

RESULT 3

CAP CORGL STANDARD; PRT; 918 AA.

ID CAP CORGL

AC P12860;

DT 01-OCT-1989 (Rel. 12, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).

GN PEP OR CGL1585.

OS Corynebacterium glutamicum (Brevibacterium flavum).

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.

OX NCBI_TaxID=1718;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 13059 / AS019;
 RA MEDLINE=8938460; PubMed=279518;
 RX Eikmanns B.J., Follett M.T., Griot M.U., Sinskey A.J.,
 RT "The phosphoenolpyruvate carboxylase gene of *Corynebacterium*
 RL glutamicum: molecular cloning, nucleotide sequence, and expression.";
 RN Mol. Genet. 218:330-339(1989).
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
 RC STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
 RX MEDLINE=89326141; PubMed=2666264;
 RA O'Regan M., Thierbach G., Bachmann B., Valleau D., Lepage P.,
 RT "Cloning and nucleotide sequence of the phosphoenolpyruvate
 RL carboxylase-coding gene of *Corynebacterium glutamicum* ATCC13032.";
 RN Gene 77:237-251(1989).
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
 RX Nakagawa S.;
 RL "Complete genomic sequence of *Corynebacterium glutamicum* ATCC 13032.";
 RT Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
 CC it forms oxaloacetate, a four-carbon dicarboxylic acid source for
 CC the tricarboxylic acid cycle.
 CC -1- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
 CC phosphoenolpyruvate + CO(2).
 CC -1- ENZYME REGULATION: ACTIVITY NOT STIMULATED BY ACETYL-COA IN THE
 CC ABSENCE OF ANY ALLOSTERIC INHIBITOR, WHILE THE CORRESPONDING
 CC PROTEIN FROM *E. COLI* IS STRONGLY STIMULATED.
 CC -1- PATHWAY: Tricarboxylic acid cycle.
 CC -1- SIMILARITY: BELONGS TO THE PEPCase FAMILY.
 CC -----
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 CC -----
 CC EMBL; X14234; CAA32450.1; -
 DR EMBL; M25819; AAB3537.1; -
 DR EMBL; A09073; CAA00837.1; -
 DR EMBL; AP05279; BAB98978.1; -
 DR PIR; S05512; QYFKG.
 DR HSSP; P00864; IFYI.
 DR HAMAP; MF_00595; -; 1.
 DR InterPro; IPR001449; PEPCase.
 DR Pfam; PF00311; PEPCase; 1.
 DR PRINTS; PR00150; PEPCaseXBLASE.
 DR PROSITE; PS00393; PEPCase_2; 1.
 DR PROSITE; PS00781; PEPCase_1; 1.
 KW Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle;
 KW Complete proteome.
 KW INIT MET 0
 FT ACT_SITE 137 137 BY SIMILARITY.
 FT ACT_SITE 578 578 BY SIMILARITY.
 FT ACT_SITE 606 607 KL -> NV (IN REF. 1).
 FT CONFLICT 799 800 FT -> LP (IN REF. 1).
 FT CONFLICT 914 914 L -> V (IN REF. 1).
 SQ SEQUENCE 918 AA; 103066 MW; A56C2703169D0698 CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 918;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASWL 6
 DB 104 LDATWL 109

ID CAP CORCT STANDARD; PRT; 919 AA.
 AC 093MH3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
 GN PEP.
 OS *Corynebacterium crenatum*.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxId=168810;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD945;
 RA Liu Y., Ding J., Wang Y.;
 RT "Cloning and expression of phosphoenolpyruvate carboxylase-coding gene
 RL in *Corynebacterium crenatum* CD945.";
 CC Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
 CC it forms oxaloacetate, a four-carbon dicarboxylic acid source for
 CC the tricarboxylic acid cycle.
 CC -1- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
 CC phosphoenolpyruvate + CO(2).
 CC -1- PATHWAY: Tricarboxylic acid cycle.
 CC -1- SIMILARITY: BELONGS TO THE PEPCase FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF406314; AAK92540.1; -
 DR HAMAP; MF_00595; -; 1.
 DR InterPro; IPR001449; PEPCase.
 DR Pfam; PF00311; PEPCase; 1.
 DR PRINTS; PR00150; PEPCaseXBLASE.
 DR PROSITE; PS00781; PEPCase_1; 1.
 DR PROSITE; PS00393; PEPCase_2; 1.
 KW Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle.
 FT ACT_SITE 138 138 BY SIMILARITY.
 FT ACT_SITE 579 579 BY SIMILARITY.
 SQ SEQUENCE 919 AA; 103331 MW; 10AE3F646AFPE604 CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 919;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASWL 6
 DB 105 LDATWL 110
 RESULT 5
 CYCL_PARD SEQUENCE STANDARD; PRT; 177 AA.
 ID CYCL_PARD SEQUENCE STANDARD; PRT; 177 AA.
 AC P29899;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c-h precursor (Cytochrome C5511) (C552).
 DB MOKO.
 GN *Paracoccus denitrificans*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Paracoccus.
 OX NCBI_TaxId=266;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Pd 1222;
 RX MEDLINE=92041581; PubMed=1657871;
 van Spanning R.J.M., Wansell C.W., de Boer T., Hazelaar M.J.,

RESULT 4
 CAP CORCT

RA Anazawa H., Harms N., Oltmann L.F., Stouthamer A.H.:
 RT "Isolation and characterization of the *moxX*, *moxI*, and *moxR*
 RT genes of *Paracoccus denitrificans*: inactivation of *moxX*, *moxG*, and
 RT *moxR* and the resultant effect on methylothrophic growth.";
 RL J. Bacteriol. 173:6948-6961(1991).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=9418715; PubMed=810419;
 RA Chen L., Durlley R., Mathews F.S., Davidson V.L.:
 RT "Structure of an electron transfer complex: methylamine
 RT dehydrogenase, amicyanin, and cytochrome c511.";
 RL Science 264:86-90(1994).
 CC -1- FUNCTION: ELECTRON ACCEPTOR FOR MDH. ACTS IN METHANOL OXIDATION.
 CC THIS CYTOCHROME HAS A REDOX POTENTIAL OF ABOUT +190 MV.
 CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).
 CC -1- INDUCTION: DURING GROWTH ON METHANOL.
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 CC -----
 CC EMBL, M57684; AAA25583.1; -;
 DR PIR; B41377; B41377.
 DR PDB; 2MTA; 31-JAN-94.
 DR InterPro; IPR000345; Cytc heme bind.
 DR PROSITE; PS00190; CYTOCHROME C/ 1.
 KM Electron transport; Heme; Signal; Methanol utilization; Periplasmic;
 KW 3D-structure. 1
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 177 CYTOCHROME C-L. (BY SIMILARITY).
 FT BINDING 79 79 HEME (COVALENT) (BY SIMILARITY).
 FT BINDING 82 82 HEME (COVALENT) (BY SIMILARITY).
 FT METAL 83 83 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT STRAND 27 27
 FT STRAND 34 34
 FT STRAND 37 39
 FT HELIX 42 44
 FT HELIX 48 56
 FT HELIX 60 63
 FT TURN 65 67
 FT HELIX 68 78
 FT TURN 79 79
 FT HELIX 80 83
 FT TURN 85 86
 FT HELIX 103 106
 FT HELIX 108 117
 FT TURN 121 122
 FT TURN 127 129
 FT HELIX 132 144
 FT TURN 145 145
 FT TURN 150 151
 FT TURN 154 155
 FT HELIX 158 162
 FT TURN 163 163
 SQ SEQUENCE 177 AA; 19396 MW; 6949FBD8B2C056E CRC64;
 Query Match 87.9%; Score 29; DB 1; Length 177;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DASWL 6
 DB 152 DASWL 156
 RESULT 6
 HIS4_SHEON STANDARD; PRT; 245 AA.
 AC Q8EFB5;

DT 15-SEP-2003 (Rel. 42; Created)
 DT 15-SEP-2003 (Rel. 42; Last sequence update)
 DT 15-SEP-2003 (Rel. 42; Last annotation update)
 DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) methylideneamino]
 DE imidazole-4-carboxamide isomerase (EC 5.3.1.16)
 DE (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
 DE isomerase)
 GN HIS4 OR SO2069.
 OS *Shewanella oneidensis*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Alteromonadaceae; *Shewanella*.
 OX NCBI_Taxid=70863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NR-1;
 RX MEDLINE=22297686; PubMed=12368813;
 RA Heidelberg J.F., Paulsen I.T., Neilson K.E., Gaidos E.J., Neilson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N., Mehe B., Clayton R.A.,
 RA Meyer T., Tsapin A., Scott J., Beaman M., Brinkac L., Daugherty S.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Halt D.H., Kolonay J.F.,
 RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
 RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
 RA Mueller J., Khouri H., Gill J., Uterback T.R., McDonald L.A.,
 RA Frelblyum T.V., Smith H.O., Venter J.C., Neilson K.H., Fraser C.M.;
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT *Shewanella oneidensis*.";
 RL Nat. Biotechnol. 20:1118-1123(2002).
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-
 CC phosphoribosylamino) methylideneamino] imidazole-4-carboxamide = 5-
 CC [(5-phospho-1-deoxyribitol-5-ylamino) methylideneamino]-1-(5-
 CC phosphoribosyl)imidazole-4-carboxamide. fourth step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE HIS4 / HISP FAMILY.
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 CC EMBL, AE015648; AAN55116.1; -;
 DR TIGR; SO2069; -;
 DR HAMAP; MF_01014; -; 1.
 DR InterPro; IPR006063; His4.
 DR InterPro; IPR006062; His biosynth.
 DR Pfam; PR00977; His biosynth. 1.
 DR TIGRPFAM; TIGR00007; TIGR00007. 1.
 KW Isomerase; Histidine biosynthesis; Complete proteome.
 SQ SEQUENCE 245 AA; 26017 MW; 6D40B1B3604527DA CRC64;
 Query Match 87.9%; Score 29; DB 1; Length 245;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DASWL 6
 DB 42 DASWL 46
 RESULT 7
 THYL_CABEL STANDARD; PRT; 277 AA.
 AC P91247;
 DT 15-JUL-1998 (Rel. 36; Created)
 DT 15-JUL-1998 (Rel. 36; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Putative thiosulfate sulfurtransferase Flig11.9 (EC 2.8.1.1).
 GN Flig11.9.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhoditidae; Peloderinae; Caenorhabditis.
 OK NCBI_Taxid=6239;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brictol N2;
 RA Latreille P., Deadman R.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
 CC -1- SIMILARITY: Contains 2 rhodanese domains.
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL; U80451; AAB37840.1; --
 DR PIR; T29797; T29797.
 DR HSSP; P00586; IRRS.
 DR Wormpep; F11G11.9; CE09351.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR001307; Rhodanese.
 DR Pfam; PF00581; Rhodanese; 1.
 DR SMART; SM00450; RHOD; 1.
 DR PROSITE; PS00683; RHODANES_2; FALSE_NEG.
 DR PROSITE; PS50206; RHODANES_3; 2.
 KW Hypothetical protein; Transferase; Repeat.
 FT DOMAIN 15 153 RHODANES_1.
 FT ACT_SITE 258 258 RHODANES_2.
 FT ACT_SITE 258 258 BY SIMILARITY.
 SQ SEQUENCE 277 AA; 30699 MW; 25BDF666CE12824C CRC64;
 Query Match 87.9%; Score 29; DB 1; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASW 5
 DB 22 LDASW 26
 RESULT 8
 YDBC_ECOLI STANDARD; PRT; 286 AA.
 AC P25906;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical oxidoreductase ydbc (EC 1.-.-.-).
 GN YDBC OR B1406.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OK NCBI_Taxid=562;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92190338; PubMed=1665988;
 RA Moszer I., Glaser P., Danchin A.;
 RT "Multiple 18 insertion sequences near the replication terminus in
 RL Escherichia coli K-12."
 RL Biochimie 73:1361-1374(1991).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426677; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Alba H., Baba T., Fujita K., Hayaishi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
 RA Oshima T., Saito N., Samped G., Seki Y., Sivasubram S.,
 RA Tagami H., Takeuchi J., Takemoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map."
 RL DNA Res. 3:363-377(1996).
 RN (4)
 RP SEQUENCE OF 1-69 FROM N.A.
 RC STRAIN=M / ATCC 11105;
 RX MEDLINE=98421522; PubMed=9748275;
 RA Ferrandez A., Minambres B., Garcia B., Olivera E.R., Luengo J.M.,
 RA Garcia J.L., Diaz E.;
 RT "Carbonylism of phenylacetic acid in Escherichia coli. Characterization
 RT of a new aerobic hybrid pathway".
 RL J. Biol. Chem. 273:25974-25986(1998).
 CC -1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
 CC -----
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 CC -----
 CC EMBL; X62680; AAC44553.1; --
 DR EMBL; AE000238; CAAC74488.1; --
 DR EMBL; D90779; BAA15021.1; --
 DR EMBL; X97452; CAA6103.1; --
 DR PIR; A48399; A48399.
 DR HSSP; P06332; 1HW6.
 DR Ecogene; EG11309; Ydbc.
 DR InterPro; IPR001395; Aldo/Ket_red.
 DR Pfam; PF00248; Aldo_ket_red.
 DR PRINTS; PR00069; ALDKETREDTASE.
 DR PRODOM; PD000288; Aldo/ket_red; 1.
 KW Hypothetical protein; Oxidoreductase; Complete proteome.
 SQ SEQUENCE 286 AA; 30706 MW; 82B587AEA91158F9 CRC64;
 Query Match 87.9%; Score 29; DB 1; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DASWL 6
 DB 92 DASWL 96
 RESULT 9
 THTR_CHICK STANDARD; PRT; 289 AA.
 AC P25324;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese).
 GN TST.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OK NCBI_Taxid=9031;
 RN (1)
 RP SEQUENCE.

RC TISSUE=Liver;
 RX MEDLINE=9113289; PubMed=2275748;
 RA Kohanski R.A., Heinrichson R.L.;
 RT "Primary structure of avian hepatic rhodanese.";
 RL J. Protein Chem. 9:369-377(1990).
 CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE
 DETOXIFICATION.
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
 CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
 THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
 CC -1- SIMILARITY: Contains 2 rhodanese domains.
 DR HSP; P00586; 1RHS.
 DR PIR; A37209; A37209.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR001307; Rhodanese.
 DR Pfam; PF00581; Rhodanese; 2.
 DR SMART; SM00450; RHOD; 2.
 DR PROSITE; PS00380; RHODANES_1; 1.
 DR PROSITE; PS00683; RHODANES_2; 1.
 DR PROSITE; PS00206; RHODANES_3; 2.
 KM Transferrase; Mitochondrion; Repeat.
 FT DOMAIN 24 142
 FT DOMAIN 143 158
 FT DOMAIN 172 284
 FT ACT_SITE 186 186
 FT ACT_SITE 244 244
 FT ACT_SITE 245 245
 FT ACT_SITE 246 246
 FT ACT_SITE 246 246
 FT SEQUENCE 289 AA; 32286 MW; 8BFCF71DE0B2BA4 CRC64;
 SO
 Query Match 87.9%; Score 29; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
 DB 31 LDASW 35

RESULT 10
 THTR RAT STANDARD; PRT; 295 AA.
 AC P24379;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thiosulfate sulfotransferase (EC 2.8.1.1) (Rhodanese) (Fragment).
 GN TST.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=91207296; PubMed=2018478;
 RA Weiland K.L., Dooley T.P.;
 RT "Molecular cloning, sequencing and characterization of cDNA to rat
 liver rhodanese, a thiosulphate sulphurtransferase.";
 RL Biochem. J. 275:227-231(1991).
 RN [2]
 RP MUTAGENESIS.
 RC TISSUE=Liver;
 RX MEDLINE=95332330; PubMed=7608189;
 RA Nagahara N., Okazaki T., Nishino T.;
 RT "Cytosolic mercaptopyruvate sulfurtransferase is evolutionarily

RT related to mitochondrial rhodanese. Striking similarity in active site
 RT amino acid sequence and the increase in the mercaptopyruvate
 RT sulfurtransferase activity of rhodanese by site-directed
 RT mutagenesis";
 RL J. Biol. Chem. 270:16230-16235(1995).
 CC -1- FUNCTION: INVOLVED IN THE FORMATION OF IRON-SULFUR COMPLEXES,
 CYANIDE DETOXIFICATION OR MODIFICATION OF SULFUR-CONTAINING
 ENZYMES. OTHER THIOL COMPOUNDS, BESIDES CYANIDE, CAN ACT AS SULFUR
 ION ACCEPTORS. ALSO HAS WEAK MERCAPTOPYRUVATE SULFURTRANSFERASE
 (MST) ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
 CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
 THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
 CC -1- SIMILARITY: Contains 2 rhodanese domains.
 CC -----
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 CC -----
 DR EMBL; X56228; CAA39677.1; -;
 DR PIR; S15081; S15081.
 DR HSP; P00586; 1RHS.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR001307; Rhodanese.
 DR Pfam; PF00581; Rhodanese; 2.
 DR SMART; SM00450; RHOD; 2.
 DR PROSITE; PS00380; RHODANES_1; 1.
 DR PROSITE; PS00683; RHODANES_2; 1.
 DR PROSITE; PS00206; RHODANES_3; 2.
 KM Transferrase; Mitochondrion; Repeat.
 FT NON_TER 1 1
 FT DOMAIN 23 141
 FT DOMAIN 142 157
 FT DOMAIN 171 286
 FT ACT_SITE 185 185
 FT ACT_SITE 246 246
 FT ACT_SITE 247 247
 FT ACT_SITE 248 248
 FT ACT_SITE 247 247
 FT MUTAGEN K->S; DECREASED RHODANES ACTIVITY;
 FT MUTAGEN 248 248
 FT SEQUENCE 295 AA; 33176 MW; 24C55B35690934E1 CRC64;
 SO
 Query Match 87.9%; Score 29; DB 1; Length 295;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
 DB 30 LDASW 34

RESULT 11
 RECO ANASP STANDARD; PRT; 296 AA.
 AC Q8YPL9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA repair protein reco (Recombination protein O).
 GN RECO OR ALR4175.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

OX NCBI_TaxID=103690;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Matnabe A., Iriuchi M., Ishikawa A., Kawasumi K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
 RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium *Anabaena* sp. strain PCC 7120.";
 RL DNA Res. 8:205-213 (2001).
 CC -1- FUNCTION: Involved in DNA repair and recombination
 CC -1- SIMILARITY: BELONGS TO THE RECO FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE RECO FAMILY.
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 CC -----
 DR EMBL: AP003595; BAB75874.1; -.
 DR PIR: AH2327; AH2327.
 DR HAMAP: MF_00201; -; 1.
 DR InterPro: IPR003717; RECO.
 DR Pfam: PF02565; RECO; 1.
 DR DNA repair: DNA recombination; Complete proteome.
 SQ SEQUENCE 296 AA; 32728 MW; A5B3D540F162BE72 CR664;
 QY Query Match 87.9%; Score 29; DB 1; Length 296;
 DB Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DASWL 6
 DB 256 DASWL 260
 RESULT 12
 THTM_HUMAN STANDARD; PRT; 296 AA.
 ID THTM_HUMAN
 AC P25325; 075750;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 3-mercapto-pyruvate sulfoltransferase (EC 2.8.1.2) (MST).
 GN MST OR TS12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92062122; PubMed=1953758;
 RA Pallini R., Guazzi G.C., Cannela C., Cacace M.G.;
 RT "Cloning and sequence analysis of the human liver rhodanese:
 RT comparison with the bovine and chicken enzymes.";
 RL Biochem. Biophys. Res. Commun. 180:887-893 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
 RA Clamp M., Smith L.J., Alnecough R., Almeida J.P., Babbage A.K.,
 RA Bagguley C., Bailey J., Bartow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,

RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grahame D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kerahaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leverhulme M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McLean O.T.,
 RA McElay J., McLaren S., McMurtry A.A., Milne S.D., Mortimore B.J.C.T.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson S., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L.,
 RA Scott C.E., Sehra H.K., Skuse C.D., Smalley S., Smith M.L.,
 RA Soderlund M., Spraggon L., Steward C.A., Sullivan J.E., Swann R.M.,
 RA Vandin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilner T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
 RA Roe B.A., Chan F., Chu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Lon P., Malat B., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Mux P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
 RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
 RA Emanuel H.E., Shaikh T., Kurahashi H., Salter S., Budarf M.L.,
 RA McEneaney B.S., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
 RA Kim U.J., Shizuya H., Simon M.I., Dunham J.P., Feyzad M., Kedra D.,
 RA Seroussi E., Franssen I., Tapia I., Bruder C.B., O'Brien K.P.,
 RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
 RA Tilahun Y., Wright H.;
 RT "The DNA sequence of human chromosome 22.";
 RL Nature 402:469-495 (1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow, Muscle, and Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen G.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang Y., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Uvedin T.B., Toshlyuk S., Carantini P., Prange C.,
 RA Bona S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Rausk S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Schnerker A., Schein J.E., Jones S.J.M., Werra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: TRANSFER OF A SULFUR ION TO CYANIDE OR TO OTHER THIOL
 CC COMPOUNDS. ALSO HAS WEAK RHODANSE ACTIVITY. MAY HAVE A ROLE IN
 CC CYANIDE DEGRADATION OR IN THIOSULFATE BIOSYNTHESIS.
 CC -1- CATALYTIC ACTIVITY: 3-mercapto-pyruvate + cyanide = pyruvate +
 CC thio-cyanate.
 CC -1- SUBUNIT: MONOMER OR DISULFIDE-LINKED HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
 CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
 CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
 CC -1- SIMILARITY: Contains 2 rhodanese domains.
 CC -1- CAUTION: Was originally (Ref.1) thought to be rhodanese.
 CC -----
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DR EMBL; X59434; CAA42060.1; -;
 DR EMBL; Z73420; CAA97763.1; -;
 DR EMBL; BC003508; AAH03508.1; -;
 DR EMBL; BC016737; AAH16737.1; -;
 DR EMBL; BC018717; AAH18717.1; -;
 DR PIR; JH0461; R0HU.
 DR HSSP; P00586; IRHS.
 DR Genew; HGNC:7223; MPST.
 DR MIM; 602496; -;
 DR GO; GO:0004792; F:chitosulfate sulfotransferase activity; TAS.
 DR GO; GO:0009440; P:cyanate carbonylism; TAS.
 DR GO; GO:0009636; P:response to toxin; TAS.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR001307; Rhodanese.
 DR Pfam; PF00581; Rhodanese; 2.
 DR SMART; SM00450; RHOD; 2.
 DR PROSITE; PS00380; RHODANSE_1; 1.
 DR PROSITE; PS00683; RHODANSE_2; 1.
 DR PROSITE; PS50206; RHODANSE_3; 2.
 DR TRANSFERRASE; Repeat.
 FT INIT MET 0 BY SIMILARITY.
 FT DOMAIN 24 143 RHODANSE 1.
 FT DOMAIN 144 159 HINGE.
 FT DOMAIN 173 287 RHODANSE 2.
 FT ACT_SITE 187 187 SUBSTRATE (MERCAPTOPYRUVATE) BINDING
 (BY SIMILARITY).
 FT ACT_SITE 196 196 SUBSTRATE (MERCAPTOPYRUVATE) BINDING
 (BY SIMILARITY).
 FT ACT_SITE 247 247 RRE -> TQ (IN REP. 1).
 FT CONFLICT 45 47
 FT SEQUENCE 296 AA; 33047 MW; 1991F0F1CAE8CB81 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 296;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
 |||||
 DB 31 LDASW 35

RESULT 13
 ID THRM RAT STANDARD; PRT; 296 AA.
 AC P97532;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 3-mercaptopyruvate sulfotransferase (EC 2.8.1.2) (MST).
 GN MPST.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS.
 RC STRAIN=WiStar; TISSUE=Liver;
 RX MEDLINE=97066916; PubMed=8910318;
 RA Nagahara N., Nishino T.;
 RT "Role of amino acid residues in the active site of rat liver
 RT mercaptopyruvate sulfotransferase. CDNA cloning, overexpression, and
 RT site-directed mutagenesis.";
 RL J. Biol. Chem. 271:27395-27401 (1996).
 RN [2]
 RP SEQUENCE OF 8-76 AND 146-284, AND CHARACTERIZATION.
 RC STRAIN=WiStar; TISSUE=Liver;

RX MEDLINE=95332330; PubMed=7608189;
 RA Nagahara N., Okazaki T., Nishino T.;
 RT "Cytosolic mercaptopyruvate sulfotransferase is evolutionarily
 RT related to mitochondrial rhodanese. Striking similarity in active site
 RT amino acid sequence and the increase in the mercaptopyruvate
 RT sulfotransferase activity of rhodanese by site-directed
 RT mutagenesis.";
 RL J. Biol. Chem. 270:16230-16235 (1995).
 CC -1- FUNCTION: TRANSFERS A SULFUR ION TO CYANIDE OR TO OTHER THIOL
 CC COMPOUNDS. ALSO HAS WEAK RHODANSE ACTIVITY. MAY HAVE A ROLE IN
 CC CYANIDE DEGRADATION OR IN THIOSULFATE BIOSYNTHESIS.
 CC -1- CATALYTIC ACTIVITY: 3-mercaptopyruvate + cyanide = pyruvate +
 CC thiocyanate.
 CC -1- SUBUNIT: MONOMER OR DISULFIDE-LINKED HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (MOSTLY) AND MITOCHONDRIAL.
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
 CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
 CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
 CC -1- PTM: THE N-TERMINAL IS BLOCKED.
 CC -1- SIMILARITY: Contains 2 rhodanese domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; D50564; BAA09127.1; -;
 DR HSSP; P00586; IRHS.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR001307; Rhodanese.
 DR Pfam; PF00581; Rhodanese; 2.
 DR SMART; SM00450; RHOD; 2.
 DR PROSITE; PS00380; RHODANSE_1; 1.
 DR PROSITE; PS00683; RHODANSE_2; 1.
 DR PROSITE; PS50206; RHODANSE_3; 2.
 DR TRANSFERRASE; Mitochondrion; Repeat.
 FT INIT MET 0
 FT DOMAIN 24 143 RHODANSE 1.
 FT DOMAIN 144 159 HINGE.
 FT DOMAIN 173 287 RHODANSE 2.
 FT ACT_SITE 187 187 SUBSTRATE (MERCAPTOPYRUVATE) BINDING.
 FT ACT_SITE 196 196 SUBSTRATE (MERCAPTOPYRUVATE) BINDING.
 FT ACT_SITE 247 247
 FT MUTAGEN 187 187
 FT MUTAGEN 196 196
 FT MUTAGEN 247 247
 FT MUTAGEN 248 248
 FT MUTAGEN 249 249
 FT MUTAGEN 249 249
 FT SEQUENCE 296 AA; 32809 MW; 0BCC176AC14C717C CRC64;

Query Match 87.9%; Score 29; DB 1; Length 296;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
 |||||
 DB 31 LDASW 35

RESULT 14
 ID THRM BOVIN STANDARD; PRT; 296 AA.
 AC P00586;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1992 (Rel. 23, last sequence update)
 DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE Thiolate sulfotransferase (EC 2.8.1.1) (Rhodanese).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 NC NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91161544; PubMed=2002017;
 RT Miller D.M., Delgado R., Chirgwin J.M., Hardies S.C., Horowitz P.M.;
 RL "Expression of cloned bovine adrenal rhodanese.";
 J. Biol. Chem. 266:4686-4691(1991).
 RN (2)
 RP SEQUENCE OF 1-294.
 RC TISSUE=Liver;
 RX MEDLINE=79048424; PubMed=711737;
 RT Russell J., Weng L., Kelm P.S., Heinrichson R.L.;
 RL "The covalent structure of bovine liver rhodanese. Isolation and
 partial structural analysis of cyanogen bromide fragments and the
 complete sequence of the enzyme.";
 J. Biol. Chem. 253:8102-8108(1978).
 RN (3)
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=79007483; PubMed=691057;
 RA Plogman J.H., Drent G., Kalk K.H., Hol W.G.J.;
 RT "Structure of bovine liver rhodanese. 1. Structure determination at
 2.5-A resolution and a comparison of the conformation and sequence of
 its two domains.";
 J. Mol. Biol. 123:557-594(1978).
 RN (4)
 RP X-RAY CRYSTALLOGRAPHY (1.36 ANGSTROMS).
 RX MEDLINE=98437562; PubMed=9761843;
 RA Gliubich F., Berni R., Colapietro M., Barba L., Zanotti G.;
 RT "Structure of sulfur-substituted rhodanese at 1.36-A resolution.";
 Acta Crystallogr. D 54:481-486(1998).
 RN (5)
 RP ACTIVE SITE.
 RX MEDLINE=79048425; PubMed=711738;
 RA Weng L., Heinrichson R.L., Westley J.;
 RT "Active site cysteinyl and arginyl residues of rhodanese. A novel
 formation of disulfide bonds in the active site promoted by
 phenylglyoxal.";
 J. Biol. Chem. 253:8109-8119(1978).
 RN (6)
 RP MUTAGENESIS OF ARG-186 AND LYS-249.
 RX MEDLINE=94179198; PubMed=8132546;
 RA Luo G.-X., Horowitz P.M.;
 RT "The sulfotransferase activity and structure of rhodanese are
 affected by site-directed replacement of Arg-186 or Lys-249.";
 J. Biol. Chem. 269:8220-8225(1994).
 CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE
 DETOXIFICATION. BINDS MOLECULAR OXYGEN AND SULFUR.
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
 CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
 THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
 CC -1- SIMILARITY: Contains 2 rhodanese domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL, M58561; AAA30753.1; -

DR PIR: A23704; ROBO.
 DR PDB: 1RHD; 27-JAN-84.
 DR PDB: 1RHS; 21-JAN-98.
 DR PDB: 2ORA; 01-AUG-96.
 DR PDB: 1ORR; 15-OCT-96.
 DR PDB: 1BOH; 27-APR-99.
 DR PDB: 1BOI; 27-APR-99.
 DR PDB: 1DP2; 13-DEC-00.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR001307; Rhodanese.
 DR Pfam; PF00581; Rhodanese; 2.
 DR SMART; SM00450; RHOD; 2.
 DR PROSITE; PS00180; RHODANES_1; 1.
 DR PROSITE; PS00683; RHODANES_2; 1.
 DR PROSITE; PS50206; RHODANES_3; 2.
 DR TRANSFERASE; Mitochondrion; 3d-structure; Repeat.
 KW INIT MET
 FT DOMAIN 0 24 142 0
 FT 143 158
 FT DOMAIN 172 287
 FT ACT_SITE 186 186
 FT ACT_SITE 247 247
 FT ACT_SITE 248 248
 FT ACT_SITE 249 249
 FT ACT_SITE 249 249
 FT VARIANT 1 2
 FT MUTAGEN 186 186
 FT MUTAGEN 249 249
 FT CONFLICT 99 99
 FT CONFLICT 214 214
 FT CONFLICT 219 219
 FT STRAND 9 10
 FT HELIX 12 20
 FT TURN 21 22
 FT STRAND 25 25
 FT STRAND 26 27
 FT TURN 28 32
 FT TURN 38 39
 FT HELIX 43 49
 FT STRAND 51 51
 FT TURN 53 54
 FT STRAND 56 57
 FT TURN 60 62
 FT TURN 66 67
 FT HELIX 77 86
 FT TURN 87 88
 FT TURN 91 92
 FT STRAND 94 98
 FT HELIX 108 117
 FT TURN 118 119
 FT STRAND 123 126
 FT TURN 127 128
 FT HELIX 129 135
 FT TURN 136 137
 FT STRAND 141 141
 FT HELIX 158 160
 FT STRAND 161 162
 FT HELIX 164 173
 FT STRAND 177 180
 FT HELIX 184 188
 FT TURN 189 189
 FT STRAND 203 204
 FT TURN 205 206
 FT STRAND 208 209
 FT HELIX 212 215
 FT STRAND 216 216
 FT TURN 218 219
 FT STRAND 222 222
 FT HELIX 225 234
 FT TURN 235 236
 FT TURN 239 240

RHODANES 1.
 HINGE.
 RHODANES 2.
 MAY PLAY A ROLE IN SUBSTRATE BINDING.
 SUBSTRATE (THIOSULFATE) BINDING
 (BY SIMILARITY).
 SUBSTRATE (THIOSULFATE) BINDING
 (BY SIMILARITY).
 MISSING (IN SOME PREPARATIONS, BUT THESE
 STILL EXHIBIT COMPLETE ENZYME ACTIVITY).
 R->A; NO RHODANES ACTIVITY.
 D -> N (IN REF. 2).
 N -> D (IN REF. 2).
 D -> N (IN REF. 2).


```

FT STRAND 243 246
FT TURN 252 252
FT HELIX 253 262
FT TURN 263 264
FT STRAND 269 271
FT HELIX 274 281
FT HELIX 284 286
FT STRAND 287 289
FT TURN 290 291
FT STRAND 292 292
SQ SEQUENCE 296 AA; 33164 MW; C8769696FA6AC11 CRC64;

Query Match
Best Local Similarity 87.9%; Score 29; DB 1; Length 296;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
DB 31 LDASW 35

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RESULT 15
ID THTR CRIGR STANDARD; PRT; 296 AA.
AC P46635;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thiolulfate sulfotransferase (EC 2.8.1.1) (Rhodanese).
GN TST.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=1029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96106946; PubMed=8535164;
RA Trevino R.J., Hunt J., Horowitz P.M., Chirgwin J.M.;
RT "Chinese hamster rhodanese cDNA: activity of the expressed protein is
RT not blocked by a C-terminal extension.";
RL Protein Expr. Purif. 6:693-699(1995).
CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE
CC DETOXIFICATION. BINDS MOLECULAR OXYGEN AND SULFUR.
CC -1- CATALYTIC ACTIVITY: Thiolulfate + cyanide = sulfite + thiocyanate.
CC -1- SUBUNIT: Monomer (by similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
CC -1- SIMILARITY: Contains 2 rhodanese domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; U23943; AAB84305.1; -.
CC HSSP; P00586; IRHS.
CC InterPro; IPR001763; Rhodanese-like.
CC InterPro; IPR001307; Rhodanese.
CC Pfam; PF00581; Rhodanese; 2.
CC SMART; SM00450; RHOD; 2.
CC PROSITE; PS00380; RHODANES_1; 1.
CC PROSITE; PS00683; RHODANES_2; 1.
CC PROSITE; PS50206; RHODANES_3; 2.
CC Trasnferase; Mitochondrion; Repeat.
CC INIT MET 0 0
CC DOMAIN 24 142 BY SIMILARITY.
CC RHODANES 1.

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FT DOMAIN 143 158 HINGE.
FT DOMAIN 172 287 RHODANES 2.
FT ACT_SITE 186 186 MAY PLAY A ROLE IN SUBSTRATE BINDING (BY
FT ACT_SITE 247 247 SIMILARITY).
FT ACT_SITE 248 248 BY SIMILARITY.
FT ACT_SITE 249 249 SUBSTRATE (THIOSULFATE) BINDING
FT ACT_SITE 249 249 (BY SIMILARITY).
FT ACT_SITE 249 249 SUBSTRATE (THIOSULFATE) BINDING
FT ACT_SITE 249 249 (BY SIMILARITY).
SQ SEQUENCE 296 AA; 33205 MW; 8811022BF9BAD666 CRC64;

Query Match
Best Local Similarity 87.9%; Score 29; DB 1; Length 296;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
DB 31 LDASW 35

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Search completed: February 18, 2004, 14:28:08
Job time : 4.55263 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35,929 Million cell updates/sec

Title: US-09-643-260-10
Perfect score: 33
Sequence: 1 LDASWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6CTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	919	3	US-08-985-916-16
2	30	90.9	935	4	US-09-271-438A-3
3	30	90.9	935	4	US-09-271-438A-8
4	29	87.9	118	4	US-09-634-238-354
5	29	87.9	136	4	US-09-370-838-123
6	29	87.9	194	4	US-09-252-991A-22578
7	29	87.9	277	4	US-09-252-991A-26048
8	29	87.9	438	4	US-09-252-991A-16758
9	29	87.9	661	4	US-09-252-991A-18225
10	29	87.9	834	4	US-09-252-991A-17616
11	28	84.8	128	4	US-09-205-258-254
12	28	84.8	210	3	US-08-611-587-4
13	28	84.8	219	3	US-09-247-373B-52
14	28	84.8	323	3	US-09-029-213B-25
15	28	84.8	402	4	US-09-328-352-5861
16	28	84.8	442	4	US-09-252-991A-26529
17	28	84.8	511	4	US-09-252-991A-27306
18	28	84.8	523	4	US-09-323-195A-17
19	28	84.8	588	4	US-09-252-991A-18861
20	27	81.8	36	5	US-08-118-270-244
21	27	81.8	36	5	PCT-US93-08528-244
22	27	81.8	134	4	US-09-732-210-395
23	27	81.8	144	4	US-09-732-210-629
24	27	81.8	167	4	US-09-252-991A-27865
25	27	81.8	233	4	US-09-252-991A-27758
26	27	81.8	263	2	US-08-790-137-4
27	27	81.8	263	2	US-08-824-874-5

28	27	81.8	263	3	US-08-807-151-5	Sequence 5, Appl1
29	27	81.8	263	3	US-09-210-084-5	Sequence 5, Appl1
30	27	81.8	263	4	US-09-478-957-5	Sequence 5, Appl1
31	27	81.8	263	4	US-09-764-762-5	Sequence 5, Appl1
32	27	81.8	272	4	US-09-252-991A-22260	Sequence 22260, A
33	27	81.8	316	4	US-09-252-991A-18153	Sequence 18153, A
34	27	81.8	385	2	US-08-694-915-2	Sequence 2, Appl1
35	27	81.8	413	2	US-08-960-756-2	Sequence 2, Appl1
36	27	81.8	416	2	US-08-844-915-4	Sequence 4, Appl1
37	27	81.8	423	1	US-08-844-064-7	Sequence 7, Appl1
38	27	81.8	423	4	US-09-009-433-7	Sequence 7, Appl1
39	27	81.8	423	4	US-08-850-348A-2	Sequence 2, Appl1
40	27	81.8	464	4	US-09-634-238-295	Sequence 295, App
41	27	81.8	479	4	US-09-634-238-248	Sequence 248, App
42	27	81.8	561	2	US-08-532-795-2	Sequence 2, Appl1
43	27	81.8	562	2	US-08-851-567B-30	Sequence 30, Appl1
44	27	81.8	569	2	US-08-532-795-23	Sequence 23, Appl1
45	27	81.8	569	2	US-08-532-795-29	Sequence 29, Appl1

ALIGNMENTS

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RESULT 1
US-08-985-916-16
Sequence 16, Application US/08985916
Patent No. 6221636
GENERAL INFORMATION:
APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIMURA, AND TSUYOSHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: VA
ZIP: 22152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985, 916
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325658
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 919 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-916-16
Query Match 90.9%; Score 30; DB 3; Length 919;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDASWL 6
Db 105 LDATWL 110
RESULT 2
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US-09-271-438A-3
; Sequence 3, Application US/09271438A
; Patent No. 6331419
; GENERAL INFORMATION:
; APPLICANT: IZUI, Hiroshi
; APPLICANT: ONO, Eiichi
; APPLICANT: MATSUI, Kazuhiko
; APPLICANT: MORIYA, Mika
; APPLICANT: ITO, Hisao
; APPLICANT: HARA, Yoshihiko
; TITLE OF INVENTION: L-GUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
; FILE REFERENCE: 0010-0989-0
; CURRENT APPLICATION NUMBER: US/09/271,438A
; CURRENT FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: JP10-69068
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: JP10-297129
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-09-271-438A-3

Query Match 90.9%; Score 30; DB 4; Length 935;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
||:||||
Db 10 LDSSWL 15

RESULT 3
US-09-271-438A-8
; Sequence 8, Application US/09271438A
; Patent No. 6331419
; GENERAL INFORMATION:
; APPLICANT: IZUI, Hiroshi
; APPLICANT: ONO, Eiichi
; APPLICANT: MATSUI, Kazuhiko
; APPLICANT: MORIYA, Mika
; APPLICANT: ITO, Hisao
; APPLICANT: HARA, Yoshihiko
; TITLE OF INVENTION: L-GUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
; FILE REFERENCE: 0010-0989-0
; CURRENT APPLICATION NUMBER: US/09/271,438A
; CURRENT FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: JP10-69068
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: JP10-297129
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-09-271-438A-8

Query Match 90.9%; Score 30; DB 4; Length 935;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
||:||||
Db 10 LDSSWL 15

RESULT 4
US-09-634-238-354
; Sequence 354, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukale, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christenson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 354
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-354

Query Match 87.9%; Score 29; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
|||||
Db 52 LDASW 56

RESULT 5
US-09-370-838-123
; Sequence 123, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Seciat, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 123
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-123

Query Match 87.9%; Score 29; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
|||||
Db 32 LDASW 36

RESULT 6
US-09-252-991A-22578
; Sequence 22578, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22578
LENGTH: 194
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22578

Query Match 87.9%; Score 29; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DASWL 6
Db 161 LDASWL 165

RESULT 7
US-09-252-991A-26048
Sequence 26048, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26048
LENGTH: 277
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26048

Query Match 87.9%; Score 29; DB 4; Length 277;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 89 LDADWL 94

RESULT 8
US-09-252-991A-16758
Sequence 16758, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16758
LENGTH: 438
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16758

Query Match 87.9%; Score 29; DB 4; Length 438;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 142 LDTSWL 147

RESULT 9
US-09-252-991A-18225
Sequence 18225, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18225
LENGTH: 661
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18225

Query Match 87.9%; Score 29; DB 4; Length 661;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 546 LDGSL 551

RESULT 10
US-09-252-991A-17616
Sequence 17616, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17616
LENGTH: 834
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17616

Query Match 87.9%; Score 29; DB 4; Length 834;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
Db 474 LDASW 478

RESULT 11
US-09-205-258-254
; Sequence 254, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 254
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (128)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-254

Query Match 84.8%; Score 28; DB 4; Length 128;
Best Local Similarity 83.3%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;
Matches 5; Conservative

QY 1 LDASW 6
Db 14 LDASW 19

RESULT 12
US-09-611-587-4
; Sequence 4, Application US/08611587
; Patent No. 6150921
; GENERAL INFORMATION:
; APPLICANT: PANDOLFO, MASSIMO
; APPLICANT: MONTERMINI, LAURA
; APPLICANT: MOLTO, MARIA D.
; APPLICANT: KOENIG, MICHAEL
; APPLICANT: CAMPUSANO, VICTORIA
; APPLICANT: COBBEE, MIREILLE
; TITLE OF INVENTION: Direct Diagnosis of Friedreich Ataxia
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P. Patent Dept.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77010
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,587
FILING DATE: 03-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brashers-Macatee, Sarah J.
REGISTRATION NUMBER: 38,087
REFERENCE/DOCKET NUMBER: D-5901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5620
TELEFAX: 713-651-5246
TELEX: 76-2829
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
POSITION IN GENOME:
UNITS: Dp
US-08-611-587-4

Query Match 84.8%; Score 28; DB 3; Length 210;
Best Local Similarity 83.3%; Pred. NO. 6.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 198 LDLSWL 203

RESULT 13
US-09-247-373B-52
Sequence 52, Application US/09247373B
Patent No. 6168954
GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NO 52
LENGTH: 219
TYPE: PRT
ORGANISM: SOYBEAN
US-09-247-373B-52

Query Match 84.8%; Score 28; DB 3; Length 219;
Best Local Similarity 66.7%; Pred. NO. 6.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 102 LDAMI 107

RESULT 14
US-09-029-213B-25
Sequence 25, Application US/09029213B
Patent No. 6180098
GENERAL INFORMATION:

APPLICANT: CHRISTIAN, Peter D.
TITLE OF INVENTION: RECOMBINANT HELICOVERPA BACULOVIRUSES
TITLE OF INVENTION: EXPRESSING HETEROLOGOUS DNA
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDermott, Will & Emery
STREET: 600 13th Street, NW
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/029,213B
FILING DATE: 31-AUG-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Hyobuk Kim
REGISTRATION NUMBER: 41,425
REFERENCE/DOCKET NUMBER: 50179-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-756-8000
TELEFAX: 202-756-8087
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-09-029-213B-25

Query Match 84.8%; Score 28; DB 3; Length 323;
Best Local Similarity 66.7%; Pred. NO. 9.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 191 LDSSWL 196

RESULT 15
US-09-328-352-5861
Sequence 5861, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5861
LENGTH: 342
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-5861

Query Match 84.8%; Score 28; DB 4; Length 342;
Best Local Similarity 83.3%; Pred. NO. 1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 307 LDAPWL 312

Search completed: February 18, 2004, 14:41:48
Job time: 7.06579 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignment)
89.145 Million cell updates/sec

Title: US-09-643-260-9
Perfect score: 40
Sequence: 1 LNMSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	95.0	526	8 Q9B964	Q9B964 ceratopsin
2	38	95.0	3103	5 Q9GV77	Q9GV77 lysozyme
3	37	92.5	204	16 Q9KER2	Q9KER2 bacillus ha
4	37	92.5	311	16 Q9ZM07	Q9ZM07 rhizobium m
5	37	92.5	337	16 Q8UB44	Q8UB44 agrobacteri
6	37	92.5	464	12 Q9WR50	Q9WR50 macaca mula
7	36	90.0	207	16 Q8RI33	Q8RI33 leptospira
8	36	90.0	210	11 Q9EPG8	Q9EPG8 rattus norv
9	36	90.0	254	2 Q9LBY3	Q9LBY3 shewanella
10	36	90.0	330	16 Q8XYA4	Q8XYA4 ralsstonia s
11	36	90.0	380	8 Q47545	Q47545 chlamydomon
12	36	90.0	442	10 Q9PED7	Q9PED7 oryza sativ
13	36	90.0	460	8 Q8HIG1	Q8HIG1 parazen pac
14	36	90.0	460	8 Q8HL32	Q8HL32 apocycclus
15	36	90.0	460	16 Q8ZL24	Q8ZL24 salmonella
16	36	90.0	460	16 Q8ZJ28	Q8ZJ28 salmonella

17	36	90.0	464	16 Q8RCS4	Q8RCS4 thermocaneer
18	36	90.0	490	16 Q8FPI8	Q8FPI8 corynebacte
19	36	90.0	493	2 Q8GPG7	Q8GPG7 pantoea agg
20	36	90.0	520	11 Q9JH11	Q9JH11 mus musculu
21	36	90.0	520	11 Q99K28	Q99K28 mus musculu
22	36	90.0	534	11 Q9D758	Q9D758 mus musculu
23	36	90.0	590	16 Q9I496	Q9I496 pseudomonas
24	36	90.0	744	16 Q3J087	Q3J087 mycobacteri
25	36	90.0	767	16 Q8G651	Q8G651 bifidobacte
26	36	90.0	864	13 Q73637	Q73637 fugu rubrip
27	35	87.5	116	2 Q68039	Q68039 rhodobacter
28	35	87.5	135	2 Q05744	Q05744 mycobacteri
29	35	87.5	145	5 Q810L0	Q810L0 drosophila
30	35	87.5	194	16 Q8D964	Q8D964 vibrio vuln
31	35	87.5	280	5 Q22375	Q22375 caenorhabd
32	35	87.5	321	5 Q94515	Q94515 drosophila
33	35	87.5	518	16 Q98134	Q98134 rhizobium 1
34	35	87.5	599	8 Q47815	Q47815 geomya perr
35	35	87.5	740	6 Q95KVI	Q95KVI bos taurus
36	35	87.5	741	12 Q8BC12	Q8BC12 gremmentell
37	35	87.5	745	11 Q8CBT3	Q8CBT3 mus musculu
38	35	87.5	756	6 Q95KVO	Q95KVO bos taurus
39	35	87.5	770	3 Q9P491	Q9P491 trichoderma
40	35	87.5	777	3 Q59898	Q59898 ampelomyces
41	35	87.5	792	3 Q9P8J3	Q9P8J3 comelomyx
42	34	85.0	69	2 Q87032	Q87032 vibrio chol
43	34	85.0	106	11 Q8CLU5	Q8CLU5 mus musculu
44	34	85.0	151	16 Q94K44	Q94K44 streptomyce
45	34	85.0	168	4 Q96B06	Q96B06 homo sapien

ALIGNMENTS

RESULT 1

Q9B964 ID Q9B964 PRELIMINARY: PRT: 526 AA.

AC 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DR 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Cytochrome oxidase subunit I (EC 1.9.3.1) (COI) (Cytochrome c oxidase polypeptide I) (Fragment).

OS Ceratopsian nanu.

OG Ceratopsian nanu.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea; Agaonidae; Agaoninae; Ceratopsian.

OK NCBI_TaxId=130016;

RM (1)

RN SEQUENCE FROM N.A.

RP STRAIN=G077;

RA Weiblen G.D.;

RT "Phylogenetic analyses of dioecious fig pollinators based on mitochondrial DNA sequences and morphology."

RL Submitted (Oct-1999) to the EMBL/GenBank/DBS databases.

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME C + 2 H(2)O.

CC -1- PATHWAY: RESPIRATORY CHAIN, TERMINAL STEP.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY. EMBL; AF200382; AA00073.1; --

DR HSSP; P18401; 1PFT.

DR InterPro; IPR00883; COX1.

DR Pfam; PF00115; COX1; 1.

DR PRINTS; PRO1165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1, 1.
 KM COPPER; Electron transport; Heme; Inner membrane; Membrane;
 KM Oxidoreductase; Respiratory chain; Transmembrane; Transport;
 KM Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 526 AA; 59586 MW; 587F82D8C4F2B62 CRC64;

Query Match 95.0%; Score 38; DB 8; Length 526;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 6
 DB 10 LNMWSL 15

RESULT 2

Q9GV77 PRELIMINARY; PRT; 3103 AA.

AC Q9GV77;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Embryonic blastocoel extracellular matrix precursor.
 GN ECM3.
 OS Lyechinus variegatus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
 OC Lyechinus.
 OX NCBI_TaxID=7654;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20340282; PubMed=10885756;
 RA Hodor P.G., Illies M.R., Bradley S., Etensohn C.A.;
 RT "Cell-substrate interactions during sea urchin gastrulation: migrating
 primary mesenchyme cells interact with and align extracellular matrix
 fibers that contain ECM3, a molecule with NG2-like and multiple
 calcium-binding domains";
 RT Dev. Biol. 222:181-194(2000).
 RL EMBL; AF287478; AAC00570.1; -
 DR EMBL; AF287478; AAC00570.1; -
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR003644; Calx_beta.
 DR Pfam; PF03160; Calx_beta; 5.
 DR SMART; SM00112; CA; 1.
 DR SMART; SM00237; Calx_beta; 5.
 DR PROSITE; PS50268; CADHERIN_2; 1.
 KM Matrix protein; Signal.
 FT SIGNAL 1 19
 SQ SEQUENCE 3103 AA; 343770 MW; 79D7EBDE1C54393 CRC64;

Query Match 95.0%; Score 38; DB 5; Length 3103;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 6
 DB 1724 LNMWSL 1729

RESULT 3

Q9KER2 PRELIMINARY; PRT; 204 AA.

AC Q9KER2;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein BH0787.
 GN BH0787.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=86665;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirata C., Nakamura Y., Ogasawara N., Kihara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001509; BAB04506.1; -
 DR InterPro; IPR006938; DUF624; 1.
 DR Pfam; PF04854; DUF624; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 204 AA; 23786 MW; 7C476B67E71015B2 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 204;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 6
 DB 22 LNMWSL 27

RESULT 4

Q92MU7 PRELIMINARY; PRT; 311 AA.

AC Q92MU7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Putative sugar transport system permease ABC transporter protein.
 GN R02512 OR SMC01978.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Gonzy J., Bothe G., Anpe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
 RA Pohl T., Portetelle D., Puenher A., Putnais B., Rampeger U.,
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT Sinorhizobium meliloti strain 1021";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 DR EMBL; AL591790; CAC47091.1; -
 DR InterPro; IPR000515; BPD_transp.
 DR Pfam; PF00528; BPD_transp; 1.
 DR PROSITE; PS00402; BPD_TRANS_P_NN_MEMBER; 1.
 KM Complete proteome.
 SQ SEQUENCE 311 AA; 34300 MW; 4BF3497341A2C198 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 311;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 6
 DB 138 LNMWSL 143

RESULT 5

Q8UB44 PRELIMINARY; PRT; 337 AA.

AC Q8UB44;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE ABC transporter, membrane spanning protein.

GN ATU3173 OR AGR_L_3272.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium.
 NCBI_TaxID=176299;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Sedul J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet M., Grant C.,
 RA Kuyavlin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
 RA Raymond C., Rouse G., Saenphimachak C., Xu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Neeter E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58".
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qureshi B., Goldman B.S., Cao Y., Askenzai M., Halling C., Mullin L.,
 RA Houmel K., Gordon J., Vaudin M., Iakchouk O., Epp A., Liu P.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Planagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58".
 RL Science 294:2323-2328 (2001).
 DR EMBL; AB009247; AAL4389.1; -
 DR EMBL; AB008366; AAK90213.1; -
 DR InterPro; IPR000515; BPD transp.
 DR Pfam; PF00528; BPD transp. 1.
 DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; 1.
 DR Complete proteome.
 KW SEQUENCE 337 AA; 37313 MW; 0F35B9A6E0D34813 CRC64;
 SQ
 Query Match 92.5%; Score 37; DB 16; Length 337;
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6
 DB 164 LNMAWL 169

RESULT 6
 QPWR50 PRELIMINARY; PRT; 464 AA.
 AC QPWR50;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Hypothetical 52.0 kDa protein (ORF32).
 OS Macaca mulatta rhadinovirus 17577, and
 OS Macaca mulatta rhadinovirus 26-95.
 OC Vitruvise; dsDNA vitruvise, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 NCBI_TaxID=83534; 119193;
 [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Macaca mulatta rhadinovirus 17577;
 RX MEDLINE=99174001; PubMed=10074154;
 RA Seale R.P., Bergman E.P., Arheim M.K., Wong S.W.;
 RT "Sequence and genomic analysis of a rhesus macaque rhadinovirus with
 RT similarity to Kaposi's sarcoma-associated herpesvirus/human
 RT herpesvirus 8".
 RL J. Virol. 73:3040-3053 (1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RC SPECIES=Macaca mulatta rhadinovirus 26-95;
 RC STRAIN=MACACA MULATTA RHADINOVIRUS ISOLATE 26-95;
 RX MEDLINE=20173730; PubMed=10708456;
 RA Alexander L., Denekamp L., Knapp A., Auerbach M.R., Damania B.,
 RA Desrochers R.C.;
 RT "The primary sequence of rhesus monkey rhadinovirus isolate 26-95:
 RT sequence similarities to Kaposi's sarcoma-associated herpesvirus and
 RT rhesus monkey rhadinovirus isolate 17577".
 RL J. Virol. 74:3388-3398 (2000).
 DR EMBL; AF083501; AAD21358.1; -
 DR EMBL; AF210726; AAP60010.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 464 AA; 51993 MW; ADB519AB96F511E5 CRC64;
 Query Match 92.5%; Score 37; DB 12; Length 464;
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6
 DB 397 VNMSWL 402

RESULT 7
 QP81E3 PRELIMINARY; PRT; 207 AA.
 ID QP81E3;
 AC QP81E3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fritling body developmental protein S-like protein.
 DE DVS OR LA3193.
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OC NCBI_TaxID=173;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar 1a1;
 RA Ren S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB011481; AAN50391.1; -
 KW Complete proteome.
 SQ SEQUENCE 207 AA; 23460 MW; 14775910CB7BB668 CRC64;
 Query Match 90.0%; Score 36; DB 16; Length 207;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMSWL 6
 DB 157 NMSWL 161

RESULT 8
 QP8PG8 PRELIMINARY; PRT; 210 AA.
 ID QP8PG8;
 AC QP8PG8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Brain Na+/Ca++ exchanger-associated protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RA Michaelis M.L., Hadwiger G.H., Islam S.I., Kumar K.N.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U53512; AAC38872.1; -
 DR InterPro; IPR000456; Ribosomal_L17.
 DR Pfam; PF01196; Ribosomal_L17; I.

SQ SEQUENCE 210 AA; 24405 MW; 3C9170304235B02D CRC64;

Query Match 90.0%; Score 36; DB 11; Length 210;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSW 5

126 LNMSW 130

RESULT 9

Q9LBY3 PRELIMINARY; PRT; 254 AA.

AC Q9LBY3; 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DE Quinol oxidase subunit III.

GN CyOA.

OS Shewanella violacea.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OX NCBI_TaxID=60217;

RN [1] SEQUENCE FROM N.A.

RA Quireishi M.H., Kato C., Nakasone K., Yamada M., Horikoshi K.;

RT "Pressure-regulation of a membrane-bound quinol oxidase in a deep-sea

piezophilic bacterium, Shewanella violacea."

RL Submitted (0CT-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB033827; BAA94864.1; -.

DR HSSP; P18400; 1CYW.

DR Interpro; IPR001505; Copper CuA.

DR Interpro; IPR006333; CyOA II.

DR Prodom; PD000131; Copper CuA; 1.

DR TIGRPM; TIGR01433; CyOA.1.

SQ SEQUENCE 254 AA; 28657 MW; F1870460580ACED CRC64;

Query Match 90.0%; Score 36; DB 2; Length 254;

Best Local Similarity 83.3%; Pred. No. 2.6e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNMSW 6

84 LNMSW 89

DB 84 LNMSW 89

RESULT 10

ID Q8XYA4 PRELIMINARY; PRT; 330 AA.

AC Q8XYA4; 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DE Probable transmembrane cytochrome c ubiquinol oxidase (Subunit II)

GN Oxidoreductase protein (EC 1.10.3.-).

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Ralstoniaceae; Ralstonia.

OX NCBI_TaxID=305;

RN [1] SEQUENCE FROM N.A.

RA Salanoubat M., Genin S., Artiguenave F., Gouy J., Manganec S.,

RA Arlet M., Billault A., Brothier P., Camus J.C., Catolico L.,

RA Chander M., Cholet N., Claudel-Renard C., Cunnac S., Demange N.,

RA Gaspin C., Lavie W., Moisan A., Robert C., Saurin W., Schlex T.,

RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,

RA Weisenbach J., Boucher C.A.;

RT "genome sequence of the plant pathogen Ralstonia solanacearum.";

RL Nature 415:497-502(2002).

DR EMBL; AL646067; CAD15560.1; -.

DR Interpro; IPR001505; Copper CuA.

DR Interpro; IPR006333; CyOA II.

DR Prodom; PD000131; Copper CuA; 1.

DR TIGRPM; TIGR01433; CyOA.1.

KW Oxidoreductase; Complete proteome.

SQ SEQUENCE 330 AA; 36117 MW; B82DF14452359B8 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 330;

Best Local Similarity 83.3%; Pred. No. 3.4e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNMSW 6

153 LNMSW 158

DB 153 LNMSW 158

RESULT 11

ID Q47545 PRELIMINARY; PRT; 380 AA.

AC Q47545; 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DE Apocytochrome b.

GN Cyb OR COB.

OS Chlamydomonas eugametos.

OC Mitochondria.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

OC Chlamydomonadaceae; Chlamydomonas.

OX NCBI_TaxID=3053;

RN [1] SEQUENCE FROM N.A.

RA MEDLINE=98145434; PubMed=9484440;

RT Denovan-Wright E.M., Nedelcu A.M., Lee R.W.;

RT "Complete sequence of the mitochondrial DNA of Chlamydomonas

eugametos."

RL Plant Mol. Biol. 36:285-295(1998).

RESULT 12

ID Q9FED7 PRELIMINARY; PRT; 442 AA.

AC Q9FED7; 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DE Probable transmembrane cytochrome c ubiquinol oxidase (Subunit II)

GN Oxidoreductase protein (EC 1.10.3.-).

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Ralstoniaceae; Ralstonia.

OX NCBI_TaxID=305;

RN [1] SEQUENCE FROM N.A.

RA Salanoubat M., Genin S., Artiguenave F., Gouy J., Manganec S.,

RA Arlet M., Billault A., Brothier P., Camus J.C., Catolico L.,

RA Chander M., Cholet N., Claudel-Renard C., Cunnac S., Demange N.,

RA Gaspin C., Lavie W., Moisan A., Robert C., Saurin W., Schlex T.,

RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,

RA Weisenbach J., Boucher C.A.;

RT "genome sequence of the plant pathogen Ralstonia solanacearum.";

RL Nature 415:497-502(2002).

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AC O9FED7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P0001B06.11 protein (P0671B11.33)
GN P0001B06.11 OR P0671B11.33.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzaceae; Oryza.
OX NCB1_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GAS) genomic DNA, chromosome 1, PAC
RT clone:P0001B06."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GAS) genomic DNA, chromosome 1, PAC
RT clone:P0671B11."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002537; BAB16858.1; -
DR EMBL: AP002746; BAB12171.1; -
DR Gramene; O9FED7; -
DR InterPro; IPR000048; IQ_region.
DR Pfam; PF00612; IQ_3.
DR SMART; SM00015; IQ_1.
SQ SEQUENCE 442 AA; 48947 MW; 2F783FEBE3740632 CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 10; Length 442;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMSWL 6
DB 274 NMSWL 278

RESULT 13
O8HLG1 PRELIMINARY; PRT; 460 AA.
AC O8HLG1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NADH dehydrogenase subunit 4.
GN ND4.
OS Parazen pacificus (parazen).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Zelformes; Paracnidae; Parazen.
OX NCB1_TaxID=181440;
RN [1]
RP SEQUENCE FROM N.A.
RA Miya M.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Miya M., Takehima H., Endo H., Ishiguro N.B., Inoue J.G., Mukai T.,
RA Satoh T.P., Yamaguchi M., Kawaguchi A., Mabuchi K., Shirai S.M.,
RA Nishida M.;
RT "Major Patterns of higher teleostean phylogenies: A new perspective
RT based on 100 complete mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 26:121-138(2002).
DR EMBL: AF004433; BAC23537.1; -
RA Mitochondrion.
SQ SEQUENCE 460 AA; 51399 MW; 2CF21B48B7B6CD7A CRC64;

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Query Match
Best Local Similarity 90.0%; Score 36; DB 8; Length 460;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMSWL 6
DB 388 NMSWL 392

RESULT 14
O8HL32 PRELIMINARY; PRT; 460 AA.
AC O8HL32;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NADH dehydrogenase subunit 4.
GN ND4.
OS Aptocyclops ventricosus (smooth lumpucker).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Scorpaeniformes;
OC Corioidae; Cyclopteridae; Aptocyclops.
OX NCB1_TaxID=181459;
RN [1]
RP SEQUENCE FROM N.A.
RA Miya M.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Miya M., Takehima H., Endo H., Ishiguro N.B., Inoue J.G., Mukai T.,
RA Satoh T.P., Yamaguchi M., Kawaguchi A., Mabuchi K., Shirai S.M.,
RA Nishida M.;
RT "Major Patterns of higher teleostean phylogenies: A new perspective
RT based on 100 complete mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 26:121-138(2002).
DR EMBL: AF004443; BAC23666.1; -
RA Mitochondrion.
SQ SEQUENCE 460 AA; 51277 MW; 335D673853B97A26 CRC64;

Query Match
Best Local Similarity 90.0%; Score 36; DB 8; Length 460;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSW 5
DB 387 LNMSW 391

RESULT 15
O8ZL24 PRELIMINARY; PRT; 460 AA.
AC O8ZL24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative glycosyl hydrolase family.
GN STM3775.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCB1_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L72 / SCSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Portolillo S., All J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan B., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium

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RT LT2."
RL Nature 413:852-856(2001).
DR EMBL; AE008876; AAL2633.1; -.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRIASE1.
DR ProDom; PD000650; Glyco_hydro_1; 1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
KW Hydrolase; Hypothetical protein; Complete proteome.
SQ SEQUENCE 460 AA; 53173 MW; 1FC5F45D6E96709 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 460;

Best Local Similarity 100.0%; Pred.No. 4.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6

DB 418 NWSWL 422

Search completed: February 18, 2004, 14:35:46
Job time : 19.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-9
Perfect score: 40
Sequence: 1 LNM5WL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	204	1 YTI6_CAEEL	Q10919 caenorhabdi
2	36	90.0	767	1 MERE_BIFLO	Q8651 bifidobacte
3	35	87.5	325	1 RIR2_MYCLE	Q9cbq2 mycobacteri
4	35	87.5	745	1 IKKA_HUMAN	Q15111 h inhibitor
5	35	87.5	745	1 IKKA_MOUSE	Q60680 m inhibitor
6	35	87.5	756	1 IKKG_HUMAN	Q14920 homo sapien
7	35	87.5	757	1 IKKG_MOUSE	Q88351 mus musculu
8	35	87.5	757	1 IKKG_RAT	Q9qy78 rattus norv
9	34	85.0	154	1 Y451_SYNY3	P29920 paracoccu
10	34	85.0	345	1 NCO8_PAPDE	P42032 rhododact
11	34	85.0	345	1 NUOH_RHOCA	P06591 escherichia
12	34	85.0	444	1 T1SD_ECOLI	Q10187 schizosacch
13	34	85.0	612	1 YAMD_SCHPO	Q24488 drosophila
14	34	85.0	685	1 ROR1_DROME	Q33822 aserina pe
15	33	82.5	54	1 ATP8_ASTPE	Q88343 wlgglewort
16	33	82.5	157	1 RHM_WIGBR	P30535 bos tauris
17	33	82.5	169	1 PKBS_BOVIN	P30536 homo sapien
18	33	82.5	169	1 PKBS_HUMAN	P50637 mus musculu
19	33	82.5	169	1 PKBS_MOUSE	P16257 rattus norv
20	33	82.5	169	1 PKBS_MOUSE	P21995 mus musculu
21	33	82.5	330	1 EMB_MOUSE	Q02761 rhododact
22	33	82.5	444	1 CYB_MOUSE	P12768 streptomyce
23	33	82.5	455	1 PIR_STRGR	P31348 influenza a
24	33	82.5	470	1 NRAM_IKLE	P31349 influenza a
25	33	82.5	470	1 NRAM_IKLE	P03469 influenza a
26	33	82.5	470	1 NRAM_IKLE	P03469 influenza a
27	33	82.5	479	1 LMRB_BAGSU	P44105 haemophilus
28	33	82.5	514	1 T3YH_HAKIN	P44105 haemophilus
29	33	82.5	529	1 YOP4_CAEEL	Q08531 caenorhabdi
30	33	82.5	627	1 YHE0_YEAST	P36731 saccharomyc
31	33	82.5	735	1 DHR2_YEAST	P36731 saccharomyc
32	33	82.5	752	1 8511_TRYCR	P12629 trypanosoma
33	33	82.5	877	1 SULH_SCHPO	Q74377 schizosacch

34	33	82.5	1053	1 HMDH_SCHPO	Q10283 schizosacch
35	33	82.5	1564	1 N184_SCHPO	Q9p7m8 schizosacch
36	33	82.5	1951	1 VGF1_IBVD	P27920 avian infec
37	32	80.0	53	1 ATP8_ANOGA	P34836 anopheles g
38	32	80.0	53	1 ATP8_ANOGU	P34836 anopheles g
39	32	80.0	53	1 ATP8_ARTSF	Q37707 atremia san
40	32	80.0	54	1 ATP8_COHLO	Q9afp7 cochlioniyla
41	32	80.0	54	1 ATP8_PANLI	P12697 paracentroc
42	32	80.0	55	1 ATP8_STRPU	P15997 strongyloce
43	32	80.0	151	1 CT78_HUMAN	Q9br46 homo sapien
44	32	80.0	154	1 Y66A_METUA	P81329 methanococc
45	32	80.0	181	1 ISP2_VIRCH	Q9kre2 vibrio chol

ALIGNMENTS

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RESULT 1
YTI6_CAEEL STANDARD; PRT; 204 AA.
AC Q10919;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 23.6 kDa protein B0252.6 in chromosome II.
GN B0252.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z., Waterston R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC
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CC -----
CC EMBL; U23453; AAC46760.1; -.
CC PIR; T15295; T15295.
CC WormPep; B0252.6; CB02422.
CC DR Hypothetical protein.
CC KW SEQUENCE 204 AA; 23610 MW; 59FB15536CD22F43 CRC64;
CC -----
Query Match 90.0%; Score 36; DB 1; Length 204;
Best local similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 NMSWL 6
DB 96 NMSWL 100

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RESULT 2

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MERE_BIFLO STANDARD; PRT; 767 AA.
ID MERE_BIFLO
AC Q8651;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 5-methyltetrahydropteroylglutamate--homocysteine methyltransferase
DE (EC 2.1.1.14) (methionine synthase, vitamin-B12 independent isozyme)
DE (Cobalamin-independent methionine synthase).
GN MERE OR B10798.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.

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OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karmaliantzou M., Snel B., Vilianova D., Berger B.,
RA Peesl G., Zwaenen M.-C., Desiere F., Bork P., Delley M.,
RA Fridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -1- FUNCTION: Catalyzes the transfer of a methyl group from 5-
CC methyltetrahydrofolate to homocysteine resulting in methionine
CC formation (by similarity).
CC -1- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-L-glutamate + L-
CC homocysteine = tetrahydropteroyltri-L-glutamate + L-methionine.
CC -1- COFACTOR: zinc; binds one ion per subunit (by similarity).
CC -1- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
CC -1- SIMILARITY: Belongs to the vitamin-B12 independent methionine
CC synthase family.
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-----
DR EMBL; AE014702; AAN24613.1; -
DR HAMM; MF 00172; -1
DR InterPro; IPR002629; Methionine_synth.
DR InterPro; IPR006276; Met_syn_B12ind.
DR Pfam; PF01717; Methionine_synth; 1.
DR ProDom; PD004692; Methionine_synth; 2.
DR TIGRfam; TIGR01371; met_syn_B12ind; 1.
KW Transferase; Methyltransferase; Methionine biosynthesis; zinc; Repeat;
KM Complete proteome.
FT METAL 652 ZINC (BY SIMILARITY).
FT METAL 654 ZINC (BY SIMILARITY).
FT METAL 737 ZINC (BY SIMILARITY).
SQ SEQUENCE 767 AA; 85358 MW; 839AC62929F9D26 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 767;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWSM 5
DB 569 LNMWSM 573

RESULT 3
RIR2_MYCLE STANDARD; PRT; 325 AA.
AC 09CR02;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonucleoside-diphosphate reductase beta chain (EC 1.1.7.4.1)
DE (Ribonucleotide reductase small subunit).
GN NRDP OR ML1731.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11334002;
RA Cole S.T., Sigmeister K., Parthali J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungell K., Basham D., Brown D., Chillingworth T., Connor R.,

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RA Davies R.M., Devlin K., Duthey S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornby T., Jagels K., Lacroix C., Maclean J., Moulé S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus."
RL Nature 409:1007-1011(2001).
CC -1- FUNCTION: CATALYZES THE BIOSYNTHESIS OF DEOXYRIBONUCLEOTIDES FROM
CC THE CORRESPONDING RIBONUCLEOTIDES, PRECURSORS THAT ARE NECESSARY
CC FOR DNA SYNTHESIS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside diphosphate + oxidized
CC thiorodoxin + (H2O) = ribonucleoside diphosphate + reduced
CC thiorodoxin.
CC -1- COFACTOR: BINDS 2 IRON IONS (BY SIMILARITY).
CC -1- PATHWAY: DNA replication pathway; first step.
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE
CC SMALL CHAIN FAMILY. MORE SIMILAR TO ENTEROBACTERIAL NRDP THAN TO
CC NRDP.
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DR EMBL; AL583923; CAC30684.1; -
DR PIR; B87125; B87125.
DR HSSP; P17424; 2R2F.
DR Lepoma; ML1731; -
DR InterPro; IPR000358; Ribonuc1 reductase.
DR Pfam; PF00268; ribonuc_red_sm1.1.
DR PROSITE; PS00369; RIBORED_SMALL; 1.
KW Oxidoreductase; DNA replication; iron; Complete proteome.
FT METAL 73 IRON 1 (BY SIMILARITY).
FT METAL 104 IRON 1 AND 2 (BY SIMILARITY).
FT METAL 107 IRON 1 (BY SIMILARITY).
FT METAL 164 IRON 2 (BY SIMILARITY).
FT METAL 198 IRON 2 (BY SIMILARITY).
FT METAL 201 IRON 2 (BY SIMILARITY).
FT ACT_SITE 111 BY SIMILARITY.
SQ SEQUENCE 325 AA; 37316 MW; A80D29751183358B CRC64;

Query Match 87.5%; Score 35; DB 1; Length 325;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWSM 6
DB 15 LNMWSM 20

RESULT 4
IKKA_HUMAN STANDARD; PRT; 745 AA.
ID IKKA_HUMAN
AC 015111; 014666; Q13132; Q92467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
DE (I kappa-B kinase alpha) (IKK- $\alpha$ ) (IKK-A) (I $\kappa$ B $\alpha$  kinase)
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
GN CHUK OR IKK $\alpha$ .
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RC TISSUE-T-cell;
RX MEDLINE=9738646; PubMed=9244310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
RT "Identification and characterization of an IkappaB kinase."; *Cell* 90:373-383(1997).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97394460; PubMed=9252186;
RA DiDonato J.A., Hayekawa M., Rothwarf D.M., Zandi E., Karin M.;
RT "A cytokine-responsive IkappaB kinase that activates the transcription factor NF-kappaB"; *Nature* 388:548-554(1997).
RN [3]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND SER-176.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L., Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation."; *Science* 278:860-866(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and embryonic tissues but localized to different human chromosomes."; *Gene* 222:331-40(1998).
RN [5]
RP SEQUENCE OF 32-745 FROM N.A.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=96258427; PubMed=8777433;
RA Connolly M.A., Marcu K.B.;
RT "CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase catalytic domain."; *Cell* Mol. Biol. Res. 41:537-549(1995).
RN [6]
RP PHOSPHORYLATION BY MAP3K4/NIK, AND MUTAGENESIS OF SER-176; THR-179 AND SER-180.
RX MEDLINE=98188283; PubMed=9550446;
RA Ling L., Cao Z., Goeddel D.V.;
RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of Ser-176."; *Proc. Natl. Acad. Sci. U.S.A.* 95:3792-3797(1998).
RN [7]
RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
RX MEDLINE=99413720; PubMed=10485710;
RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M., Donner D.B.;
RT "NF-kappaB activation by tumour necrosis factor requires the Akt serine-threonine kinase."; *Nature* 401:82-85(1999).
RN [8]
RP IKKA-IKKB BINDING.
RX MEDLINE=99212141; PubMed=10195894;
RA Delhase M., Hayekawa M., Chen Y., Karin M.;
RT "Positive and negative regulation of IkappaB kinase activity through IKKbeta subunit phosphorylation."; *Science* 284:309-313(1999).
RN [9]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase."; *Mol. Cell. Biol.* 18:7336-7343(1998).
RN [10]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;

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RA Jobin C,Sartor R,B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am.J.Physiol. 276:C451-C462(2000).
RN [(1)]
RP SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKKB AND IKBG.
RX MEDLINE=21968797; PubMed=11971985;
RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
R O'Walley B.W.;
RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RT activity by I kappa B kinase.";
RL Mol. Cell. Biol. 22:3549-3561(2002).
CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3.
CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated
CC when dephosphorylated.
CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
CC also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MAP3K4/NIK, MEKK1, IRAK and IKK-alpha-p65-p50
CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
CC a complex composed of NCOA2, NCOA3, IKKB, IKBG and CREBBP.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- PPM: Phosphorylated by MAP3K4/NIK, AKT and to a lesser extent by
CC MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IRAKPB KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL; AF012890; AAC51662.1; -.
DR EMBL; AF009225; AAC51671.1; -.
DR EMBL; AF080157; AAD08996.1; -.
DR EMBL; U22512; AAC50713.1; -.
DR HSSP; Q63450; 1A06.
DR Genew; HGNC:1974; CHUK.
DR MIM; 600664; -.
DR GO; GO:0005737; C:cytosolam; TAS.
DR GO; GO:0008384; F:Ikappab kinase activity; TAS.
DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
DR GO; GO:0007252; P:i-kappab phosphorylation; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPRO00719; Prot_kinase.
DR InterPro; IPRO02290; Ser_thr_pkinase.
DR InterPro; IPRO01245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SMO0220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR PROSITE; PSS0011; PROTEIN KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 302 PROTEIN KINASE.
FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 738 743 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 144 144 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).
FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14).
FT MOTIFEN 23 23 T-S-A: LOSS OF PHOSPHORYLATION AND DECREASE OF KINASE ACTIVITY.
```


FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->M: LOSS OF AUTOPHOSPHORYLATION.
 FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF ACTIVITY.
 FT MUTAGEN 176 176 S->B: FULL ACTIVATION.
 FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
 FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
 FT CONFLICT 543 543 E->G (IN REF. 2).
 FT CONFLICT 604 604 L->R (IN REF. 5).
 FT CONFLICT 679 680 TS->AY (IN REF. 5).
 FT CONFLICT 684 684 P->A (IN REF. 3 AND 5).
 FT CONFLICT 687 687 TS->DL (IN REF. 5).
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
 Query Match 87.5%; Score 35; DB 1; Length 745;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6
 Db 738 LDMSWL 743

RESULT 5
 ID IKKA_MOUSE STANDARD; PRT; 745 AA.
 AC 060680; Q9D2X3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (I κ B 2.7.1.1-)
 DE (1-kappa-B kinase alpha) (IKK α) (IKK-A) (I κ B kinase)
 DE (1-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
 kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1KX).
 GN CHUK OR IKKA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/c;
 RX MEDLINE=96044444; PubMed=7556004;
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 chromosome 10 and mouse chromosome 19.";
 RL Genomics 27:348-351(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/c;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connolly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 families of interacting proteins, contains a serine-threonine kinase
 catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Fukuishi Y., Kono H., Adachi J., Fukuda S.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kodera K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
 RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kienl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Bocelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gietzung S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyoka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Konteak S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=20198447; PubMed=10733566;
 RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R.,
 RA Gelezianus R., Marcu K.B.;
 RT "Functional isoforms of I κ B kinase alpha (IKK α) lacking
 RT leucine zipper and helix-loop-helix domains reveal that IKK α and
 RT IKK β have different activation requirements.";
 RL Mol. Cell. Biol. 20:2635-2649(2000).
 RN [5]
 RP PHOSPHORYLATION BY MAP3K14/NIK.
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of I κ B kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RP IKK-A-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delnase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of I κ B kinase activity through
 RT IKK β subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [7]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of I κ B kinase by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [8]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-gamma/IKK-epsilon.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q60680-1; Sequence=Displayed;
 CC Name=2; Synonyms=Delta LH;
 CC IsoId=Q60680-2; Sequence=VSP_004866; VSP_004867;
 CC Name=3; Synonyms=Delta H;
 CC IsoId=Q60680-3; Sequence=VSP_004866, VSP_004869;
 CC TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
 CC 3 are expressed predominantly in brain and T-lymphocytes.
 CC -1- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
 CC E11, E15 and E17 days. In the limb development, its expression
 CC predominates in the limb buds at E12.5 day.

RP IDENTIFICATION IN A COMPLEX WITH CREBBP, NCOA2, NCOA3, IKKA AND IKKB.
 RX MEDLINE=21968797; PubMed=11971985;
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 O'Malley B.W.;
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
 activity by I kappa B kinase.";
 RL Mol. Cell. Biol. 22:3549-3561(2002).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 the dissociation of the inhibitor/NF-kappa-B complex and
 ultimately the degradation of the inhibitor. Also phosphorylates
 NCOA3 (by similarity).
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50
 complex. Phosphorylated IKB-alpha is further released from the
 complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
 and CREBBP.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
 muscle, kidney, pancreas, spleen, thymus, prostate, testis and
 peripheral blood.
 CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
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 DR EMBL; AF029664; AAC51860.1; -;
 DR EMBL; AF080158; AAD08997.1; -;
 DR EMBL; AF031416; AAC64675.1; -;
 DR EMBL; BC006231; AAH06231.1; -;
 DR HSSP; Q63450; 1A06.
 DR Genew; HGNC:5960; IKKBK.
 DR MIM; 603258; -;
 DR GO; GO:0005737; C:cytoplasm; NAS.
 DR GO; GO:0005524; P:ATP binding activity; NAS.
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; NAS.
 DR GO; GO:0016563; P:transcriptional activator activity; NAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR002290; Ser Thr kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00240; Ubiquitin; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS0011; PROTEIN KINASE DM; 1.
 KM Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT NP BIND 737 742 NEMO-BINDING.
 FT ACT_SITE 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT MOD_SITE 145 145 BY SIMILARITY.
 FT MOD_RSS 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RSS 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RSS 181 181 PHOSPHORYLATION.
 FT MTAGN 44 44 K-2A: LOSS OF KINASE ACTIVITY AND NO
 EFFECT ON BINDING TO NIK.
 FT MTAGN 177 177 S-2A: DECREASE OF ACTIVITY.
 FT MTAGN 177 177 S-2B: FULL ACTIVATION.
 FT MTAGN 181 181 S-2A: DECREASE OF ACTIVITY.
 FT MTAGN 181 181 S-2B: FULL ACTIVATION.
 FT CONFLICT 231 255 WSKVRKSKSEVDIVSBDLNGTVWF -> CYRMMPGTVAHS

FT FT CNPSTLGGGRGRI (IN REF. 5).
 FT CONFLICT 425 425 Q -> H (IN REF. 1).
 SQ SEQUENCE 756 AA; 86563 MW; F9C4DF671AE9E14E CRC64;
 Query Match 87.5%; Score 35; DB 1; Length 756;
 Best Local Similarity 83.3%;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNMSTL 6
 Db 737 LDMSTL 742
 RESULT 7
 ID IKKB MOUSE STANDARD; PRT; 757 AA.
 AC 088351; Q9RLJ6;
 DT 16-OCT-2001 (Rel. 40. Created)
 DT 16-OCT-2001 (Rel. 40. Last sequence update)
 DT 28-FEB-2003 (Rel. 41. Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIB).
 GN IKKB OR IKKB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SOURCE: FROM N.A. AND PHOSPHORYLATION BY MEKK1.
 RC STRAIN=C57BL/6; TISSUE=spleen;
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 Okumura K.;
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 protein kinase/ERK kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
 constitutively phosphorylates serine residues of Ikb.";
 RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE=99455228; PubMed=10523828;
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
 developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [5]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 inflammation and protection.";
 RL Am. J. Physiol. 278:G451-G462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 the dissociation of the inhibitor/NF-kappa-B complex and
 ultimately the degradation of the inhibitor. Also phosphorylates
 NCOA3.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can

CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P55-P50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKs
 CC and CREBBP (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
 CC -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
 CC the mouse embryo, at E9.5 day its expression begins to be
 CC localized to the brain, neural ganglia, neural tube, and in liver
 CC at E12.5 day. At E15.5 day, the expression is further restricted
 CC to specific tissues of the embryo.
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF026524; AAC23557.1; -
 CC EMBL: AF088910; AAD52095.1; -
 CC HSSP: Q63450; 1A06.
 CC MGD: MGI:1338071; Ikkb.
 CC InterPro: IPR000719; Prot Kinase.
 CC InterPro: IPR002290; Ser Thr kinase.
 CC InterPro: IPR001245; Tyr kinase.
 CC Pfam: PF00069; kinase_1.
 CC PRINTS: PR00109; TYRKINASE.
 CC PRODOM: PD000001; Prot Kinase; 1.
 CC PROSITE: PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 CC PROSITE: PS00108; PROTEIN KINASE ST; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC phosphorylation.
 CC KW DOMAIN 15 300 PROTEIN KINASE.
 CC FT 458 479 LEUCINE-ZIPPER (POTENTIAL).
 CC FT DOMAIN 737 742 NEMO-BINDING.
 CC FT NP_BIND 21 29 ATP (BY SIMILARITY).
 CC FT BINDING 44 44 ATP (BY SIMILARITY).
 CC FT ACT_SITE 145 145 ATP (BY SIMILARITY).
 CC FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 CC FT CONFLICT 56 56 N -> D (IN REF. 2).
 CC FT CONFLICT 343 343 N -> D (IN REF. 2).
 CC FT CONFLICT 356 356 K -> E (IN REF. 2).
 CC FT CONFLICT 390 390 L -> F (IN REF. 2).
 CC FT CONFLICT 406 406 P -> Q (IN REF. 2).
 CC FT FT 573 573 K -> R (IN REF. 2).
 CC FT CONFLICT 736 757 TLDSWLTQWEDERCLSEQACD -> VTA (IN REF.
 CC FT SEQUENCE 757 AA; 86690 MW; PED962095449C5E CRC64;
 CC Query Match 87.5%; Score 35; DB 1; Length 757;
 CC Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 LKMSWL 6
 CC DB 737 LKMSWL 742
 CC
 CC RESULT 8
 CC ID IKKB_RAT STANDARD; PRT; 757 AA.
 CC AC Q9QY78;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)
 DE (I-kappa-B-kinase beta) (IKK-beta) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 OX [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.
 RT "IKK beta in megakaryocyte differentiation."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., D'Onato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase."
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection."
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-alpha-P55-P50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKs, IKKs
 CC and CREBBP (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
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 CC -----
 CC EMBL: AF15282; AAF21978.1; -
 CC HSSP: Q63450; 1A06.
 CC InterPro: IPR000719; Prot Kinase.
 CC InterPro: IPR002290; Ser Thr kinase.
 CC InterPro: IPR001245; Tyr kinase.
 CC Pfam: PF00069; kinase_1.
 CC PRINTS: PR00109; TYRKINASE.
 CC PRODOM: PD000001; Prot Kinase; 1.
 CC PROSITE: PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 CC PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC phosphorylation.
 CC KW DOMAIN 15 300 PROTEIN KINASE.
 CC FT 458 479 LEUCINE-ZIPPER (POTENTIAL).
 CC FT DOMAIN 737 742 NEMO-BINDING.
 CC FT NP_BIND 21 29 ATP (BY SIMILARITY).
 CC FT BINDING 44 44 ATP (BY SIMILARITY).
 CC FT ACT_SITE 145 145 ATP (BY SIMILARITY).
 CC FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 CC FT SEQUENCE 757 AA; 86690 MW; PED962095449C5E CRC64;
 CC Query Match 87.5%; Score 35; DB 1; Length 757;
 CC Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 LKMSWL 6
 CC DB 737 LKMSWL 742
 CC
 CC RESULT 8
 CC ID IKKB_RAT STANDARD; PRT; 757 AA.
 CC AC Q9QY78;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)

FT MOD RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 757 AA; 86866 MW; 3AF6A6A7DF91F9C CRC64;

Query Match 87.5%; Score 35; DB 1; Length 757;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 6
 DB 737 LNMWSL 742

RESULT 9
 ID Y451_S1YNY3 STANDARD; PRT; 154 AA.
 AC P74576;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein s110451.
 GN S110451.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97061201; PubMed=8905231;
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nanno K.,
 RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Rep. 3:109-136(1996).
 CC -1- SIMILARITY: BELONGS TO THE UPF0039 (ELAA) FAMILY.

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 CC -----
 CC CC EMBL; D90917; BAA18794.1; -
 CC DR PIR; S76882; S76882.
 CC DR InterPro; IPR00182; GCS5acetyltransf.
 CC DR Pfam; PF00583; Acetyltransf. 1.
 CC KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 154 AA; 17612 MW; C84777660627F9C2 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 154;
 Best Local Similarity 80.0%; Pred. No. 49;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 5
 DB 3 LNMWSL 7

RESULT 10
 ID N008_PARDE STANDARD; PRT; 345 AA.
 AC P29920;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NADH-quinone oxidoreductase chain 8 (EC 1.6.99.5) (NADH dehydrogenase
 DE I, chain 8) (NDH-1, chain 8).
 GN N008.

OS Paracoccus denitrificans.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Paracoccus.
 OX NCBI_TaxID=266;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13543; PubMed=8422400;
 RA Xu X., Matsumo-Yagi A., Yagi T.;
 RT "DNA sequencing of the seven remaining structural genes of the gene
 RT cluster encoding the energy-transducing NADH-quinone oxidoreductase
 RT of Paracoccus denitrificans.";
 RL Biochemistry 32:968-981(1993).
 CC -1- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
 CC sulfur (Fe-S) centers, to quinones in the respiratory chain. The
 CC immediate electron acceptor for the enzyme in this species is
 CC believed to be ubiquinone. Couples the redox reaction to proton
 CC translocation (for every two electrons transferred, four hydrogen
 CC ions are translocated across the cytoplasmic membrane), and thus
 CC conserves the redox energy in a proton gradient.
 CC -1- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
 CC -1- SUBUNIT: COMPOSED OF 14 DIFFERENT SUBUNITS. SUBUNITS N007-14
 CC CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.

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 CC -----
 CC DR EMBL; L02354; AAA25592.1; -
 CC DR PIR; C45456; C45456.
 CC DR InterPro; IPR001694; Resp_NADH_dh1.
 CC DR Pfam; PF00146; NADHdh1.
 CC DR PROSITE; PS00667; COMPLEX1_ND1_1; 1.
 CC DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
 CC KW Oxidoreductase; NAD; Quinone; Ubiquinone; Transmembrane.
 FT TRANSMEM 15 35 POTENTIAL.
 FT TRANSMEM 82 102 POTENTIAL.
 FT TRANSMEM 115 135 POTENTIAL.
 FT TRANSMEM 161 181 POTENTIAL.
 FT TRANSMEM 190 210 POTENTIAL.
 FT TRANSMEM 253 273 POTENTIAL.
 FT TRANSMEM 278 298 POTENTIAL.
 FT TRANSMEM 309 329 POTENTIAL.
 SQ SEQUENCE 345 AA; 38751 MW; E33B667B5E9506B4 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 345;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNMWSL 6
 DB 191 LNMWSL 196

RESULT 11
 ID N008_RHOCA STANDARD; PRT; 345 AA.
 AC P42032;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NADH-quinone oxidoreductase chain H (EC 1.6.99.5) (NADH dehydrogenase
 DE I, chain H) (NDH-1, chain H).
 GN N008 OR NDHA.
 OS Rhodobacter capsulatus (Rhodospirillum rubrum capsulata).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Rhodobacter.

```

OX  NCBI_TaxID=1061;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 33303 / B10;
RA  MEDLINE=92233948; PubMed=1568483;
RX  Dupuis A.;
RT  "Identification of two genes of Rhodobacter capsulatus coding for
RT  proteins homologous to the ND1 and 23 kDa subunits of the
RT  mitochondrial complex I."
RL  FEBS Lett. 301:215-218(1992).
CC  -1- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
CC  sulfur (Fe-S) centers, to quinones in the respiratory chain. The
CC  immediate electron acceptor for the enzyme in this species is
CC  believed to be ubiquinone. Couples the redox reaction to proton
CC  translocation (for every two electrons transferred, four hydrogen
CC  ions are translocated across the cytoplasmic membrane), and thus
CC  conserves the redox energy in a proton gradient.
CC  -1- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF029365; AAC24997.1; -
DR  EMBL; Z11611; CAA77684.1; -
DR  PIR; S23368; S23368.
DR  InterPro; IPR001694; Resp_NADH_dh1.
DR  Pfam; PF00136; NADHdh_1.
DR  PROSITE; PS00667; COMPLEX1_ND1_1; 1.
DR  PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW  Oxidoreductase; NAD; Quinone; Ubiquinone; Transmembrane.
FT  TRANSMEM 14
FT  TRANSMEM 84 104
FT  TRANSMEM 115 135
FT  TRANSMEM 161 181
FT  TRANSMEM 190 210
FT  TRANSMEM 248 268
FT  TRANSMEM 277 297
FT  TRANSMEM 309 329
SQ  SEQUENCE 345 AA; 37852 MW; 5F9E9D640D911854 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 345;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNMWMTL 6
DB 191 LNMWMTL 196

RESULT 12
T1SD_ECOLI STANDARD; PRT; 444 AA.
AC P06991;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Type I restriction enzyme EcodI specificity protein (S protein)
DE (S.EcodI).
GN HSDS OR HSS.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D / E166;

```

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RX MEDLINE=83216118; PubMed=6304321;
RA Gough J.A., Murray N.E.;
RT "Sequence diversity among related genes for recognition of specific
RT targets in DNA molecules."
RL J. Mol. Biol. 166:1-19(1983).
CC -1- FUNCTION: THE M AND S SUBUNITS TOGETHER FORM A METHYLTRANSFERASE
CC (MTASE) THAT METHYLATES TWO ADENINE RESIDUES IN COMPLEMENTARY
CC STRANDS OF BIPARTITE DNA RECOGNITION SEQUENCE. IN THE PRESENCE OF
CC THE R SUBUNIT THE COMPLEX CAN ALSO ACT AS AN ENDONUCLEASE, BINDING
CC TO THE SAME TARGET SEQUENCE BUT CUTTING THE DNA SOME DISTANCE FROM
CC THIS SITE. WHETHER THE DNA IS CUT OR MODIFIED DEPENDS ON THE
CC METHYLATION STATE OF THE TARGET SEQUENCE. WHEN THE TARGET SITE IS
CC UNMODIFIED, THE DNA IS CUT. WHEN THE TARGET SITE IS
CC METHYLATED, THE COMPLEX ACTS AS A MAINTENANCE MTASE MODIFYING
CC THE DNA SO THAT BOTH STRANDS BECOME METHYLATED. SUBUNIT S DICTATES
CC DNA SEQUENCES SPECIFICITY. THE ECODI ENZYME RECOGNIZES 5'-
CC TTA(N7)GTCT-3'.
CC -1- SUBUNIT: THE TYPE I RESTRICTION/MODIFICATION SYSTEM IS COMPOSED
CC OF THREE POLYPEPTIDES R,M AND S.
CC -1- DOMAIN: CONTAINS TWO DNA RECOGNITION DOMAINS, EACH SPECIFYING
CC RECOGNITION OF ONE OF THE TWO DEFINED COMPONENTS OF THE TARGET
CC SEQUENCE.
CC -1- SIMILARITY: BELONGS TO THE TYPE-I RESTRICTION SYSTEM S METHYLASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR  EMBL; V00287; CAA23553.1; -
DR  REBASE; 3640; S.EcodI.
DR  InterPro; IPR000055; Rest mod DNA.
DR  Pfam; PF01420; Methylase S; 2.
KW  Restriction system; DNA-Binding.
SQ  SEQUENCE 444 AA; 49893 MW; 14BE17B5325294F0 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 444;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMSWMTL 6
DB 215 NMSWMTL 219

RESULT 13
YAWD_SCHPO STANDARD; PRT; 612 AA.
AC Q10187;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein C3F10.13 in chromosome I.
GN SPAC3F10.13.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,

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RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voiclaert G., Aert R., Robben J., Grymptre B.,
 RA Wellens J., Vanstele E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Moesli D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Mambut R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mortier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Poretsky J.,
 RA Shpakovski G.V., Uesery D., Barrell B.G., Nurse P.,
 RT "the genome sequence of Schizosaccharomyces pombe.",
 RL Nature 415:871-880(2002).
 CC -1- SIMILARITY: Contains 1 UBA domain.
 CC -----
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DR EMBL; 269369; CA93311.1; -.
 DR PIR; T38714; T38714.
 DR GeneDB SPombe; SPAC3F10.13; -.
 DR InterPro; IPR000449; UBA_domain.
 DR Pfam; PF00627; UBA_1.
 DR SMART; SM00165; UBA_1.
 DR PROSITE; PS50030; UBA; 1.
 KW Hydrochemical protein; Glycoprotein; Transmembrane.
 FT TRANSMEM 91 111
 FT TRANSMEM 437 457
 FT DOMAIN 3 42
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 416 416 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 612 AA; 68720 MW; 38PDPF3808F554CD CRC64;

Query March 85.0%; Score 34; DB 1; Length 612;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMSWL 6
 DB 296 NMSWI 300

RESULT 14
 ROR1 DROME STANDARD; PRT; 685 AA.
 AC Q24488;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transmembrane receptor Ror precursor
 DE (EC 2.7.1.112) (drom).
 GN ROR OR CG4926.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC STRAIN=Cancon-S; TISSUE=Larval brain;
 RX MEDLINE=93348222; PubMed=8394009;
 RA Wilson C., Gopherman D.C.I., Steller H.;
 RT "Dros. a potential neurotrophic receptor gene, encodes a Drosophila
 RT homolog of the vertebrate Ror family of Trk-related receptor tyrosine
 RT kinases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Cenniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton R.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer J.R.G., Champe M., Pfeiffer B.D.,
 RA Wen K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Milos G.L.G.,
 RA Abell J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flook A., Gabrielian A.B., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
 RA Jalali M., Kalish F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Sliker E., Sliker E., Sliker E., Simpson M., Skupski M.P., Smith T.,
 RA Sliker E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zheng F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE OF 545-597 FROM N.A.
 RX MEDLINE=98401146; PubMed=9731193;
 RA Oates A.C., Wollberg P., Achen M.G., Milke A.F.;
 RT "Sampling the genomic pool of protein tyrosine kinase genes using the
 RT polymerase chain reaction with genomic DNA.";
 RL Biochem. Biophys. Res. Commun. 249:660-667(1998).
 CC -1- FUNCTION: Tyrosine-protein kinase receptor that functions during
 CC early stages of neuronal development.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in neurons of the developing nervous
 CC system.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ROR
 CC SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 frizzled (FZ) domain.
 CC -----
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignment)

87.531 Million cell updates/sec

Title: US-09-643-260-9

Perfect score: 40

Sequence: 1 LNMWML 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	204	2 C83748	hypothetical prote
2	37	92.5	337	2 AG2946	hypothetical prote
3	37	92.5	337	2 C98336	probable integral
4	36	90.0	204	2 T15295	hypothetical prote
5	36	90.0	380	2 T11041	ubiquinol-cytochro
6	36	90.0	460	2 AG0965	probable glycosyl
7	36	90.0	590	2 C83491	hypothetical prote
8	36	90.0	744	2 T10035	hypothetical prote
9	35	87.5	116	2 T03472	conserved hypotet
10	35	87.5	321	2 T24773	hypothetical prote
11	35	87.5	325	2 B87125	ribonucleotide red
12	35	87.5	745	1 T49101	conserved helix-10
13	35	87.5	777	2 T09056	glucan 1,3-beta-gl
14	34	85.0	154	2 S76882	hypothetical prote
15	34	85.0	345	2 C45456	NADH2 dehydrogenas
16	34	85.0	345	2 S22368	NADH2 dehydrogenas
17	34	85.0	355	2 F70983	probable serine pr
18	34	85.0	612	2 T38714	hypothetical prote
19	34	85.0	685	1 A48289	neurotrophic recep
20	34	85.0	903	2 E88221	protein T01H3.2 [1
21	34	85.0	919	2 T37062	probable transcrip
22	34	85.0	980	2 T24336	hypothetical prote
23	34	85.0	1147	2 T35781	hypothetical prote
24	33	82.5	52	2 D90532	hypothetical prote
25	33	82.5	54	2 S70600	H+-transporting tw
26	33	82.5	72	2 AD2464	hypothetical prote
27	33	82.5	169	2 T38724	mitochondrial benz
28	33	82.5	169	2 JCI393	benzodiazepine rec
29	33	82.5	169	2 I57953	peripheral-type be

30	33	82.5	169	2 A53405	peripheral-type be
31	33	82.5	169	2 S14257	benzodiazepine rec
32	33	82.5	169	2 A39473	peripheral-type be
33	33	82.5	169	2 JEO149	ABC transporter su
34	33	82.5	275	2 AB2466	ABC transporter su
35	33	82.5	281	2 AF2161	cation-efflux syst
36	33	82.5	289	2 AB2953	ATP synthase A cha
37	33	82.5	310	2 C84701	hypothetical prote
38	33	82.5	315	2 A86710	transposase of 159
39	33	82.5	315	2 G86712	transposase of 159
40	33	82.5	315	2 D86741	transposase of 159
41	33	82.5	315	2 G86787	transposase of 159
42	33	82.5	315	2 G86794	transposase of 159
43	33	82.5	315	2 C86814	transposase of 159
44	33	82.5	315	2 B86837	transposase of 159
45	33	82.5	315	2 B86860	transposase of 159

ALIGNMENTS

RESULT 1

C83748 hypothetical protein BH0787 [imported] - Bacillus halodurans (strain C-125)

C/Spectrum: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #ext_change 15-Jun-2001

C/Accession: C83748

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maeno, N.; Fujii, F.; Hi

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans an

A/Reference number: AB1650, NCBI:20512582, PMID:11056132

A/Accession: C83748

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-204 <STO>

A/Cross-references: GB:AP001509; GB:BA000004; NID:gl0173176; PIDN:BA04506.1; GSPDB:GN

A/Experimental source: strain C-125

C/Genetics:

A/Gene: BH0787

C/Superfamily: Bacillus subtilis conserved hypothetical protein yest

Query Match
Best Local Similarity 92.5% Score 37; DB 2; Length 204;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWML 6
|||:
Db 22 LNMWML 27

RESULT 2

AG2946 hypothetical protein Atcu173 [imported] - Agrobacterium tumefaciens (strain C58, Dupont

C/Spectrum: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #ext_change 16-Nov-2002

C/Accession: AG2946

R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,

erige, G.; Gilliet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ber, E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577, NCBI:21608550; PMID:11743193

A/Accession: AG2946

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-337 <KUR>

A/Cross-references: GB:AB008689; PIDN:AAL43989.1; PID:gl7741546; GSPDB:GN00187

A/Experimental source: strain C58 (Dupont)

C/Genetics:

A/Gene: Atcu173

A/Map position: linear chromosome

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
 A/Reference number: A82950; MUID:20437337; PMID:10984043
 A/Accession: C83491
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-590 <STO>
 A/Cross-references: GB:AE004553; GB:AE004091; NID:G9947164; PIDN:ANG04631.1; GSPDB:GN001
 A/Experimental source: strain PA01
 C/Genetics:
 A/Gene: PA1242

Query Match 90.0%; Score 36; DB 2; Length 590;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNMSWL 5
 |||||
 Db 360 LNMSWL 364

RESULT 8
 T10035
 Hypothetical protein MLCB628.16c - *Mycobacterium leprae*
 C/Species: *Mycobacterium leprae*
 C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
 C/Accession: T10035
 R./Eigmeier, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
 Mol. Microbiol. 7, 197-206, 1993
 A/Title: Use of an ordered cosmid library to deduce the genomic organization of *Mycobact*
 A/Reference number: Z16917; MUID:93388700; PMID:8446027
 A/Accession: T10035
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-744 <EIG>
 A/Cross-references: EMBL:Y14967; NID:G2370268; PIDN:CAA5203.1; PID:G2370283
 C/Genetics:
 A/Note: MLCB628.16c

Query Match 90.0%; Score 36; DB 2; Length 744;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NMSWL 6
 |||||
 Db 265 NMSWL 269

RESULT 9
 T03472
 conserved hypothetical protein - *Rhodobacter capsulatus*
 C/Species: *Rhodobacter capsulatus*
 C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
 C/Accession: T03472
 R./Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fomstein, M.
 Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
 A/Title: Sequence of a 189-kb segment of the chromosome of *Rhodobacter capsulatus* SB1003
 A/Reference number: Z14955; MUID:9744404; PMID:9256421
 A/Accession: T03472
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-116 <VLC>
 A/Cross-references: EMBL:AF010496; NID:G3128256; PIDN:ACI6125.1; PID:G3128273
 C/Genetics:
 A/Map position: 1

Query Match 87.5%; Score 35; DB 2; Length 116;
 Best Local Similarity 83.3%; Pred. No. 56;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNMSWL 6

Db 63 LSMSWL 68
 |||||

RESULT 10
 T24773
 Hypothetical protein T10B10.8 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C/Accession: T24773
 R./Sims, M.
 submitted to the EMBL Data Library, May 1996
 A/Reference number: Z19934
 A/Accession: T24773
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-321 <MTL>
 A/Cross-references: EMBL:Z72514; PIDN:CAA96680.1; GSPDB:GN00028; CESP:T10B10.8
 A/Experimental source: clone T10B10
 C/Genetics:
 A/Gene: CESP:T10B10.8
 A/Map position: X
 A/Introns: 40/3; 54/2; 64/3; 123/3; 229/2; 262/3

Query Match 87.5%; Score 35; DB 2; Length 321;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LNMSWL 6
 |||||

Db 221 LNMSWL 226

RESULT 11
 B87125
 ribonucleoside reductase small subunit (imported) - *Mycobacterium leprae*
 C/Species: *Mycobacterium leprae*
 C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 C/Accession: B87125
 R./Cole, S.T.; Eigmeier, K.; Parthill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; I
 R.; Davies, R.M.; Devlin, K.; Duthey, S.; Felwell, T.; Fraser, A.; Hamlin, N.; Holroy
 eam, M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001
 A/Title: Massive gene decay in the leprosy bacillus.
 A/Reference number: A86909; MUID:21128732; PMID:11234002
 A/Accession: B87125
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-325 <STO>
 A/Cross-references: GB:AL450380; NID:G13093483; PIDN:CAC30684.1; GSPDB:GN00147
 C/Genetics:
 A/Gene: nrdf
 C/Superfamily: ribonucleoside-diphosphate reductase beta

Query Match 87.5%; Score 35; DB 2; Length 325;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNMSWL 6
 |||||

Db 15 LNMSWL 20

RESULT 12
 I49101
 conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.1-) CHUK - mouse
 C/Species: *Mus musculus* (house mouse)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: I49101
 R./Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
 Genomics 27, 348-351, 1995
 A/Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome

A:Reference number: 149101; MUID:960444444; PMID:7558004
A:Accession: 149101
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-745 <PSS>
A:Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493
C:Gene: CHUK
C:Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homolog
C:Keywords: ATP; phosphotransferase
F:13-283/Domain: protein kinase homology <KIN>

Query Match 87.5%; Score 35; DB 1; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6
DB 738 LDMSWL 743

RESULT 13
T09056
glucan 1,3-beta-glucosidase (EC 3.2.1.58) - *Ampelomyces quisqualis*
N:Alternate names: exo-beta-1,3-glucanase
C:Species: *Ampelomyces quisqualis*
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T09056
R:Rotem, Y.; Yarden, O.; Stetzberg, A.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z16541
A:Accession: T09056
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-777 <ROT>
A:Cross-references: EMBL:AF029354; NID:g3004862; PID:g3004863
A:Experimental source: strain AQ10
C:Gene: exga
C:Genetics:
A:Description: catalyzes the hydrolysis of beta-D-glucose units from the non-reducing end
C:Keywords: glycosidase; hydrolase

Query Match 87.5%; Score 35; DB 2; Length 777;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6
DB 266 MNMNL 271

RESULT 14
S76882
hypothetical protein - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S76882
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-116, 1996
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
S.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76882
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-154 <KAN>
A:Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAAL8794.1; PID:g165388
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Start codon: GTG

C:Superfamily: hypothetical protein b2267

Query Match 85.0%; Score 34; DB 2; Length 154;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSW 5
DB 3 INMSW 7

RESULT 15
C45456
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - *Paracoccus denitrificans*
N:Alternate names: NADH-quinone oxidoreductase chain I
C:Species: *Paracoccus denitrificans*
C>Date: 24-Feb-1994 #sequence_revision 15-Oct-1994 #text_change 03-Jun-2002
C:Accession: C45456
R:Xu, X.; Matsuno-Yagi, A.; Yagi, T.
Biochemistry 32, 968-981, 1993
A>Title: DNA sequencing of the seven remaining structural genes of the gene cluster encoding
A:Reference number: A45456; MUID:93136200; PMID:8422400
A:Accession: C45456
A:Molecule type: DNA
A:Residues: 1-345 <XU>
A:Cross-references: GB:L02354; NID:g150606; PIDN:AA25592.1; PID:g150608
A:Note: sequence extracted from NCBI backbone (NCBIN:123409, NCBI:123413)
C:Genetics:
A:Gene: NQ08
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C:Keywords: membrane-associated complex; NAD; oxidative phosphorylation; oxidoreductase

Query Match 85.0%; Score 34; DB 2; Length 345;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNMSWL 6
DB 191 LNMYWL 196

Search completed: February 18, 2004, 14:38:43
Job time : 7.5921 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39, Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-9

Perfect score: 40

Sequence: 1 LNWSWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	117	4	US-09-149-476-360 Sequence 360, App
2	36	90.0	609	2	US-09-252-991A-20134 Sequence 20134, A
3	35	87.5	745	2	US-08-887-518-3 Sequence 3, Appl
4	35	87.5	745	2	US-09-023-321-3 Sequence 3, Appl
5	35	87.5	745	2	US-08-890-853-4 Sequence 4, Appl
6	35	87.5	745	2	US-09-032-475-3 Sequence 3, Appl
7	35	87.5	745	2	US-09-099-125A-4 Sequence 4, Appl
8	35	87.5	745	2	US-09-099-125A-4 Sequence 4, Appl
9	35	87.5	745	2	US-09-032-475-4 Sequence 4, Appl
10	35	87.5	745	3	US-08-890-854-4 Sequence 4, Appl
11	35	87.5	745	3	US-09-023-324-4 Sequence 4, Appl
12	35	87.5	745	3	US-09-168-629-2 Sequence 2, Appl
13	35	87.5	745	3	US-08-910-820-10 Sequence 10, Appl
14	35	87.5	745	3	US-08-810-131A-2 Sequence 4, Appl
15	35	87.5	745	4	US-09-109-986-4 Sequence 10, Appl
16	35	87.5	745	4	US-09-844-908-10 Sequence 3, Appl
17	35	87.5	745	4	US-09-868-758-3 Sequence 4, Appl
18	35	87.5	756	2	US-08-887-518-4 Sequence 4, Appl
19	35	87.5	756	2	US-09-023-321-4 Sequence 4, Appl
20	35	87.5	756	2	US-08-890-853-2 Sequence 2, Appl
21	35	87.5	756	2	US-09-032-475-4 Sequence 2, Appl
22	35	87.5	756	2	US-09-099-125A-2 Sequence 2, Appl
23	35	87.5	756	2	US-09-099-125A-2 Sequence 2, Appl
24	35	87.5	756	3	US-09-032-476-2 Sequence 2, Appl
25	35	87.5	756	3	US-08-890-854-2 Sequence 2, Appl
26	35	87.5	756	3	US-09-023-324-2 Sequence 15, Appl
27	35	87.5	756	3	US-09-168-629-15 Sequence 15, Appl

28	35	87.5	756	3	US-08-910-820-9 Sequence 9, Appl
29	35	87.5	756	4	US-09-109-986-2 Sequence 2, Appl
30	35	87.5	756	4	US-09-844-908-9 Sequence 9, Appl
31	35	87.5	756	4	US-09-868-758-4 Sequence 4, Appl
32	35	87.5	997	4	US-09-417-197-123 Sequence 123, App
33	35	87.5	997	4	US-09-417-197-121 Sequence 121, App
34	34	85.0	144	4	US-09-252-991A-21138 Sequence 21138, A
35	34	85.0	355	3	US-08-818-112-79 Sequence 79, Appl
36	34	85.0	355	4	US-08-818-111-80 Sequence 80, Appl
37	34	85.0	355	4	US-09-056-556-79 Sequence 79, Appl
38	34	85.0	454	4	US-09-072-596-80 Sequence 80, Appl
39	34	85.0	454	4	US-09-252-991A-28780 Sequence 28780, A
40	33	82.5	151	4	US-09-252-991A-23526 Sequence 23526, A
41	33	82.5	303	4	US-09-252-991A-19160 Sequence 19160, A
42	33	82.5	455	2	US-09-134-001C-4443 Sequence 4443, Ap
43	33	82.5	455	2	US-08-272-255-14 Sequence 14, Appl
44	33	82.5	455	5	PCT-US95-08565-14 Sequence 14, Appl
45	33	82.5	471	4	US-08-311-731A-168 Sequence 168, App

ALIGNMENTS

RESULT 1
US-09-149-476-360
Sequence 360, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149, 476
EARLIER FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 90.0%; Score 36; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSW 5
| | | | |
DB 30 LNMSW 34

RESULT 2
US-09-252-991A-20134
Sequence 20134, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20134

LENGTH: 609

TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20134

Query Match 90.0%; Score 36; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSW 5
| | | | |
DB 379 LNMSW 383

RESULT 3
US-08-887-518-3
Sequence 3, Application US/08887518
Patent No. 5843721

GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA

ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

QY 1 LNMSW 6
| | | | |
DB 379 LNMSW 383

NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 87.5%; Score 35; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6
| | | | |
DB 738 LNMSWL 743

RESULT 4
US-09-023-321-3
Sequence 3, Application US/09023321
Patent No. 5844073

GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 87.5%; Score 35; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6
| | | | |
DB 738 LNMSWL 743

Db 738 LDMWSWL 743

RESULT 5

US-08-890-853-4
Sequence 4, Application US/08890853
Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
ATTORNEY/AGENT INFORMATION:
MORONICZ, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 87.5%; Score 35; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMWSWL 6
Db 738 LDMWSWL 743

RESULT 6

US-09-032-475-3
Sequence 3, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
APPLICANT: Roche, Mike
ATTORNEY/AGENT INFORMATION:
MORONICZ, John
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 87.5%; Score 35; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMWSWL 6
Db 738 LDMWSWL 743

RESULT 7

US-09-099-125A-4
Sequence 4, Application US/09099125A
Patent No. 5916760
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
ATTORNEY/AGENT INFORMATION:
MORONICZ, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-09-125A-4

Query Match
Best Local Similarity 87.5%; Score 35; DB 2; Length 745;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWML 6
DB 738 LDMWML 743

RESULT 8
US-09-099-124A-4
Sequence 4, Application US/09099124A
Patent No. 5939302
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,124A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-09-099-124A-4

Query Match
Best Local Similarity 87.5%; Score 35; DB 2; Length 745;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWML 6
DB 738 LDMWML 743

RESULT 9
US-09-032-476-4
Sequence 4, Application US/09032476
Patent No. 6235492
GENERAL INFORMATION:
APPLICANT: Roche, Mike

APPLICANT: Cao, Zhaodan
APPLICANT: R gnter, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-09-032-476-4

Query Match
Best Local Similarity 87.5%; Score 35; DB 3; Length 745;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWML 6
DB 738 LDMWML 743

RESULT 10
US-08-890-854-4
Sequence 4, Application US/08890854
Patent No. 6235512
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-854-4

Query Match 87.5%; Score 35; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNWSWL 6
|:|||||
Db 738 LDMSWL 743

RESULT 11
US-09-023-324-4
Sequence 4, Application US/09023324
Patent No. 6235513
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaoan
APPLICANT: R. gnier, Catherine
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,324
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 87.5%; Score 35; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNWSWL 6
|:|||||
Db 738 LDMSWL 743

RESULT 12
US-09-168-629-2
Sequence 2, Application US/09168629
Patent No. 6242253
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: Didonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: I κ B Kinase, Subunits Thereof, and Methods of Using Same
FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 2
LENGTH: 745
TYPE: PRT
ORGANISM: Homo sapiens
US-09-168-629-2

Query Match 87.5%; Score 35; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNWSWL 6
|:|||||
Db 738 LDMSWL 743

RESULT 13
US-08-910-820-10
Sequence 10, Application US/08910820
Patent No. 6258579
GENERAL INFORMATION:
APPLICANT: Mercurio, Frank
APPLICANT: Zhu, Hengyi
APPLICANT: Barbosa, Miguel
APPLICANT: Li, Gian
APPLICANT: Murray, Brian W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-910-820-10

Query Match 87.5%; Score 35; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
|:|||||
DB 738 LDWSWL 743

RESULT 14
US-08-810-131A-2
Sequence 2, Application US/08810131A
Patent No. 6268194
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: Didonato, Joseph A.
APPLICANT: Rochwart, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using
TITLE OF INVENTION: Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,131A
FILING DATE: 25-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-131A-2

Query Match 87.5%; Score 35; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
|:|||||
DB 738 LDWSWL 743

RESULT 15
US-09-109-986-4
Sequence 4, Application US/09109986
Patent No. 6479266
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaoan
APPLICANT: R ghter, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,986
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890, 854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-109-986-4

Query Match 87.5%; Score 35; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
|:|||||
DB 738 LDWSWL 743

Search completed: February 18, 2004, 14:41:48
Job time : 8.06579 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-8
Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_Archea:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_Mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
15: SP_Virus:*
16: SP_Bacteriophage:*
17: SP_Archaeo:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	92.3	387	10 Q8LJE0	Q8LJE0 oryza sativ
2	36	92.3	482	5 Q9VQ45	Q9VQ45 drosophila
3	36	92.3	544	10 Q9FEB1	Q9FEB1 oryza sativ
4	36	92.3	645	8 Q61620	Q61620 balanogloss
5	36	92.3	740	6 Q95KVL	Q95KVL bos taurus
6	36	92.3	745	11 Q8CET3	Q8CET3 mus muscula
7	36	92.3	756	6 Q95KVO	Q95KVO bos taurus
8	35	89.7	48	16 Q8VKA2	Q8VKA2 mycobacteri
9	35	89.7	110	16 Q8DY14	Q8DY14 streptococc
10	35	89.7	173	17 Q9HHF7	Q9HHF7 halobacteri
11	35	89.7	196	13 Q9YH31	Q9YH31 notophthalm
12	35	89.7	276	2 Q47020	Q47020 escherichia
13	35	89.7	311	5 Q94380	Q94380 caenorhabdi
14	35	89.7	371	5 Q25333	Q25333 leishmania
15	35	89.7	387	16 Q8YFW8	Q8YFW8 bruceella me
16	35	89.7	390	16 Q8G212	Q8G212 bruceella bu

17	35	89.7	391	2 Q8KPQ4	Q8KPQ4 synechococc
18	35	89.7	391	16 Q8YPT8	Q8YPT8 anabaena sp
19	35	89.7	469	10 Q8RXB1	Q8RXB1 phaeodactyl
20	35	89.7	481	11 Q8VCV5	Q8VCV5 mus musculu
21	35	89.7	522	10 Q9SJ13	Q9SJ13 arabidopsis
22	35	89.7	522	10 Q8LAH9	Q8LAH9 arabidopsis
23	35	89.7	522	10 Q8HL75	Q8HL75 arabidopsis
24	35	89.7	604	4 Q9Y475	Q9Y475 homo sapien
25	35	89.7	645	2 Q69315	Q69315 thermus sp.
26	35	89.7	645	2 Q8GEA9	Q8GEA9 thermus sp.
27	35	89.7	683	4 Q8GDU7	Q8GDU7 homo sapien
28	35	89.7	823	5 Q8SC00	Q8SC00 encephalit
29	35	89.7	1173	16 Q8ERJ0	Q8ERJ0 oceanobacti
30	35	89.7	1345	16 Q9L060	Q9L060 streptomyce
31	35	89.7	1367	16 Q9PPR8	Q9PPR8 ureaplasma
32	35	89.7	1379	13 P79701	P79701 coturnix co
33	35	89.7	1591	3 Q9HPW1	Q9HPW1 ashbya gos
34	35	89.7	2054	5 Q9GZ13	Q9GZ13 rhodobacter
35	34	87.2	116	2 Q68039	Q68039 rhodobacter
36	34	87.2	135	2 Q05744	Q05744 mycobacteri
37	34	87.2	145	5 Q810L0	Q810L0 drosophila
38	34	87.2	248	4 Q8W205	Q8W205 homo sapien
39	34	87.2	321	5 Q94515	Q94515 drosophila
40	34	87.2	355	16 Q07175	Q07175 mycobacteri
41	34	87.2	395	17 Q97V10	Q97V10 sulfobolus
42	34	87.2	398	16 P74568	P74568 synechocyst
43	34	87.2	465	16 Q8P701	Q8P701 xanthomonas
44	34	87.2	469	16 Q8PG82	Q8PG82 xanthomonas
45	34	87.2	471	16 Q8P416	Q8P416 xanthomonas

ALIGNMENTS

RESULT 1

Q8LJE0 PRELIMINARY; PRT; 387 AA.
AC Q8LJE0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P0496H05.7 protein.
GN P0496H05.7.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriophytidae; Oryzaceae; Oryza.
OX NCBI_TaxID:39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone: P0496H05.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003267; BAC03279.1; -.
DR Gene, Q8LJE0; -.
SQ SEQUENCE 387 AA; 41273 MW; C3D070B59608ACB CRC64;

Query Match 92.3%; Score 36; DB 10; Length 387;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
DB 242 VEWMSWL 247

RESULT 2
ID Q9VQ45 PRELIMINARY; PRT; 482 AA.
AC Q9VQ45;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-OCT-2002 (TREMblrel. 22, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
 DE CG31664 protein.
 GN CG31933 OR CG15622.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=1073112;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Deason K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasse K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegvam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kienle S., Kulp D., Lai Z.,
 RA Kimmel B.E., Kodly C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris D., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacble J.M.,
 RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupel M.P., Smith T.,
 RA Spier E., Spradling A.C., Stepleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassenaar D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Fortiera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howard T.J.,
 RA Idegvam C., Jalali M., Kruse D., Li P., Mattei B., Mostrel A.,
 RA Mcintosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacble J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phoumenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Strapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "sequencing of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Miera S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kankner J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Seale S.M.J., Smith B., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Flybase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003585; AAF51336.2; -;
 DR Flybase; PBgn0051664; CG31664.
 DR Flybase; PBgn0051933; CG31933.
 DR InterPro; IPR004245; DUF229.
 DR Pfam; PF02995; DUF229; 1.
 SQ SEQUENCE 482 AA; 55495 MW; A91F2D2DFDPC5D CRC64;

Query Match 92.3%; Score 36; DB 5; Length 482;
 Best Local Similarity 83.3%; Pred. NO. 5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEWSWL 6
 Db 57 VEWSWL 62

RESULT 3
 ID Q9FEE1 PRELIMINARY; PRT; 544 AA.
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2003 (TREMblrel. 23, last sequence update)
 DT 01-MAR-2003 (TREMblrel. 26, last annotation update)
 DE Putative cytochrome P450.
 GN P0688A04.9 OR P0006C01.24.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriatridae; Oryzaceae; Oryza.
 NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Saeki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone: P0688A04.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Saeki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone: P0688A04.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Saeki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone: P006C01.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1-SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL; AP002839; BAB19103.1; -;
 DR EMBL; AP002744; BAB19082.1; -;
 DR Gramene; Q9FEE1; -;
 DR InterPro; IPR001128; Cytochrome_P450.
 DR Pfam; PF00067; P450; 1.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 KW Heme; Monooxygenase; Oxidoreductase.
 SQ SEQUENCE 544 AA; 60867 MW; 273EAF5966D1A024 CRC64;

Query Match 92.3%; Score 36; DB 10; Length 544;
 Best Local Similarity 83.3%; Pred. NO. 5.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
 Db 48 LEWAML 53

RESULT 4

063620 PRELIMINARY; PRT; 645 AA.
 ID 063620;
 AC 063620;
 DT 01-ANG-1998 (TRENBLrel. 07, Created)
 DT 01-ANG-1998 (TRENBLrel. 07, Last sequence update)
 DE 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE NADH dehydrogenase subunit 5.
 OS Balanoglossus carnosus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Hemichordata; Enteropneusta; Ptychodermidae;
 OC Balanoglossus.
 OX NCBI_TaxID=35080;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99016090; PubMed=9799263;
 RA Caestreana J., Feldmaier-Fuchs G., Yokobori S., Satoh N., Paabo S.;
 RT "The mitochondrial genome of the hemichordate Balanoglossus carnosus
 and the evolution of deuterostome mitochondria."
 RL Genetics 150:1115-1123(1998).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98188267; PubMed=9520430;
 RA Caestreana J., Feldmaier-Fuchs G., Paabo S.;
 RT "Codon reassignment and amino acid composition in hemichordate
 mitochondria."
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3703-3707(1998).
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Caestreana J., Feldmaier-Fuchs G., Paabo S.;
 RT Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
 RL EMBL; AF051097; AAD11945.1; -
 DR InterPro; IPR003916; NADHb oxreds.
 DR InterPro; IPR001750; Oxidored_q1_N.
 DR InterPro; IPR001516; Oxidored_q1_N.
 DR Pfam; PF00662; oxidored_q1_N; 1.
 DR PRINTS; PR01434; NADHGNAS5.
 KM NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
 SQ SEQUENCE 645 AA; 6945 MW; C8A498941B61F92 CRC64;

Query Match 92.3%; Score 36; DB 8; Length 645;
 Best Local Similarity 83.3%; Pred. No. 6.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEWSWL 6
 Db 96 LEWAML 101

RESULT 5

095KV1 PRELIMINARY; PRT; 740 AA.
 ID 095KV1;
 AC 095KV1;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE 1kB kinase-alpha.
 GN BIKALPHA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Rottenberg S., Dobbelaere D.A.E., Heusler V.T.;
 RT "Identification and characterization of the bovine 1kB kinases (IKTs)

RT alpha, beta and gamma",
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AJ141455; CAC3686.1; -
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SMO0220; S_trc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 740 AA; 84343 MW; 01903BE1F44D176 CRC64;

Query Match 92.3%; Score 36; DB 6; Length 740;
 Best Local Similarity 83.3%; Pred. No. 7.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEWSWL 6
 Db 738 LDMSWL 738

RESULT 6

08CBT3 PRELIMINARY; PRT; 745 AA.
 ID 08CBT3;
 AC 08CBT3;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Conserved helix-loop-helix ubiquitous kinase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RL 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK035326; BAC29034.1; -
 SQ SEQUENCE 745 AA; 84770 MW; 48C9B01C17A61184 CRC64;

Query Match 92.3%; Score 36; DB 11; Length 745;
 Best Local Similarity 83.3%; Pred. No. 7.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEWSWL 6
 Db 738 LDMSWL 743

RESULT 7

095KV0 PRELIMINARY; PRT; 756 AA.
 ID 095KV0;
 AC 095KV0;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE 1kB kinase-beta.
 GN BIKBETA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.

RA Rotenberg S., Dobbelaere D.A.E., Heusler V.T.;
 RT "Identification and characterization of the bovine Ikb kinases (IKBs)
 RT alpha, beta and gamma";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AJ144556; CAC3687.1; -
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR PRODOM: PD000001; Prot_kinase; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SO SEQUENCE 756 AA; 86647 MW; A072D15614A176B5 CRC64;

Query Match 92.3%; Score 36; DB 6; Length 756;
 Best Local Similarity 83.3%; Pred. No. 7.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSML 6
 |||||
 Db 737 LEWSML 742

RESULT 8
 ID Q8VXB2 PRELIMINARY; PRT; 48 AA.
 AC Q8VXB2;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein MT0946.
 GN MT0946
 OS Mycobacterium tuberculosis
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwin M.L., Haft D., Hickey B.,
 RA Kojanay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,
 RA Bhat W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE006980; AAK45193.1; -
 DR TIGR: MT0946; -
 KW Hypothetical protein.
 SO SEQUENCE 48 AA; 5265 MW; COBPA9D6A2EFBD6 CRC64;

Query Match 89.7%; Score 35; DB 16; Length 48;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EWSML 6
 |||||
 Db 14 EWSML 18

RESULT 9
 ID Q8DY14 PRELIMINARY; PRT; 110 AA.
 AC Q8DY14;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN SAG1496.

OS Streptococcus agalactiae (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=2222988; PubMed=12200547;
 RA Tetteilin H., Maignan V., Cieleszyc M.J., Eisen J.A., Peterson S.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margalit I., Read T.D.,
 RA Dehoff L.C., Wolf A.M., Beaman M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kojanay J.F., Madupu R., Lewis M.R.,
 RA Radu D., Fedorova N.B., Scanlan D., Khouri H., Scallan S.,
 RA Carly H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 RA Jacobson E.T., Breton C., Gall G., Martini G., Vengli F., Malone D.,
 RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V Streptococcus agalactiae";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
 DR EMBL: AE014260; AAN00363.1; -
 DR TIGR: SAG1496; -
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 110 AA; 12689 MW; 243D6B9029709A4 CRC64;

Query Match 89.7%; Score 35; DB 16; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSM 5
 |||||
 Db 14 LEWSM 18

RESULT 10
 ID Q9HHP7 PRELIMINARY; PRT; 173 AA.
 AC Q9HHP7;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Vng6292C.
 GN Vng6292C.
 OS Halobacterium sp. (strain NRC-1).
 OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahatras G.G., Berguist B., Pan M.,
 RA Shukla H.D., Laskey S.R., Bailga N.S., Thorsen V., Shroona J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Meli R., Go Y.A.,
 RA Leitauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonaki P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Ienparger T.A., Peck R.F., Pohlischer M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 RT "Genome sequence of Halobacterium species NRC-1";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL: AE005159; AAG20929.1; -
 DR InterPro: IPR001584; Rve.
 DR Pfam: PF00665; rve; 1.
 KW Plasmid; Complete proteome.
 SO SEQUENCE 173 AA; 20267 MW; E8B02BDC76ED4371 CRC64;

Query Match 89.7%; Score 35; DB 17; Length 173;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EWSML 6
 |||||

DB 42 EMSWL 46

RESULT 11

O9YH31 PRELIMINARY; PRT; 196 AA.

AC O9YH31

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Putative fibroblast growth factor-4.

OS Notophtalmus viridescens (Baseter newt) (Triturus viridescens).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae; Notophtalmus.

OC NCB1_Taxid=8316;

OX (1)

RP SEQUENCE FROM N.A.

RA Wei Y.;

RT "Putative Newt Fibroblast Growth Factor-4.";

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U76998; AAC98812.1; -.

DR HSSP; P09038; 1BPF.

DR InterPro; IPR001064; Crystal1in.

DR InterPro; IPR002348; IL1_HBGF.

DR Pfam; PF00167; FGF_1.

DR PRINTS; PR00262; IL1HBGF.

DR ProDom; PD000831; IL1_HBGF; 1.

DR SMART; SM00442; FGF_1.

DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.

DR PROSITE; PS00247; HBGF_FGF_1.

SO SEQUENCE 196 AA; 22033 MW; AC4686CD989C6EAF CRC64;

Query Match 89.7%; Score 35; DB 13; Length 196;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSW 5

DB 37 LEWSW 41

RESULT 12

O47020 PRELIMINARY; PRT; 276 AA.

AC O47020;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Hypothetical protein.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

OC NCB1_Taxid=562;

OX (1)

RP SEQUENCE FROM N.A.

RA STRAIN=K-12;

RC MEDLINE=82059454; PubMed=6272196;

RA An G., Bendjak D.S., Mamelak L.A., Friesen J.D.;

RT "Organization and nucleotide sequence of a new ribosomal operon in Escherichia coli containing the genes for ribosomal proteins S2 and elongation factors T8.";

RT Nucleic Acids Res. 9:4163-4172(1981).

RL (2)

RP SEQUENCE FROM N.A.

RA STRAIN=K-12;

RC MEDLINE=83309630; PubMed=6343085;

RA Stephens P.E., Darlison M.G., Lewis H.M., Guest J.R.;

RT "The pyruvate dehydrogenase complex of Escherichia coli K12. Nucleotide sequence encoding the pyruvate dehydrogenase component.";

RT Eur. J. Biochem. 133:155-162(1983).

RL (3)

RP SEQUENCE FROM N.A.

RC STRAIN=K-12;

RX MEDLINE=83234434; PubMed=6345153;

RA Stephens P.E., Darlison M.G., Lewis H.M., Guest J.R.;

RT "The pyruvate dehydrogenase complex of Escherichia coli K12. Nucleotide sequence encoding the dihydrolipoamide acetyltransferase component.";

RT Eur. J. Biochem. 133:481-489(1983).

RL (4)

RP SEQUENCE FROM N.A.

RA STRAIN=K-12;

RX MEDLINE=84004369; PubMed=6352260;

RA Stephens P.E., Lewis H.M., Darlison M.G., Guest J.R.;

RT "Nucleotide sequence of the lipoamide dehydrogenase gene of Escherichia coli K12.";

RT Eur. J. Biochem. 135:519-527(1983).

RL (5)

RP SEQUENCE FROM N.A.

RA STRAIN=K-12;

RX MEDLINE=85054973; PubMed=6094577;

RA Richard C., Richard F., Martin C., Haziza C., Patte J.C.;

RT "Regulation of expression and nucleotide sequence of the Escherichia coli dapp gene.";

RT J. Biol. Chem. 259:14824-14828(1984).

RL (6)

RP SEQUENCE FROM N.A.

RA STRAIN=K-12;

RX MEDLINE=85127060; PubMed=3882429;

RA Broome-Smith J.K., Edelman A., Younis S., Spratt B.G.;

RT "The nucleotide sequences of the porA and porB genes encoding penicillin-binding proteins 1A and 1B of Escherichia coli K12.";

RT Eur. J. Biochem. 147:437-446(1985).

RL (7)

RP SEQUENCE FROM N.A.

RA STRAIN=K-12;

RX MEDLINE=86085668; PubMed=3079747;

RA Coulton J.W., Mason P., Cameron D.R., Carmel G., Jean R., Rode H.N.;

RT "Protein fusions of beta-galactosidase to ferrichrome-iron receptor of Escherichia coli K-12.";

RT J. Bacteriol. 165:181-192(1986).

RL (8)

RP SEQUENCE FROM N.A.

RA STRAIN=K-12;

RX MEDLINE=86278132; PubMed=3015933;

RA Breton R., Saniacou H., Papayannopoulos I., Blamann K., Lapointe J.;

RT "Glutaryl-tRNA synthetase of Escherichia coli. Isolation and primary structure of the glx gene and homology with other aminoacyl-tRNA synthetases.";

RT J. Biol. Chem. 261:10610-10617(1986).

RL (9)

RP SEQUENCE FROM N.A.

RA STRAIN=K-12;

RX MEDLINE=87014116; PubMed=3020380;

RA Koester W., Braun V.;

RT "Iron hydroxamate transport of Escherichia coli: Nucleotide sequence of the fnuB gene and identification of the protein.";

RT Mol. Gen. Genet. 204:435-442(1986).

RL (10)

RP SEQUENCE FROM N.A.

RA STRAIN=K-12;

RX MEDLINE=87083395; PubMed=3025182;

RA Chye M.L., Pittard J.;

RT "Transcription control of the arop gene in Escherichia coli K-12: Analysis of operator mutants.";

RT J. Bacteriol. 169:386-393(1987).

RL (11)

RP SEQUENCE FROM N.A.

RA STRAIN=K-12;

RX MEDLINE=87109068; PubMed=3027045;

RA Ben-Basat A., Bauer K., Chang S.Y., Myambo K., Boosman A., Chang S.;

RT "Processing of the initiation methionine from proteins: Properties of the Escherichia coli methionine aminopeptidase and its gene structure.";

RT J. Bacteriol. 169:751-757(1987).

RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=8727948; PubMed=3301821;
 RA Coulton J.W., Mason P., Allatt D.D.;
 RT "fhuc and fhud genes for iron (III)-ferrichrome transport into
 RL Escherichia coli K-12.";
 RN J. Bacteriol. 169:3844-3849(1987).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=88058963; PubMed=3316212;
 RA Taber C.W., Taber H.;
 RT "The speeded operon of Escherichia coli: Formation and processing of
 RL a proenzyme form of 8-adenosylmethionine decarboxylase.";
 RN J. Biol. Chem. 262:16037-16040(1987).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=8815237; PubMed=2450046;
 RA Gebhard W., Schreilmueller T., Hochstrasser K.;
 RT "Complementary DNA and derived amino acid sequence of the precursor of
 RL one of the three protein components of the inter-alpha-trypsin
 RN inhibitor complex.";
 RN FEBS Lett. 229:63-67(1988).
 RN [15]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=89061679; PubMed=2904262;
 RA Andrews S.C., Guest J.R.;
 RT "Nucleotide sequence of the gene encoding the GMP reductase of
 RL Escherichia coli K12.";
 RN Biochem. J. 255:35-43(1988).
 RN [16]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=88227880; PubMed=3372485;
 RA Mellano M.A., Cooksey D.A.;
 RT "Nucleotide sequence and organization of copper resistance genes from
 RL Pseudomonas syringae pv. tomato.";
 RN J. Bacteriol. 170:2879-2883(1988).
 RN [17]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=89155419; PubMed=2537812;
 RA Liu J., Parkinson J.S.;
 RT "Genetics and sequence analysis of the pcnB locus, an Escherichia coli
 RL gene involved in plasmid copy number control.";
 RN J. Bacteriol. 171:1254-1261(1988).
 RN [18]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=89008347; PubMed=3049588;
 RA Sung Y., Fuchs J.A.;
 RT "Characterization of the cym operon in Escherichia coli K12.";
 RN J. Biol. Chem. 263:14769-14775(1988).
 RN [19]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=89057448; PubMed=3057437;
 RA Lapiduska B., Sharma S., Georgopoulos C.;
 RT "Sequence analysis and regulation of the htrA gene of Escherichia
 RL coli: A sigma-32-independent mechanism of heat-inducible
 RN transcription.";
 RN Nucleic Acids Res. 16:10053-10067(1988).
 RN [20]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=90128278; PubMed=2693214;
 RA Roncero M.I., Jepsen L.P., Stroman P., van Heeswijk R.;
 RT "Characterization of a leuA gene and an Ars element from Nucor
 RL Gene 84:335-343(1989).

RN [21]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=89327165; PubMed=2666401;
 RA Xie Q.W., Taber C.W., Taber H.;
 RT "Spermidine biosynthesis in Escherichia coli the promoter and the
 RL termination regions of the speed operon.";
 RN J. Bacteriol. 171:4457-4465(1989).
 RN [22]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=90113890; PubMed=2691840;
 RA Lindquist S., Gallent M., Lindberg F., Normark S.;
 RT "Signaling proteins in enterobacterial ampC beta-lactamase
 RL regulation.";
 RN Mol. Microbiol. 3:1091-1102(1989).
 RN [23]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=90202727; PubMed=2180916;
 RA Kang P.-J., Craig E.A.;
 RT "Identification and characterization of a new Escherichia coli gene
 RL that is a dosage-dependent suppressor of a dnaK deletion mutation.";
 RN J. Bacteriol. 172:2055-2064(1990).
 RN [24]

Query Match 89.7%; Score 35; DB 2; Length 276;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EMSWL 6
 Db 9 EMSWL 13

RESULT 13
 ID 094380 PRELIMINARY; PRT; 311 AA.
 AC 094380;
 DT 01-FEB-1997 (TRMBLrel. 02, Created)
 DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
 DE ZC47.13 protein.
 GN ZC47.13.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McMurtry A.A.;
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RT Science 282:2012-2018(1998).
 RL EMBL; Z81141; CAB03488.2; -
 DR WormDep; ZC47.13; CE25668.
 DR InterPro; IPR002900; DUF38.
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF01827; FTH; 1.
 SQ SEQUENCE 311 AA; 36603 MW; 928464208868C48B CRC64;

Query Match 89.7%; Score 35; DB 5; Length 311;
 Best Local Similarity 83.3%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EMSWL 6

Db 295 LEWEMWL 300

RESULT 14

Q25333 PRELIMINARY; PRT; 371 AA.
 AC Q25333;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Surface antigen P2 (Fragment).
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=V121;
 RX MEDLINE=92105105; PubMed=1761547;
 RA Murray P.J., Spithill T.W.;
 RT "Variants of a Leishmania Surface Antigen Derived from a Multigenic Family."
 RL J. Biol. Chem. 266:24477-24484 (1991).
 DR EMBL; X57134; CAA40413.1; -.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR InterPro; IPR02965; P-rich_extensn.
 DR Pfam; PF00560; LRR; 2.
 DR PRINTS; PR01217; PRICHEXTENSN.
 DR PROSITE; PSS0502; LRR_PS; 1.
 FT NON_TER
 SQ SEQUENCE 371 AA; 39765 MW; 82D0A0BE163E247D CRC64;

Query Match 89.7%; Score 35; DB 5; Length 371;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EMSWL 6
 |||||
 Db 1 EMSWL 5

RESULT 15

Q81FW8 PRELIMINARY; PRT; 387 AA.
 AC Q81FW8;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Mannose-6-phosphate isomerase (EC 5.3.1.8).
 GN BMEI1394.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=1175668;
 RA Delvecchio V.G., Kapratel V., Redkar R.J., Patra G., Mujer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jabloncki L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
 RA Selkov E., Elzer P.H., Haglid S., O'Callaghan D., Teleson J.-J.,
 RA Haseikorn R., Kyriades N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 Brucella melitensis."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
 DR EMBL; AB009577; AAU52575.1; -.
 KW isomerase; Complete proteome.
 SQ SEQUENCE 387 AA; 44267 MW; 4E1F33C64461663F CRC64;

Query Match 89.7%; Score 35; DB 16; Length 387;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EMSWL 6

Db 245 EMSWL 249

Search completed: February 18, 2004, 14:35:44
 Job time : 18.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 / Search time 3.55263 Seconds
(without alignment)
79.423 Million cell updates/sec

Title: US-09-643-260-8

Perfect score: 39

Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt 41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	92.3	745	1 IKXA_HUMAN	O15111 h inhibitor
2	36	92.3	745	1 IKXA_MOUSE	O60680 m inhibitor
3	36	92.3	756	1 IKXB_HUMAN	O14920 homo sapien
4	36	92.3	757	1 IKXB_MOUSE	O88351 mus musculu
5	36	92.3	757	1 IKXB_RAT	O96778 rattus norv
6	35	89.7	400	1 HOPC_ECOLI	P36646 escherichia
7	34	87.2	334	1 GTRB_BOVIN	P58354 bos taurus
8	34	87.2	477	1 GTRB_HUMAN	O94764 homo sapien
9	34	87.2	477	1 GTRB_MOUSE	O91121 rattus norv
10	34	87.2	478	1 GTRB_RAT	O91121 rattus norv
11	34	87.2	685	1 RORI_DROME	O24488 drosophila
12	33	84.6	512	1 VG29_BPMU	O91121 rattus norv
13	33	84.6	777	1 TDR1_HUMAN	O91121 rattus norv
14	33	84.6	928	1 TDR1_MOUSE	O91121 rattus norv
15	33	84.6	1698	1 Y076_HUMAN	O91121 rattus norv
16	32	82.1	83	1 VG41_BPMU	O91121 rattus norv
17	32	82.1	94	1 VG41_BPMU	O91121 rattus norv
18	32	82.1	296	1 CYOA_BUCAL	P57544 buchnera ap
19	32	82.1	307	1 OOK2_ACEAC	P50553 acetobacter
20	32	82.1	314	1 CYOA_PSEPU	O91121 rattus norv
21	32	82.1	362	1 D2UP_YEAST	P32347 saccharomyc
22	32	82.1	375	1 D12_CREAL	O81931 crepis alpi
23	32	82.1	387	1 MANA_RHIME	P29954 rhizobium m
24	32	82.1	561	1 RK_BOVIN	P28327 bos taurus
25	32	82.1	563	1 RK_HUMAN	O15835 homo sapien
26	32	82.1	564	1 RK_MOUSE	O91121 rattus norv
27	32	82.1	564	1 RK_RAT	O91121 rattus norv
28	32	82.1	576	1 GRKE_HUMAN	P43350 homo sapien
29	32	82.1	576	1 GRKE_MOUSE	O70293 mus musculu
30	32	82.1	576	1 GRKE_RAT	P97711 rattus norv
31	32	82.1	578	1 GRK4_HUMAN	P32298 homo sapien
32	32	82.1	580	1 GRKS_BOVIN	P43249 bos taurus
33	32	82.1	590	1 GRKS_HUMAN	P34947 homo sapien

34	32	82.1	590	1 GRKS_RAT	O62833 rattus norv
35	32	82.1	642	1 YORI_CABEL	O09537 caenorhabdi
36	32	82.1	714	1 GRK2_DROME	P32866 drosophila
37	32	82.1	775	1 ECEL_MOUSE	O91120 mus musculu
38	32	82.1	775	1 ECEL_RAT	O91121 rattus norv
39	32	82.1	826	1 CRVA_BACCH	O98597 bacillus th
40	32	82.1	842	1 AMPN_LACDL	P37896 lactobacilli
41	32	82.1	983	1 BEP3_CHICK	P29318 gallus gall
42	32	82.1	983	1 BEP3_HUMAN	P29320 homo sapien
43	32	82.1	983	1 BEP3_MOUSE	P29319 mus musculu
44	32	82.1	984	1 BEP3_RAT	O08680 rattus norv
45	32	82.1	1039	1 GUNB_CAUSA	P10474 c endogluc

ALIGNMENTS

RESULT 1
ID IKXA_HUMAN STANDARD, PRT, 745 AA.
AC O15111; 014666; 013132; 092467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.-)
DE (I-kappa-B kinase 1) (IKK-1) (IKK-1) (IKK-1) (IKK-1) (IKK-1)
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
GN CHUK OR IKK-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
ON NCBI_Taxid=9606;
RX [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RC TISSUE=T-cell;
RA MEDLINE=97386461; PubMed=9244310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Roche M.;
RT "Identification and characterization of an IkappaB kinase";
RL Cell 90:373-383(1997).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC MEDLINE=97394468; PubMed=9252186;
RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi B., Karin M.;
RT "A cytokine-responsive IkappaB kinase that activates the transcription
RT factor NF-kappaB";
RL Nature 388:548-554(1997).
RN [3]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
RP SER-176.
RC TISSUE=Cervical carcinoma;
RA MEDLINE=96008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT NF-kappaB activation";
RL Science 278:860-866(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA MEDLINE=99032998; PubMed=9813330;
RA Hu M.C.-T., Wang Y.-P.;
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes";
RL Gene 222:31-40(1998).
RN [5]
RP SEQUENCE OF 32-745 FROM N.A.
RC TISSUE=Cervical carcinoma;
RA MEDLINE=96258427; PubMed=8777433;
RA Connelly M.A., Marcu K.B.;
RT "CHUK, a new member of the helix-loop-helix and leucine zipper
RT families of interacting proteins, contains a serine-threonine kinase
RT catalytic domain";

RL Cell. Mol. Biol. Res. 41:537-549(1995).
 [6]
 RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
 RP AND SER-180.
 RX MEDLINE=98188283; PubMed=9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
 Ser-176.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 [7]
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RX MEDLINE=99413720; PubMed=10485710;
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
 RA Donner D.B.;
 RT "NF-kappaB activation by tumor necrosis factor requires the Akt
 serine-threonine kinase.";
 RL Nature 401:82-85(1999).
 [8]
 RN IKK-1/KKB BINDING.
 RP MEDLINE=99212141; PubMed=10195894;
 RA Delhaese M., Hayekawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 IkappaB subunit phosphorylation.";
 RL Science 284:309-313(1999).
 [9]
 RN IKK PHOSPHORYLATION.
 RP MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 [10]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I-kappa B/NF-kappa B system: a key determinant of mucosal
 inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 [11]
 RP SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKKB AND IKBK.
 RX MEDLINE=21968797; PubMed=11971985;
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 RA O'Malley B.W.;
 RT "Regulation of SRC-3 (PCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
 activity by I kappa B kinase.";
 RL Mol. Cell. Biol. 22:3549-3561(2002).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 the dissociation of the inhibitor/NF-kappa-B complex and
 ultimately the degradation of the inhibitor. Also phosphorylates
 NCOA3.
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated
 when dephosphorylated.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 also bind to MAP3K14/NIK, MEKK1, IKAP and IKK-alpha-P65-P50
 complex. A weak interaction with TRAF2 cannot be excluded. Part of
 a complex composed of NCOA2, NCOA3, IKKB, IKKKG and CREBBP.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; AF012890; AAC51662.1; -
 DR EMBL; AF009225; AAC51671.1; -
 DR EMBL; AF080157; AAD08996.1; -
 DR EMBL; U22512; AAC50713.1; -
 DR HSR; 063450; 1A06.
 DR Genew; HGNC:1974; CHUK.
 DR MIM; 600664; -
 DR GO; GO:0005737; Cytoplasm; TAS.
 DR GO; GO:0008384; F:IkappaB kinase activity; TAS.
 DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
 DR GO; GO:0007252; P:I-kappaB phosphorylation; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR000719; Prot. kinase.
 DR InterPro; IPR002290; Ser. thr. kinase.
 DR InterPro; IPR001245; Tyr. kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot. kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 KM DOMAIN 15 302
 FT DOMAIN 15
 FT DOMAIN 455 476
 FT DOMAIN 738 743
 FT NP BIND 21 29
 FT BINDING 44 44
 FT ACT SITE 144 144
 FT MOD RES 23 23
 FT MOD RES 176 176
 FT MUTAGEN 23 23
 FT MUTAGEN 44 44
 FT MUTAGEN 44 44
 FT MUTAGEN 176 176
 FT MUTAGEN 176 176
 FT MUTAGEN 176 176
 FT MUTAGEN 179 179
 FT MUTAGEN 180 180
 FT CONFLICT 543 543
 FT CONFLICT 604 604
 FT CONFLICT 679 680
 FT CONFLICT 684 684
 FT CONFLICT 686 687
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
 Query Match 92.3%; Score 36; DB 1; Length 745;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LEMSWL 6
 Db 738 LDMSWL 743
 RESULT 2
 ID IKKA MOUSE STANDARD; PRT; 745 AA.
 AC 060680; Q9D2X3;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 15-SEP-2003 (Rel. 42; Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
 DE (I-kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkappaB kinase)
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
 kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1KX).
 GN CHUK OR IKKA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN-BALB/C.
 RX MEDLINE=9604444; PubMed=755804,
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 RL chromosome 10 and mouse chromosome 19.";
 RN Genomics 27:348-351(1995).
 RP [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN-BALB/C.
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connolly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RL Cell. Mol. Res. 41:537-549(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC STRAIN-CS7BL/6J; TISSUE=Colon.
 RX MEDLINE=21085660; PubMed=11217851,
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kawakawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Knehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Scambly F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
 RA Blake J., Bonfelli D., Boljunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guelincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
 RA Lyons P., Marchionni L., Maehama M., Mazzarelli J., Mombaerts P.,
 RA Norodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schonbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kontuski S.,
 RA Hayashizaki Y.;
 RL "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=20198447; PubMed=10733566;
 RA McGentle F.R., Connolly M.A., Balzarano D., Mueller J.R.,
 RA Gelezianas R., Marcu K.B.;
 RT "Functional isoforms of Ikappab kinase alpha (IKKalpha) lacking
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
 RT IKKbeta have different activation requirements.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RP IKK- α BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhaese M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of Ikappab kinase activity through
 RT Ikappa subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [7]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of Ikappab kinases by mitogen-activated protein
 RT kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).

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[8]
RN REVIEW
RX MEDLINE=20178139; PubMed=10712233;
RA "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection."
RL Am. J. Physiol. 278:C451-C462(2000).
CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
the dissociation of the inhibitor/NF-kappa-B complex and
ultimately the degradation of the inhibitor. Also phosphorylates
NCOA3.
CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated
when dephosphorylated.
CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
also as an homodimer. Directly interacts with IKK-gamma/MEMO.
CC Heterodimers form the active complex. The tripartite complex can
also bind to MAP3K14/NIK, MEKK1, IKAP and IKB-alpha-P65-P50
complex. A weak interaction with TRAF2 cannot be excluded. Part of
a complex composed of NCOA2, NCOA3, IKKB, IKBG and CREBBP (by
similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1;
IsoId=Q60680-1; Sequence=displayed;
Name=2; Synonyms=Delta LH;
IsoId=Q60680-2; Sequence=VSP_004866, VSP_004867;
Name=3; Synonyms=Delta H;
IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;
-1- TISSUE SPECIFICITY: Ubiquitous only for Isoform 1, Isoforms 2 and
3 are expressed predominantly in brain and T-lymphocytes.
-1- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
E11, E15 and E17 days. In the limb development, its expression
predominates in the limb buds at E12.5 day.
-1- PPM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
MEKK1, and dephosphorylated by PP2A, Autophosphorylated.
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
IKAPPAB KINASE SUBFAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL, U13473; AAC52589.1; -.
DR EMBL, AK018671; BAB31335.1; -.
DR PIR, I49101; I49101.
DR HSSP, Q63450; IA06.
DR MGD, MGI:99484; Chuk.
DR InterPro, IPRO00719; Prot_kinase.
DR InterPro, IPRO02290; Ser_Thr_kinase.
DR InterPro, IPRO01245; Tyr_kinase.
DR Pfam, PF00069; pkinase.1.
DR PRINTS, PR00109; TYRKINASE.
DR ProDom, PD000001; Prot_kinase.1.
DR PROSITE, PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE, PS00108; PROTEIN_KINASE_ST.1.
DR PROSITE, PSS0011; PROTEIN_KINASE_DOM.1.
KM Transferase; Serine/threonine-protein kinase; ATP-binding;
Phosphorylation; Alternative splicing.
KV DOMAIN 15 300
FT FT 455 476 LEUCINE_ZIPPER (POTENTIAL).
FT DOMAIN 738 743 MEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 144 144 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT)
(BY SIMILARITY).
FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14)
(BY SIMILARITY).
FT
```


DR HSSP: 063450; 1A06.
 DR Genew; HGNC:5960; IKKB.
 DR MIM; 603258; -.
 DR GO; GO:0005737; C:cytoplasm; NAS.
 DR GO; GO:0005524; F:ATP binding activity; NAS.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
 DR GO; GO:0016563; F:transcriptional activator activity; NAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00240; ubiquitin; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION.
 FT MOD_RES 181 181 PHOSPHORYLATION.
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO EFFECT ON BINDING TO NIK.
 FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
 FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
 FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
 FT CONFICT 231 255 WHSKVRCKSEVDIVSDNLGTYKF -> CVRMMPGVTHAS
 FT CONFICT 231 255 CNPTLGGGRW (IN REF. 5).
 FT FT 0 -> H (IN REF. 1).
 SQ CONFLICT 425 425
 SQ SEQUENCE 756 AA; 86563 MM; P9CADPF671ABE14E CRC64;

Query Match 92.3%; Score 36; DB 1; Length 756;
 Best Local Similarity 83.3%; Pred. NO. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LEWSWL 6
 Db 737 LDMSWL 742

RESULT 4
 IKKB_MOUSE STANDARD; PRT; 757 AA.
 ID IKKB_MOUSE
 AC 088351; Q9RIJ6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN
 RX [1]
 RP SEQUENCE FROM N.A. AND PHOSPHORYLATION BY MEKK1.
 RC STRAIN=C57BL/6; TISSUE=Spleen;
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of I-kappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
 RT constitutively phosphorylates serine residues of Ikb.";
 RL Submitted (Aug-1998) to the EMBL/GenBank/DDA databases.
 RN [3]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE=94455228; PubMed=10523828;
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates I-kappaB kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didenko J.A., Iin A.;
 RT "Coordinate regulation of I-kappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [5]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P65-P50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
 CC and CREBBP (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
 CC -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
 CC the mouse embryo, at E9.5 day its expression begins to be
 CC localized to the brain, neural ganglia, neural tube, and in liver
 CC at E12.5 day. At E15.5 day, the expression is further restricted
 CC to specific tissues of the embryo.
 CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; AF026524; AAC23557.1; -
 CC EMBL; AF088910; AAD52095.1; -
 DR HSSP: 063450; 1A06.
 DR MIM; 603450; 1A06.
 DR MIM; 603450; 1A06.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation.

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FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 737 742 MEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 56 56 N -> D (IN REF. 2).
FT CONFLICT 343 343 N -> E (IN REF. 2).
FT CONFLICT 356 356 K -> R (IN REF. 2).
FT CONFLICT 390 390 L -> F (IN REF. 2).
FT CONFLICT 406 406 P -> Q (IN REF. 2).
FT CONFLICT 573 573 K -> R (IN REF. 2).
FT CONFLICT 736 757 TLDMSWLQMEDEERCSLEQACD -> VTA (IN REF. 2).
SQ SEQUENCE 757 AA; 86690 MM; PED962P095449CSE CRC64;

Query Match 92.3%; Score 36; DB 1; Length 757;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
DB 737 LDMSWL 742

RESULT 5
IKKB_RAT STANDARD; PRT; 757 AA.
AC Q9QY78;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE (1-kappa-B-kinase Deca) (IKKB) (IKK-beta) (IKK-B) (1-kappa-B kinase 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKKB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RA Zhan Y., Sun S., David K.;
RT "IKK beta in megakaryocyte differentiation.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99036236; PubMed=9819420;
RA Nemoto S., Didonato J.A., Lin A.;
RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [3]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B complex and the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates NCOA3.
CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but also as a homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MEK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50 complex. Phosphorylated IKK-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB and CREBBP (by similarity).

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK. Weakly autophosphorylated.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPAB KINASE SUBFAMILY.
CC -----
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CC -----
CC EMBL; AF15282; AAF21978.1; -.
DR HSSP; 063450; 1A06.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
SQ SEQUENCE 757 AA; 86866 MM; 3AFB46ATDF91F9C CRC64;

Query Match 92.3%; Score 36; DB 1; Length 757;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
DB 737 LDMSWL 742

RESULT 6
HOFC_ECOLI STANDARD; PRT; 400 AA.
AC P36646; P75648;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein transport protein hofc.
DE HOFC OR HOFC OR BO106.
GN Bacteriella coli.
OS Bacteriella coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Bacteriella.
OX NCBI_TaxId=562;
RN [1]
RA SEQUENCE FROM N.A.
RP STRAIN=K12;
RX MEDLINE=95047556; PubMed=7959070;
RA Whitchurch C.B., Matlick J.S.;
RT "Involved in protein secretion, DNA uptake and the assembly of type-4 fimbriae in other Bacteria.";
RL Gene 150:9-15(1994).
RN [2]
RA SEQUENCE FROM N.A.
RP STRAIN=K12 / WJ110;
RX MEDLINE=94261430; PubMed=8202364;

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RA Fujita N., Mori H., Yura T., Ishihama A.;
 "Systematic sequencing of the *Escherichia coli* genome: analysis of
 the 2.4-4.1 min (110,917-193,643 bp) region.";
 Nucleic Acids Res. 22:1637-1639(1994).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatner F.R.; Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:123-124(1997).
 RN [4]
 RP SEQUENCE OF 165-400 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=89061679; PubMed=2904262;
 RA Andrews S.C., Guest J.R.;
 RT "Nucleotide sequence of the gene encoding the GMP reductase of
Escherichia coli K12.";
 RL Biochem. J. 255:35-43(1988).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 (Probable).
 CC -1- SIMILARITY: BELONGS TO THE PUF/OUTP/EXEP/XSP/KCP FAMILY.
 CC -1- CAUTION: REF.2 AND REF.4 SEQUENCES DIFFER IN THE N- AND C-TERMINAL
 AS WELL AS IN THE CENTRAL PART DUE TO FRAMESHIFTS.
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 or send an email to license@isb-sdb.ch).
 CC -----
 DR EMBL; L28105; AAC36925.1; -
 DR EMBL; D26562; -; NOT ANNOTATED_CDS.
 DR EMBL; AE000119; AAC73217.1; -
 DR EMBL; X07917; -; NOT ANNOTATED_CDS.
 DR PIR; B64733; B64733.
 DR EcGene; EG11798; hofC.
 DR InterPro; IPR003104; hofC.
 DR InterPro; IPR001992; BacF_sect_syecII.
 DR Pfam; PF00482; GSP1_F_1.
 DR PRINTS; PR00812; BCTERIALGSP.
 DR PROSITE; PS00874; T2SP_F_1.
 KW Transport; Transmembrane; Inner membrane; Complete proteome.
 FT TRANSMEM 165 185 POTENTIAL.
 FT TRANSMEM 209 229 POTENTIAL.
 FT TRANSMEM 370 390 POTENTIAL.
 FT CONFLICT 1 39 MASKED(MRWGIGTGDGNADGMLWASRTLLMALQQM
 -> MAVNSGAGAAVAVQVLT (IN REF. 1).
 SQ SEQUENCE 400 AA; 44450 MW; 9D37333B87AE0D5 CRC64;
 QY Query Match 89.7%; Score 35; DB 1; Length 400;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 EWSWL 6
 DB 215 EWSWL 219
 RESULT 7
 GTR8_BOVIN STANDARD; PRT; 334 AA.
 AC PS8354;
 DT 28-FEB-2003 (rel. 41, Last Created)
 DT 28-FEB-2003 (rel. 41, Last sequence update)
 DT 28-FEB-2003 (rel. 41, Last annotation update)
 DE Solute carrier family 2, facilitated glucose transporter, member 8
 (Glucose transporter type 8) (Glucose transporter type XI) (Fragment).

GN SLC2A8 OR GLUT8 OR GLUTX1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=2148267; PubMed=11599048;
 RA Augustin R., Pocar P., Navarrete-Santos A., Wrenzycki C., Gandolfi F.,
 RA Niemann H., Fischer B.;
 RT "Glucose transporter expression is developmentally regulated in in
 vitro derived bovine preimplantation embryos.";
 RL Mol. Reprod. Dev. 60:370-376(2001).
 CC -1- FUNCTION: Insulin-regulated facilitative glucose transporter.
 CC Binds cytochalasin B in a glucose-inhibitable manner. Seems to be
 CC a dual-specific sugar transporter as it is inhibitable by
 CC fructose (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Principally
 CC intracellular. May move between intracellular vesicles and the
 CC plasma membrane. The dileucine internalization motif is critical
 CC for intracellular sequestration (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
 CC TRANSPORTERS SUBFAMILY.
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 or send an email to license@isb-sdb.ch).
 CC -----
 DR EMBL; AF321324; AAK69606.1; -
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR005828; Sug_transporter.
 DR Pfam; PF00083; sugar_tr_1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; PARTIAL.
 KW Transport; Sugar transporter; Transmembrane; Multigene family.
 FT DOMAIN 1 14
 FT TRANSMEM 15 14 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 36 35 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 39 38 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 60 113 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 114 134 7 (POTENTIAL).
 FT DOMAIN 135 149 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 150 170 8 (POTENTIAL).
 FT DOMAIN 171 176 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 177 197 9 (POTENTIAL).
 FT DOMAIN 198 224 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 225 245 10 (POTENTIAL).
 FT DOMAIN 246 261 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 262 282 11 (POTENTIAL).
 FT DOMAIN 283 295 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 296 316 12 (POTENTIAL).
 FT DOMAIN 317 334 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 334 AA; 36659 MW; 0BE9B670ADAB71DD CRC64;
 QY Query Match 87.2%; Score 34; DB 1; Length 334;
 Best Local Similarity 83.3%; Pred. No. 11e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 LEWSWL 6
 DB 35 LEWSWL 40
 RESULT 8
 GTR8_HUMAN STANDARD; PRT; 477 AA.

AC Q9NT64; Q9NSC4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Solute carrier family 2, facilitated glucose transporter, member 8
 GN (Glucose transporter type 8) (Glucose transporter type XI).
 GN SLC2A8 OR GLUT8 OR GLUTX1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RC MEDLINE=20283667; PubMed=10821868;
 RA Doege H., Schuermann A., Bahrenberg G., Brauers A., Joest H.-G.;
 RT "GLUT8, a novel member of the sugar transporter facilitator family with
 RT glucose transport activity.";
 RL J. Biol. Chem. 275:16275-16280(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20138191; PubMed=10671487;
 RA Ibbertson M.R., Uldry M.A., Thorens B.;
 RT "GLUTX1, a novel mammalian glucose transporter expressed in the
 RT central nervous system and insulin-sensitive tissues.";
 RL J. Biol. Chem. 275:4607-4612(2000).
 CC -1- FUNCTION: Insulin-regulated facilitative glucose transporter.
 CC Binds cytochalasin B in a glucose-inhibitable manner. Seems to be
 CC a dual-specific sugar transporter as it is inhibitable by
 CC fructose (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Principally
 CC intracellular. May move between intracellular vesicles and the
 CC plasma membrane. The dileucine internalization motif is critical
 CC for intracellular sequestration (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in testis, but not in
 CC testicular carcinoma. Lower amounts present in most other tissues.
 CC -1- INDUCTION: In testis, downregulated by estrogen.
 CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
 CC TRANSPORTERS SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL, Y17801; CAB89809.1; -;
 CC DR EMBL, AJ245937; CAB75702.1; -;
 CC DR Genew; HGNC:13812; SLC2A8.
 DR MIM; 605245; -;
 DR GO; GO:0005887; C:Integral to plasma membrane; TAS.
 DR GO; GO:0005355; P:glucose transporter activity; TAS.
 DR GO; GO:0005975; P:carbohydrate metabolism; TAS.
 DR GO; GO:0015758; P:glucose transport; TAS.
 DR InterPro; IPR007114; MRS.
 DR InterPro; IPR005828; Sub_transporter.
 DR InterPro; IPR005829; Sug_transporter.
 DR InterPro; IPR003663; Sugar_transpt.
 DR Pfam; PF00083; sugar_tr; 1.
 DR PRINTS; PRO0171; SUGRTNSPORT.
 DR TIGRPRM6; TIGR00879; SP; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
 DR Transport; Sugar transporter; Transmembrane; Glycoprotein;
 KW Multigene family.
 KM
 FT DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 26 46 1 (POTENTIAL).
 FT DOMAIN 47 70 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 71 91 2 (POTENTIAL).
 FT DOMAIN 92 96 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 97 117 3 (POTENTIAL).

FT DOMAIN 118 127 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 128 148 4 (POTENTIAL).
 FT DOMAIN 149 156 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 157 177 5 (POTENTIAL).
 FT DOMAIN 178 182 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 183 202 6 (POTENTIAL).
 FT DOMAIN 204 226 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 227 277 7 (POTENTIAL).
 FT DOMAIN 278 292 8 (POTENTIAL).
 FT TRANSMEM 293 313 9 (POTENTIAL).
 FT DOMAIN 314 319 10 (POTENTIAL).
 FT TRANSMEM 320 340 11 (POTENTIAL).
 FT DOMAIN 341 367 12 (POTENTIAL).
 FT TRANSMEM 368 388 13 (POTENTIAL).
 FT DOMAIN 389 404 14 (POTENTIAL).
 FT TRANSMEM 405 425 15 (POTENTIAL).
 FT DOMAIN 426 438 16 (POTENTIAL).
 FT TRANSMEM 439 459 17 (POTENTIAL).
 FT DOMAIN 460 477 18 (POTENTIAL).
 FT SITE 12 13 DILEUCINE INTERNALIZATION MOTIF (BY
 FT SIMILARITY).
 FT CARBOHYD 349 349 N-LINKED (GLCNAC. .) (By similarity).
 FT CONFLICT 377 377 S -> N (IN REF. 2).
 FT CONFLICT 456 457 FS -> LF (IN REF. 2).
 FT CONFLICT 462 462 T -> I (IN REF. 2).
 SQ SEQUENCE 477 AA; 50792 MW; 0848094B40AE76 CRC64;
 Query Match 87.2%; Score 34; DB 1; Length 477;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEWSML 6
 Db 179 LEWRWL 184
 RESULT 9
 GTR8_MOUSE STANDARD; PRT; 477 AA.
 ID GTR8_MOUSE Q9UJF3; Q9UJF4; Q9UJF5;
 AC Q9UJF3; Q9UJF4; Q9UJF5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Solute carrier family 2, facilitated glucose transporter, member 8
 GN (Glucose transporter type 8) (Glucose transporter type XI).
 GN SLC2A8 OR GLUT8 OR GLUTX1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20138191; PubMed=10671487;
 RA Ibbertson M.R., Uldry M.A., Thorens B.;
 RT "GLUTX1, a novel mammalian glucose transporter expressed in the
 RT central nervous system and insulin-sensitive tissues.";
 RL J. Biol. Chem. 275:4607-4612(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RC MEDLINE=20283667; PubMed=10821868;
 RA Doege H., Schuermann A., Bahrenberg G., Brauers A., Joest H.-G.;
 RT "GLUT8, a novel member of the sugar transporter facilitator family with
 RT glucose transport activity.";
 RL J. Biol. Chem. 275:16275-16280(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Embryonic carcinoma;
 RC MEDLINE=20319023; PubMed=10860996;
 RA Karayannopoulos M.O., Chi M.-Y., Cui Y., Pingsterhaus J.M.,
 RA McKnight R.A., Mueckler S.U., Moley K.H.;
 RT "GLUT8 is a glucose transporter responsible for insulin-stimulated
 RT glucose uptake in the blastocyst.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:7313-7318(2000).
 RN [41]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Ola; TISSUE=Spleen;
 RX MEDLINE=21547794; PubMed=11689004;
 RA Schoepers A., Doege H., Joost H.-G., Schnermann A.;
 RT "Mouse GLUT8, genomic organization and regulation of expression in
 3T3-L1 adipocytes by glucose";
 RL Biochem. Biophys. Res. Commun. 288:969-974(2001).
 CC -1- FUNCTION: Insulin-regulated facilitative glucose transporter.
 CC Binds cytochalasin B in a glucose-inhibitable manner. Seems to be
 CC a dual-specific sugar transporter as it is inhibitable by
 CC fructose.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Principally
 CC intracellular. May move between intracellular vesicles and the
 CC plasma membrane. The dileucine internalization motif is critical
 CC for intracellular sequestration (by similarity). Insulin induces a
 CC change in the intracellular localization and gives rise to
 CC insertion in the plasma membrane.
 CC -1- TISSUE SPECIFICITY: Highest level of expression in placenta and
 CC testis. Highly expressed in adult and pubertal testis, but not
 CC prepubertal testis. Lower levels of expression in brain, liver,
 CC heart, kidney, fat and skeletal muscle.
 CC -1- DEVELOPMENTAL STAGE: High expression in blastocysts.
 CC -1- SIMILARITY: Inhibited under glucose deprivation.
 CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
 CC TRANSPORTERS SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: AJ245936; CAB5719.1; -.
 CC EMBL: Y17802; CAB89815.1; -.
 CC EMBL: AF232061; AAF78366.1; -.
 CC EMBL: AJ413951; CAC88690.1; -.
 CC MGI: MGI:1860103; SLC2A8.
 CC DR GO: GO:0005887; C: integral to plasma membrane; IDA.
 CC DR GO: GO:0005536; F: glucose binding activity; IDA.
 CC DR GO: GO:0005355; F: glucose transporter activity; IDA.
 CC DR GO: GO:0015758; F: glucose transporter; IDA.
 CC DR GO: GO:0008286; P: insulin receptor signaling pathway; IDA.
 CC DR GO: GO:0001666; P: response to hypoxia; IDA.
 CC DR InterPro: IPR007114; MFS.
 CC DR InterPro: IPR005828; Sub transporter.
 CC DR InterPro: IPR005829; Sug transporter.
 CC DR InterPro: IPR003663; Sugar_transpt.
 CC Pfam: PF00083; sugar_tr; 1.
 CC DR PRINTS: PRO0171; SUGRTNSPORT.
 CC DR TIGRFAMs: TIGR00879; SP; 1.
 CC DR PROSITE: PS00216; SUGAR_TRANSPORT_1; 1.
 CC DR PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
 CC KW Transport; Sugar transport; Transmembrane; Glycoprotein;
 CC Multigene family.
 CC KM
 CC FT DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 26 46 1 (POTENTIAL).
 CC FT DOMAIN 47 70 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 71 91 2 (POTENTIAL).
 CC FT DOMAIN 92 96 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 97 117 3 (POTENTIAL).
 CC FT DOMAIN 118 127 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 128 148 4 (POTENTIAL).
 CC FT DOMAIN 149 156 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 157 177 5 (POTENTIAL).
 CC FT DOMAIN 178 182 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 183 203 6 (POTENTIAL).
 CC FT DOMAIN 204 257 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 258 278 7 (POTENTIAL).
 CC FT DOMAIN 279 293 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 294 314 8 (POTENTIAL).
 FT DOMAIN 315 320 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 321 341 9 (POTENTIAL).
 FT DOMAIN 342 367 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 368 388 10 (POTENTIAL).
 FT DOMAIN 389 404 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 405 425 11 (POTENTIAL).
 FT DOMAIN 426 438 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 439 459 12 (POTENTIAL).
 FT DOMAIN 460 477 CYTOPLASMIC (POTENTIAL).
 FT SITE 12 13 DILEUCINE INTERNALIZATION MOTIF (BY
 FT SIMILARITY).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC...) (By similarity).
 FT CONFLICT 39 39 S -> N (IN REF. 1).
 FT CONFLICT 94 94 S -> A (IN REF. 2 AND 4).
 FT CONFLICT 429 429 S -> N (IN REF. 1).
 SQ SEQUENCE 477 AA; 51523 MW; A3753FB34E452P9A CRC64;
 Query Match 87.2%; Score 34; DB 1; Length 477;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EWSMTL 6
 Db 179 LEWRWL 184
 RESULT 10
 GTR8_RAT
 ID GTR8_RAT STANDARD; PRT; 478 AA.
 AC Q9J21; Q9J21; Q9J21; Q9J21; Q9J21; Q9J21; Q9J21; Q9J21; Q9J21; Q9J21;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Solute carrier family 2, facilitated glucose transporter, member 8
 DE (glucose transporter type 8) (Glucose transporter type XI).
 GN SLC2A8 OR GLUT8 OR GLUTX1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS OF LEU-12 AND
 RP LEU-13.
 RC TISSUE=Testis;
 RX MEDLINE=20138191; PubMed=10671487;
 RA Ibberson M.R., Uldry M.A., Thorens B.;
 RT "GLUTX1, a novel mammalian glucose transporter expressed in the
 RT central nervous system and insulin-sensitive tissues";
 RL J. Biol. Chem. 275:4607-4612(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Ishihashi K.;
 RT "Molecular cloning of a new putative glucose transporter";
 RL Submitted (Oct-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20283667; PubMed=10821868;
 RA Doege H., Schnermann A., Bahrendberg C., Brauers A., Joost H.-G.;
 RT "GLUT8, a novel member of the sugar transport facilitator family with
 RT glucose transport activity";
 RL J. Biol. Chem. 275:16275-16280(2000).
 CC -1- FUNCTION: Insulin-regulated facilitative glucose transporter.
 CC Binds cytochalasin B in a glucose-inhibitable manner. Seems to be
 CC a dual-specific sugar transporter as it is inhibitable by
 CC fructose.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Principally
 CC intracellular. May move between intracellular vesicles and the
 CC plasma membrane. The dileucine internalization motif is critical
 CC for intracellular sequestration.
 CC -1- TISSUE SPECIFICITY: Highly expressed in adult and pubertal testis,
 CC but not prepubertal testis. Moderate expression in hypothalamus,


```

RA Nakajima Y., Miuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA Yamada K., Fujii Y., Oaki K., Hiraio M., Omori Y., Ota T., Suzuki Y.,
RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA Isegaki T., Sugano S.;
RT "NEBO human cDNA sequencing project";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- TISSUE SPECIFICITY: Testis and ovary specific.
CC -1- SIMILARITY: Contains 3 Tudor domains.
CC -----
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CC -----
DR EMBL; AF285591; AKK31970.1; -.
DR EMBL; AK024735; BAB14982.1; -.
DR Genew; HGNC:11712; TDRD1.
DR MIM; 605796; -.
DR InterPro; IPR001097; Maternal_tudor.
DR InterPro; IPR002999; Tudor.
DR Pfam; PF00567; TUDOR; 3.
DR SMART; SM00333; TUDOR; 3.
DR PROSITE; PS50304; TUDOR; 3.
KW Repeat.
FT DOMAIN 138 197 TUDOR 1.
FT DOMAIN 359 418 TUDOR 2.
FT DOMAIN 587 645 TUDOR 3.
FT CONFLICT 737 737 T -> M (IN REF. 2).
FT CONFLICT 775 777 VKS -> KKKKK (IN REF. 2).
SQ SEQUENCE 777 AA; 86762 MW; A733B80D3D76AB8C CRC64;

Query March 84.6%; Score 33; DB 1; Length 777;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWT 6
Db 300 LEWTVW 305

RESULT 14
TDR1_MOUSE STANDARD; PRT; 928 AA.
AC O99MT1;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tudor domain containing protein 1.
GN TDRD1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary, and Testis;
RX MEDLINE=2117548; PubMed=11279525;
RA Wang P.J., McCarrey J.R., Yang F., Page D.C.;
RT "An abundance of X-linked genes expressed in spermatogonia.";
RL Nat. Genet. 27:422-426(2001).
CC -1- TISSUE SPECIFICITY: Testis and ovary specific.
CC -1- SIMILARITY: Contains 4 Tudor domains.
CC -----
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CC -----
DR EMBL; AF285591; AKK31970.1; -.
DR MGD; MGI:1933218; Tdrd1.
DR InterPro; IPR001097; Maternal_tudor.
DR InterPro; IPR002999; Tudor.
DR Pfam; PF00567; TUDOR; 4.
DR SMART; SM00333; TUDOR; 4.
DR PROSITE; PS50304; TUDOR; 4.
KW Repeat.
FT DOMAIN 63 123 TUDOR 1.
FT DOMAIN 292 351 TUDOR 2.
FT DOMAIN 512 571 TUDOR 3.
FT DOMAIN 738 796 TUDOR 4.
SQ SEQUENCE 928 AA; 103050 MW; 9CCF0DBA3AF671AF CRC64;

Query March 84.6%; Score 33; DB 1; Length 928;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWT 6
Db 453 LEWTVW 458

RESULT 15
Y076_HUMAN STANDARD; PRT; 1698 AA.
AC Q14959;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein KIAA0076.
GN KIAA0076.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96051398; PubMed=7584044;
RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
RA Seki N., Kawarabayashi Y., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. II.
RT The coding sequences of 40 new genes (KIA0041-KIA0080) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 1:223-229(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marishta K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Tohyiuki S., Carninci P., Prange C.,
RA Bosa S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Rohak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton B., Kettman W., Madan A., Kodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallue D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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DR EMBL: D38548; BAA05551.1; --
DR EMBL: BC033647; AAH33647.1; --
KW Hypothetical Protein.
SQ SEQUENCE 1698 AA; 19118 MW; 57B11CC478E3EEDA CRC64;

Query Match 84.6%; Score 33; DB 1; Length 1698;
Best Local Similarity 66.7%; Pred. No. 7.5e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEWSWL 6
|:|:|
DB 1446 LOWTWL 1451

Search completed: February 18, 2004, 14:28:06
Job time : 4.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: us-09-643-260-8

Perfect score: 39

Sequence: 1 LEKSWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 761:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	92.3	645	2 T11137	NADH2 dehydrogenas
2	36	92.3	745	2 I49101	conserved helix-lo
3	35	89.7	150	2 PNO444	Ig heavy chain V r
4	35	89.7	242	2 T27590	hypothetical prote
5	35	89.7	371	2 S20075	promastigote surfa
6	35	89.7	387	2 AD3426	mannose-6-phosphat
7	35	89.7	391	2 AG2318	hypothetical prote
8	35	89.7	400	2 B64733	protein transport
9	35	89.7	474	1 G2MS11	Ig gamma-2b chain
10	35	89.7	522	2 A84606	hypothetical prote
11	35	89.7	1367	2 H82874	conserved hypotet
12	35	89.7	1379	2 UC4954	vascular endotheli
13	35	89.7	2054	2 T32413	probable acetyl-Co
14	34	87.2	116	2 T03472	conserved hypotet
15	34	87.2	117	2 S03289	Ig heavy chain pre
16	34	87.2	133	2 PC1155	Ig heavy chain pre
17	34	87.2	355	2 F70983	probable serine pr
18	34	87.2	395	2 E90438	hypothetical prote
19	34	87.2	398	2 S76763	hypothetical prote
20	34	87.2	685	1 A48289	neurotrophic recep
21	34	87.2	919	2 T37062	probable transcrip
22	34	87.2	1139	2 A10379	probable potassium
23	33	84.6	160	2 E71560	hypothetical prote
24	33	84.6	161	2 C81711	conserved hypotet
25	33	84.6	267	2 G90579	hypothetical prote
26	33	84.6	273	2 AB1696	PTS mannose-specif
27	33	84.6	272	2 AH1324	PTS mannose-specif
28	33	84.6	322	2 A13395	NADH2 dehydrogenas
29	33	84.6	358	2 AD2878	iron-chelator utl1

30	33	84.6	358	2 P97654	mxkB protein (AF29
31	33	84.6	480	2 T24087	hypothetical prote
32	33	84.6	700	2 T24092	hypothetical prote
33	33	84.6	723	2 T32136	hypothetical prote
34	33	84.6	783	2 F88808	protein R09E10.3 (
35	33	84.6	903	2 T20804	hypothetical prote
36	33	84.6	1753	2 T00350	hypothetical prote
37	32	82.1	72	2 AD2464	hypothetical prote
38	32	82.1	83	2 S30986	gene 41 protein -
39	32	82.1	94	2 F72804	gp41 protein - Myc
40	32	82.1	100	2 AG0447	probable phage-rel
41	32	82.1	122	2 S63909	Ig V-D-J region (M
42	32	82.1	132	2 S65785	mel-13a protein -
43	32	82.1	154	2 A72029	conserved hypotet
44	32	82.1	154	2 H86594	CT556 hypothetical
45	32	82.1	203	2 T50421	hypothetical prote

ALIGNMENTS

RESULT 1

T11137

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - acorn worm mitochondrion

C/Species: mitochondrion Balanoglossus carnosus

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #ext_change 03-Jun-2002

C/Accession: T11137

R/Castresana, J.; Faldutier-Fuchs, G.; Yokobori, S.; Sach, N.; Paabo, S.

Genetics 150, 1115-1123, 1998

A/Title: The mitochondrial genome of the hemichordate Balanoglossus carnosus and the e

A/Reference number: Z17250; MIMD:199016080; PMID:9799263

A/Accession: T11137

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-645 <CAS>

A/Cross-references: EMBL:AF051097; NID:G3065680; PID:G3065682; PIDN:AAD11945.1

A/Genome: mitochondrion

C/Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match

Best Local Similarity 92.3%; Score 36; DB 2; Length 645;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEKSWL 6
|||||
DB 96 LEKSWL 101

RESULT 2

I49101

conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.1-) CHUK - mouse

C/Species: Mus musculus (house mouse)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 10-Sep-1999

C/Accession: I49101

R/Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.

Genomics 27, 348-351, 1995

A/Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome

A/Reference number: I49101; MIMD:19604444; PMID:7558004

A/Accession: I49101

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-745 <RBS>

A/Cross-references: EMBL:U12473; NID:G1079492; PIDN:AAC52589.1; PID:G1079493

A/Genes: CHUK

C/Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homo-

C/Keywords: ATP; phosphotransferase

F/13-283/Domain: protein kinase homology <KIN>

Query Match 92.3%; Score 36; DB 1; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEWSML 6
 DB 738 LDMSWL 743

RESULT 3

IG heavy chain V region precursor - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C/Accession: P00444

A/Residues: 1-150 <KAL>

A/Reference number: P00444; MUID:93138402; PMID:1339379

A/Accession: P00444

A/Molecule type: mRNA

A/Residues: 1-150 <KAL>

C/Cross-references: GB:I02346

C/Keywords: heterotetramer; immunoglobulin

F/1-19/DNA: signal sequence #status predicted <SIG>

F/20-150/Product: Ig heavy chain V region #status predicted <MAT>

F/34-117/DNA: variable region <VRG>

F/34-117/DNA: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 89.7%; Score 35; DB 2; Length 150;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSML 6

DB 1 MEMSML 6

RESULT 4

T27590

hypothetical protein ZC47.13 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C/Accession: T27590

R/McMurray, A.

submitted to the EMBL Data Library, October 1996

A/Reference number: Z20391

A/Accession: T27590

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-242 <WIL>

A/Cross-references: EMBL:281141; PIDN:CA03488.1; CESP:ZC47.13

A/Experimental source: clone ZC47

C/Genetics:

A/Introns: 172/3

C/Superfamily: Caenorhabditis elegans hypothetical protein ZC47.9

Query Match

Best Local Similarity 89.7%; Score 35; DB 2; Length 242;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEWSML 6

DB 226 LEWML 231

RESULT 5

S20075

Promastigote surface antigen P2 (clone 2.5) precursor - Leishmania major (fragment)

C/Species: Leishmania major

C/Date: 13-Jan-1995 #sequence_revision 06-Feb-1998 #text_change 31-Jan-2000

C/Accession: S20075; C41710

R/Murray, P.J.; Spithill, T.W.

J. Biol. Chem. 266, 24477-24484, 1991

A/Title: Variants of a Leishmania surface antigen derived from a multigenic family.

A/Reference number: A41710; MUID:92105105; PMID:1761547

A/Accession: S20075

A/Molecule type: mRNA

A/Residues: 1-371 <MUR>

A/Cross-references: EMBL:X57134; NID:99580; PID:99581

C/Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol link

F/1-343/Product: promastigote surface antigen P2 (fragment) #status predicted <PSA>

F/344-371/DNA: carboxyl-terminal propeptide #status predicted <CTP>

F/343/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Aap) (in mature fo

Query Match

Best Local Similarity 89.7%; Score 35; DB 2; Length 371;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSML 6

DB 1 EWSML 5

RESULT 6

AD3426

mannose-6-phosphate isomerase (EC 5.3.1.8) [imported] - Brucella melitensis (strain 161

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C/Accession: AD3426

R/DelVecchio, V.G.; Kapural, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen Brucella melite

A/Reference number: AD3426; PMID:11756688

A/Accession: AD3426

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1387 <KUR>

A/Cross-references: GB:AB008917; PIDN:AA152575.1; PID:gl7983392; GSPDB:GN00190

A/Experimental source: strain 16M

C/Genetics:

A/Map position: 1

C/Keywords: intramolecular oxidoreductase; isomerase

Query Match

Best Local Similarity 89.7%; Score 35; DB 2; Length 387;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSML 6

DB 245 EWSML 249

RESULT 7

AG2318

hypothetical protein all4102 [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C/Accession: AG2318

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriqul

DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A

A/Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AG2318

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1391 <KUR>

A/Cross-references: GB:BA000019; PIDN:BA075801.1; PID:gl7133237; GSPDB:GN00179

A/Experimental source: strain PCC 7120

C/Genetics:

A/Gene: all4102

Query Match 89.7%; Score 35; DB 2; Length 391;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEWSML 6
 |||||
 Db 37 LEWDML 42

RESULT 8

protein transport protein hofc - Escherichia coli (strain K-12)
 B64733
 C:Species: Escherichia coli
 C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #ext_change 01-Mar-2002
 C:Accession: B64733; S45184; S45183
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A>Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: B64733
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-400 <BLAT>
 A:Cross-references: GB:AE000119; GB:U00096; NID:91786283; PIDN:AACT3217.1; PID:91786295;
 A:Experimental source: strain K-12, substrain MG1655
 R:Fujita, N.
 submitted to the EMBL Data Library, January 1994
 A:Reference number: S45181
 A:Accession: S45184
 A:Molecule type: DNA
 A:Residues: 'MGR', 28-147, 'PK', 150-173, 'NHGGCGNAFCVCRSLPSTREPTPHRH' <FUS>
 A:Cross-references: EMBL:D65562; NID:9473770; PIDN:BA05563.1; PID:9473774
 A:Experimental source: strain K-12
 A:Accession: S45183
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 207-366, 'NRVADHNGNMYAGCGN/SANPFRCEWMDGITYACCSTPALGDYRLKKRFGSCCTR', 'INVN
 A:Cross-references: EMBL:D65562; NID:9473770; PIDN:BA05562.1; PID:9473773
 A:Experimental source: strain K-12
 C:Genetics:
 A:Gene: hofc; hopC
 A:Superfamily: secretion protein xcpS
 C:Keywords: protein transport; transmembrane protein
 F:167-183/Domain: transmembrane #status predicted <TM1>
 F:719-735/Domain: transmembrane #status predicted <TM2>
 F:369-385/Domain: transmembrane #status predicted <TM3>

Query Match 89.7%; Score 35; DB 2; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EMSML 6
 |||||
 Db 215 EMSML 219

RESULT 9

G2MS11
 IG gamma-2b chain - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #ext_change 01-Dec-2000
 C:Accession: S25057; A02157; A26232; A26233; A53598
 R:Blattner, F.R.; Voss, A.; Nierbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
 submitted to the EMBL Data Library, July 1992
 A>Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
 A:Reference number: S25057
 A:Accession: S25057
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-474 <FIS>
 A:Cross-references: EMBL:X67210; NID:954826; PIDN:CAA7649.1; PID:954827
 R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Odate, M.; Honjo, T.

Nature 283, 786-789, 1980
 A>Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from
 A:Reference number: A02157; MUID:80120716; PMID:6766534
 A:Contents: a allele
 A:Accession: A02157

A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAN>

A:Cross-references: GB:J00461
 A>Note: the sequence was determined from the germline gene
 R:Tucker, P.W.; Marcu, K.B.; Slichter, J.L.; Blattner, F.R.
 Science 206, 1299-1303, 1979

A>Title: Structure of the constant and 3' untranslated regions of the murine gamma2b h
 A:Reference number: A26233; MUID:80081501; PMID:117548

A:Accession: MFC 11
 A:Contents: MFC 11
 A:Accession: A26235

A:Molecule type: mRNA
 A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TVU>
 A>Note: Lys-474 is probably removed posttranslationally
 R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
 Science 206, 1303-1306, 1979

A>Title: Sequence of the cloned gene for the constant region of murine gamma2b immunog
 A:Reference number: A26232; MUID:80081502; PMID:117549

A:Accession: A26232
 A:Molecule type: DNA

A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TVU>
 R:Ollio, R.; Rougeon, F.
 Nature 296, 761-763, 1982

A>Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gai
 A:Reference number: A26233; MUID:82173203; PMID:6803173

A:Contents: b allele
 A:Accession: A26233
 A:Molecule type: DNA

A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL
 A:Cross-references: GB:J00461
 R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takaha
 J. Biol. Chem. 269, 12345-12350, 1994

A>Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
 A:Reference number: A53598; MUID:94216359; PMID:7512967

A:Accession: A53598
 A>Status: preliminary
 A:Molecule type: protein

A:Residues: 234-251 <KIM>
 C:Comment: The a allele sequence is shown.

C:Genetics:
 A:Intron: 138/1; 236/1; 258/1; 368/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k)
 hain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into
 C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
 F:157-222/Domain: immunoglobulin homology <IM1>
 F:236-257/Region: hinge
 F:281-350/Domain: immunoglobulin homology <IM2>

F:387-454/Domain: immunoglobulin homology <IM3>
 F:152/Disulfide bonds: interchain (to light chain) #status predicted
 F:164-220,288-348,394-452/Disulfide bonds: #status predicted

F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
 F:324/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 89.7%; Score 35; DB 1; Length 474;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSML 6
 |||||
 Db 1 MEMSWI 6

RESULT 10

A84606
 hypothetical protein At2g21860 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #ext_change 02-Feb-2001
 C:Accession: A84606

R,lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Taiton, L.; euser, D.; Nieman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84606
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-522 <STO>
A:Cross-references: GB:AE002093; NID:g4417279; PIDN:AAD20404.1; GSPDB:GN00139
C:Genetics:
A:Gene: Atg21860
A:Map position: 2

Query Match 89.7%; Score 35; DB 2; Length 522;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSW 5
Db 341 LEWSW 345

RESULT 11
H82874
conserved hypothetical ATP/GTP-binding protein UUS71 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: H82874
R:Glass, V.I.; Leikowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: A82870
A:Accession: H82874
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1367 <GLA>
A:Cross-references: GB:AE002155; GB:AF222894; NID:g6899572; PIDN:AAF30985.1; GSPDB:GN001
C:Experimental source: serovar 3, biovar 1
C:Genetics:
A:Gene: UUS71
A:Genetic code: SGC3

Query Match 89.7%; Score 35; DB 2; Length 1367;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EWSWL 6
Db 786 EWSWL 790

RESULT 12
JC4954
vascular endothelial growth factor receptor 2 precursor - Japanese quail
N:Alternate names: Quail endothelial kinase 2; Quak 2
C:Species: Coturnix coturnix japonica (Japanese quail)
C>Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 24-Sep-1999
C:Accession: JC4954
R:Elchmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Gene 174, 3-8, 1996
A>Title: Molecular cloning of Quak 1 and 2, two quail vascular endothelial growth factor
A:Reference number: JC4953; MUID:97017121; PMID:8863722
A:Accession: JC4954
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1379 <ETC>
A:Cross-references: EMBL:X83287; NID:g619865; PIDN:CAA58267.1; PID:e283815; PID:g1707416
C:Comment: This protein is an endothelial-specific receptor and binds vascular endothelial
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homoid
C:Keywords: ATP; embryo; growth factor receptor; transmembrane protein
F,1-20/Domain: signal sequence #status predicted <SIG>

F,789-810/Domain: transmembrane #status predicted <TMM>
F,856-1188/Domain: protein kinase homology <KIN>
F,864-872/Region: protein kinase ATP-binding motif

Query Match 89.7%; Score 35; DB 2; Length 1379;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSW 5
Db 57 LEWSW 61

RESULT 13
T32413
probable acetyl-CoA carboxylase (EC 6.4.1.2) W09B6.1 [similarity] - Caenorhabditis ele
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Aug-2000
C:Accession: T32413
R:Goela, D.; Maggi, L.; Andrews, S.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid W09B6.
A:Reference number: Z21162
A:Accession: T32413
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2054 <GOB>
A:Cross-references: EMBL:AF025469; PIDN:AAJ71048.1; GSPDB:GN00020; CESP:W09B6.1
A:Experimental source: strain Bristol N2; clone W09B6
C:Genetics:
A:Gene: CESP:W09B6.1
A:Map position: 2
A:Insertion: 18/3; 50/3; 97/1; 734/2; 793/3; 1975/2; 2037/2
C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti
C:Keywords: ligase

Query Match 89.7%; Score 35; DB 2; Length 2054;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSW 5
Db 773 LEWSW 777

RESULT 14
T03472
conserved hypothetical protein - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C:Accession: T03472
R:Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fomstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A>Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB10
A:Reference number: Z14955; MUID:97404404; PMID:9256491
A:Accession: T03472
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-116 <VIC>
A:Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16125.1; PID:g3128273
C:Genetics:
A:Map position: 1

Query Match 87.2%; Score 34; DB 2; Length 116;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LEWSWL 6
Db 63 LEWSWL 68

RESULT 15

S03289
Ig heavy chain precursor V region (VAR100) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
C/Accession: S03289
R/Blanketstein, T.; Bonhomme, F.; Krawinkel, U.
Immunogenetics 26, 237-248, 1987
A/Title: Evolution of pseudogenes in the immunoglobulin V(H)-gene family of the mouse.
A/Reference number: S03289; MUID:88006305; PMID:2820872
A/Accession: S03289
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-117 <BLA>
A/Cross-references: EMBL:X06866; NID:G52454; PIDN:CAA2991.1; PID:G758157
C/Genetics:
A/Introns: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 34; DB 2; Length 117;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSVL 6
:||||:
DB 1 MEWSNV 6

Search completed: February 18, 2004, 14:38:42
Job time : 8.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds

(Without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-8

Sequence: 39
1 LEWSWL 6

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTUS COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	454	4 US-09-252-991A-28780	Sequence 28780, A
2	36	92.3	745	2 US-08-887-518-3	Sequence 3, App1
3	36	92.3	745	2 US-09-023-321-3	Sequence 3, App1
4	36	92.3	745	2 US-08-890-853-4	Sequence 4, App1
5	36	92.3	745	2 US-09-032-475-3	Sequence 3, App1
6	36	92.3	745	2 US-09-099-125A-4	Sequence 4, App1
7	36	92.3	745	2 US-09-099-125A-4	Sequence 4, App1
8	36	92.3	745	3 US-09-032-476-4	Sequence 4, App1
9	36	92.3	745	3 US-08-890-854-4	Sequence 4, App1
10	36	92.3	745	3 US-09-023-324-4	Sequence 2, App1
11	36	92.3	745	3 US-09-168-629-2	Sequence 10, App1
12	36	92.3	745	3 US-08-810-131A-2	Sequence 2, App1
13	36	92.3	745	4 US-09-109-986-4	Sequence 4, App1
14	36	92.3	745	4 US-09-844-908-10	Sequence 10, App1
15	36	92.3	745	4 US-09-868-758-3	Sequence 3, App1
16	36	92.3	745	2 US-08-887-518-4	Sequence 4, App1
17	36	92.3	745	2 US-09-023-321-4	Sequence 4, App1
18	36	92.3	745	2 US-08-890-853-2	Sequence 4, App1
19	36	92.3	745	2 US-09-032-475-4	Sequence 4, App1
20	36	92.3	745	2 US-09-099-125A-2	Sequence 2, App1
21	36	92.3	745	2 US-09-099-125A-2	Sequence 2, App1
22	36	92.3	745	3 US-09-032-476-2	Sequence 2, App1
23	36	92.3	745	3 US-08-890-854-2	Sequence 2, App1
24	36	92.3	745	3 US-09-023-324-2	Sequence 15, App1
25	36	92.3	745	3 US-09-168-629-15	Sequence 9, App1
26	36	92.3	745	3 US-08-910-820-9	Sequence 9, App1
27	36	92.3	745	3 US-08-910-820-9	Sequence 9, App1

28	36	92.3	756	4 US-09-109-986-2	Sequence 2, App1
29	36	92.3	756	4 US-09-844-908-9	Sequence 9, App1
30	36	92.3	756	4 US-09-868-758-4	Sequence 4, App1
31	36	92.3	996	4 US-09-417-197-123	Sequence 123, App
32	36	92.3	997	4 US-09-417-197-121	Sequence 121, App
33	35	89.7	137	1 US-08-392-419-2	Sequence 2, App1
34	35	89.7	140	3 US-08-836-561-27	Sequence 27, App1
35	35	89.7	140	3 US-08-836-561-63	Sequence 63, App1
36	35	89.7	140	3 US-08-836-561-74	Sequence 74, App1
37	35	89.7	140	3 US-08-836-561-78	Sequence 78, App1
38	35	89.7	140	3 US-08-836-561-83	Sequence 83, App1
39	35	89.7	140	3 US-08-579-378A-4	Sequence 4, App1
40	35	89.7	140	4 US-09-434-122-27	Sequence 27, App1
41	35	89.7	140	4 US-09-434-122-63	Sequence 63, App1
42	35	89.7	140	4 US-09-434-122-74	Sequence 74, App1
43	35	89.7	140	4 US-09-434-122-78	Sequence 78, App1
44	35	89.7	140	4 US-09-434-122-83	Sequence 83, App1
45	35	89.7	140	5 PCT-US93-11612-4	Sequence 4, App1

ALIGNMENTS

RESULT 1

US-09-252-991A-28780
; Sequence 28780, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 10/196,136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28780
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28780

Query Match 100.0%; Score 39; DB 4; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|||||

DB 305 LEWSWL 310

US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
DB 738 LDMSWL 743

RESULT 3
US-09-023-321-3
Sequence 3, Application US/09023321
Patent No. 5844073

GENERAL INFORMATION:
APPLICANT: Roche, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-09-023-321-3

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
DB 738 LDMSWL 743

RESULT 4
US-08-890-853-4
Sequence 4, Application US/08890853
Patent No. 5851812

GENERAL INFORMATION:
APPLICANT: Goedel, David V.
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
DB 738 LDMSWL 743

RESULT 5
US-09-032-475-3
Sequence 3, Application US/09032475
Patent No. 5854003

GENERAL INFORMATION:
APPLICANT: Roche, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEWSWL 6
DB 738 LDMSWL 743

RESULT 6
US-09-099-125A-4
Sequence 4, Application US/09099125A
Patent No. 5916760
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEWSWL 6
DB 738 LDMSWL 743

RESULT 7
US-09-099-124A-4
Sequence 4, Application US/09099124A
Patent No. 5939302
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,124A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-124A-4

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEWSWL 6
DB 738 LDMSWL 743

RESULT 8
US-09-032-476-4
; Sequence 4, Application US/09032476
; Patent No. 6235492
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R. Guier, Catherine
; TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent-In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,476
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-032-476-4
Query Match 92.3%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEWSWL 6
|:||||
Db 738 LDMSWL 743
RESULT 9
US-08-890-854-4
; Sequence 4, Application US/08890854
; Patent No. 6235512
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R. Guier, Catherine
; TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent-In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,854
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-890-854-4
Query Match 92.3%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEWSWL 6
|:||||
Db 738 LDMSWL 743
RESULT 10
US-09-023-324-4
; Sequence 4, Application US/09023324
; Patent No. 6235513
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R. Guier, Catherine
; TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent-In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,324
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 92.3%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
Db 738 LDMSWL 743

RESULT 11
US-09-168-629-2
Sequence 2, Application US/09168629
Patent No. 6242253
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: Didonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: Ikr kinase, Subunits Thereof, and Methods of Using Same
FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
EARLIER FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 745
TYPE: PRT
ORGANISM: Homo sapiens
US-09-168-629-2

Query Match 92.3%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
Db 738 LDMSWL 743

RESULT 12
US-08-910-820-10
Sequence 10, Application US/08910820
Patent No. 6258579
GENERAL INFORMATION:
APPLICANT: Mercutio, Frank
APPLICANT: Zhu, Hengyi
APPLICANT: Barbosa, Miguel
APPLICANT: Li, Ghan
APPLICANT: Murray, Brian W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-910-820-10

Query Match 92.3%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
Db 738 LDMSWL 743

RESULT 13
US-08-810-131A-2
Sequence 2, Application US/08810131A
Patent No. 6268194
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: Didonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,131A
FILING DATE: 25-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-131A-2

Query Match 92.3%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEMSWL 6
|:||||
Db 738 LEMSWL 743

RESULT 14
US-09-109-986-4
Sequence 4, Application US/09109986
Patent No. 6479266
GENERAL INFORMATION:
APPLICANT: Rotne, Mike
APPLICANT: Cao, Zhaoan
APPLICANT: R. Grier, Catherine
TITLE OF INVENTION: IKK-1 Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,986
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-109-986-4

Query Match 92.3%; Score 36; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. NO. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEMSWL 6
|:||||
Db 738 LEMSWL 743

RESULT 15
US-09-844-908-10
Sequence 10, Application US/09844908
Patent No. 6576437
GENERAL INFORMATION:
APPLICANT: Mercurio, Frank
APPLICANT: Zhu, Hengyi
APPLICANT: Barbosa, Miguel
APPLICANT: Li, Gian
APPLICANT: Murray, Brian W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
COMPLEX AND METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/844,908
FILING DATE: 27-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-844-908-10

Query Match 92.3%; Score 36; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. NO. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEMSWL 6
|:||||
Db 738 LEMSWL 743

Search completed: February 18, 2004, 14:41:47
Job time : 7.06579 sec

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-7

Perfect score: 38

Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	1033	4 Q8N3S6	Q8N3S6 homo sapien
2	36	94.7	488	10 Q9SEJ7	Q9SEJ7 lupinus alb
3	36	94.7	675	17 Q26849	Q26849 methanobact
4	35	92.1	91	16 Q98C88	Q98C88 rhizobium 1
5	35	92.1	116	2 Q68039	Q68039 rhodobacter
6	35	92.1	135	2 Q05744	Q05744 mycobacteri
7	35	92.1	145	5 Q810L0	Q810L0 drosophila
8	35	92.1	172	2 Q9KK81	Q9KK81 breviabacter
9	35	92.1	196	16 Q50005	Q50005 mycobacteri
10	35	92.1	197	2 Q88SV7	Q88SV7 unclutured
11	35	92.1	210	16 Q86317	Q86317 mycobacteri
12	35	92.1	321	5 Q94515	Q94515 drosophila
13	35	92.1	329	5 Q9VFY8	Q9VFY8 drosophila
14	35	92.1	398	16 Q8FMH6	Q8FMH6 bruceella su
15	35	92.1	422	16 Q92NU3	Q92NU3 rhizobium m
16	35	92.1	438	16 Q8UDU6	Q8UDU6 agrobacteri

17	35	92.1	441	16 Q8YBVO	Q8YBVO bruceella me
18	35	92.1	966	11 Q8BRK2	Q8BRK2 mus musculu
19	35	92.1	1040	10 Q8GU52	Q8GU52 oryza sativ
20	35	92.1	1055	10 Q9S722	Q9S722 arabidopsis
21	35	92.1	1057	10 Q9F17	Q9F17 arabidopsis
22	35	92.1	1058	10 Q9F1R5	Q9F1R5 arabidopsis
23	34	89.5	50	2 Q43996	Q43996 mycobacteri
24	34	89.5	77	2 Q9XIK2	Q9XIK2 pseudomonas
25	34	89.5	88	12 Q88815	Q88815 eastern equ
26	34	89.5	88	12 Q88810	Q88810 eastern equ
27	34	89.5	88	12 Q88803	Q88803 eastern equ
28	34	89.5	88	12 Q88816	Q88816 eastern equ
29	34	89.5	88	12 Q88811	Q88811 eastern equ
30	34	89.5	88	12 Q88817	Q88817 eastern equ
31	34	89.5	88	12 Q88809	Q88809 eastern equ
32	34	89.5	88	12 Q88823	Q88823 eastern equ
33	34	89.5	88	12 Q88808	Q88808 eastern equ
34	34	89.5	88	12 Q88818	Q88818 eastern equ
35	34	89.5	88	12 Q88801	Q88801 eastern equ
36	34	89.5	88	12 Q88821	Q88821 eastern equ
37	34	89.5	88	12 Q88807	Q88807 eastern equ
38	34	89.5	88	12 Q88804	Q88804 eastern equ
39	34	89.5	88	12 Q88822	Q88822 eastern equ
40	34	89.5	88	12 Q88805	Q88805 eastern equ
41	34	89.5	88	12 Q88820	Q88820 eastern equ
42	34	89.5	88	12 Q88813	Q88813 eastern equ
43	34	89.5	88	12 Q88814	Q88814 eastern equ
44	34	89.5	88	12 Q88819	Q88819 eastern equ
45	34	89.5	88	12 Q88800	Q88800 eastern equ

ALIGNMENTS

RESULT 1

Q8N3S6 PRELIMINARY; PRT; 1033 AA.
AC Q8N3S6
DT 01-OCT-2002 (TRMBLrel. 22, Created)
DT 01-OCT-2002 (TRMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP451G02.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Wamburt R., Heubner D., Mewes H.W., Well B., Wiemann S.;
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AL831955; CAD38600.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 1033 AA; 114395 MW; ED4F629A29CDB6B CRC64;

Query Match 100.0%; Score 38; DB 4; Length 1033;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
DB 557 LAMSWL 562

RESULT 2

Q9SEJ7 PRELIMINARY; PRT; 488 AA.
AC Q9SEJ7
DT 01-MAY-2000 (TRMBLrel. 13, Created)
DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TRMBLrel. 22, Last annotation update)
DE 1-antihydroxypropane-1-carboxylate synthase 3 (EC 4.4.1.14).

GN ACSJ.
 OS Lupinus albus (white lupine).
 OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid 1; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
 OX NCBI_TaxId=3870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Ultra;
 RX MEDLINE=20539411; PubMed=11089679;
 RA Bekman E.P., Saibo N.J., Di Cataldo A., Regalado A.P., Ricardo C.P.,
 Rodrigues-Pousada C.;
 RT "Differential expression of four genes encoding 1-aminocyclopropane-1-
 RT carboxylate synthase in *Lupinus albus* during germination, and in
 RT response to indole-3-acetic acid and wounding.";
 RL Planta 211:663-672(2000).
 CC -1- COPACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
 CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 DR EMBL: AF119413; AAF2211.1; -.
 DR HSSP: P37821; 1B8G.
 DR InterPro: IPR001176; ACC_synthase.
 DR InterPro: IPR004839; AminoTransferase/2.
 DR InterPro: IPR004838; NitrTransf_1.
 DR Pfam: PF00155; aminotran_1.2; 1.
 DR PRINTS: PR00753; ACCSYNTASE.
 DR PROSITE: PS00105; AA_TRANSFER_CLASS_1; 1.
 KW Lyase; Pyridoxal phosphate.
 SQ SEQUENCE 488 AA; 55026 MW; 5BB0D640DD129970 CRC64;
 Query Match 94.7%; Score 36; DB 10; Length 488;
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
 DB 479 IAMSWL 484

RESULT 3
 026849
 ID 026849 PRELIMINARY; PRT; 675 AA.
 AC 026849;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Heavy-metal transporting CPX-type ATPase.
 GN MTH755.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxId=167420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 Aldredge T., Beahrizadeh R., Blakey D., Cook R., Gilbert K.,
 Harrison D., Hoang L., Keagle P., Lum W., Pochler B., Qiu D.,
 Spadatore R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 McQuigall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 Daniels C.J., Mo J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of *Methanobacterium thermoautotrophicum*
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 DR EMBL: AE000854; AAB85258.1; -.
 DR InterPro: IPR006403; ATPase-IB1_Cu.
 DR InterPro: IPR006416; ATPase-IB_Hvy.
 DR InterPro: IPR001757; ATPase_E1-E2.

DR InterPro: IPR001756; Cu ATPase.
 DR InterPro: IPR005834; HydroLase.
 DR Pfam: PF00122; E1-E2 ATPase; 1.
 DR Pfam: PF00702; HydroLase; 1.
 DR PRINTS: PR00119; CATATPASE.
 DR PRINTS: PR00943; CUATPASE.
 DR TIGRPFAM: TIGR01511; ATPase-IB1_Cu; 1.
 DR TIGRPFAM: TIGR01525; ATPase-IB_Hvy; 1.
 DR TIGRPFAM: TIGR01494; ATPase_P-type; 3.
 DR PROSITE: PS00154; ATPASE_E1-E2; 1.
 KW Complete proteome.
 SQ SEQUENCE 675 AA; 72337 MW; 56A5D4C175C0CC6F CRC64;
 Query Match 94.7%; Score 36; DB 17; Length 675;
 Best Local Similarity 83.3%; Pred. No. 8.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
 DB 299 IAMSWL 304

RESULT 4
 098C88
 ID 098C88 PRELIMINARY; PRT; 91 AA.
 AC 098C88;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Exopolysaccharide production repressor, Exor.
 GN MRS553.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxId=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFP303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idehara K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT *Mesorhizobium loti*.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP003006; BAB51733.1; -.
 KW Complete proteome.
 SQ SEQUENCE 91 AA; 9887 MW; 10F09237249B37F0 CRC64;
 Query Match 92.1%; Score 35; DB 16; Length 91;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
 DB 18 VAMSWL 23

RESULT 5
 068039
 ID 068039 PRELIMINARY; PRT; 116 AA.
 AC 068039;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 12.6 kDa protein.
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Rhodospirillaceae; Rhodospirillum.
 OX NCBI_TaxId=1061;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=SB1003;
 RX MEDLINE=9740404; PubMed=9256491;
 RA Vlack C., Paces V., Maltsev N., Paces J., Haselkorn R., Feinstein M.;
 RT "Sequence of a 189-kb segment of the chromosome of Rhodospirillum rubrum";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
 DR EMBL; AF010496; AAC16125.1;
 DR InterPro; IPR005133; Phag_mhG_yufB.
 DR Pfam; PF03334; Phag_mhG_yufB; 1.
 DR TIGRfam; TIGR01300; CPA3_mhG_phag; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 116 AA; 12553 MW; FFB91E726D421996 CRC64;
 Query Match 92.1%; Score 35; DB 2; Length 116;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LANSWL 6
 DB 63 LANSWL 68

RESULT 6
 ID 005744 PRELIMINARY; PRT; 135 AA.
 AC 005744;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE Hypothetical 14.5 kDa protein.
 GN MLCB5.12.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Badcock K., Churcher C.M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Parthill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93188700; PubMed=8446027;
 RA Bigmeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
 RT "Use of an ordered cosmid library to deduce the genomic organization
 of Mycobacterium leprae";
 RL Mol. Microbiol. 7:197-206(1993).
 DR EMBL; Z95151; CAB08408.1;
 KW Hypothetical protein.
 SQ SEQUENCE 135 AA; 14516 MW; E7B32E2379C4888C CRC64;
 Query Match 93.1%; Score 35; DB 2; Length 135;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LANSWL 6
 DB 23 LANSWL 28

RESULT 7
 ID 081010 PRELIMINARY; PRT; 145 AA.
 AC 081010;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE CG32240-PA (GH04494P).
 GN CG32240.

OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Euphybia; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephybia; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoeklin R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H., Blazer E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abell J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,
 RA Borokov D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Crawley S., Dahlke C., Davenport U.B., Davies P.,
 RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodeon K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Laake P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodgett M., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celisner S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Barton J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Paclet J., Paragad V., Park S., Patel S., Pfeiffer B., Scheeler F.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Mista S., Crosby W.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celisner S.E.,
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smurniak R., Whitfield B.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[1]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RA Flybaas;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=Y;
RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungai C.J., Nuno J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF003481; AAM1600.1; -;
DR EMBL, BT001386; AAM7141.1; -;
SQ SEQUENCE 145 AA; 17393 MW; 4EF7D500940F762A CRC64;
QY Query Match 92.1%; Score 35; DB 5; Length 145;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 36 LAMSWL 41
QY 1 LAMSWL 6
|:|||||
Db 36 LAMSWL 41

RESULT 8
Q9KK81 PRELIMINARY; PRT; 172 AA.
ID Q9KK81
AC Q9KK81
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 18.8 kDa protein.
GN CRTK.
OS Brevibacterium linens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Brevibacteriaceae; Brevibacterium.
OX NCBI_TaxID=1703;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 20426;
RX MEDLINE=20279196; PubMed=10821176;
RA Krubasik P., Sandmann G.;
RT "A carotenogenic gene cluster from Brevibacterium linens with novel
RT lycopenase cyclase genes involved in the synthesis of aromatic
RT carotenoids";
RL MOL. Gen. Genet. 263:423-432(2000).
DR EMBL, AF139916; AAF65585.1; -;
DR InterPro; IPR006032; Ribosomal_S12_23.
DR InterPro; IPR004307; TPO_MBR.
DR Pfam; PF03073; TPO_MBR; 1.
DR PROSITE; PS00055; RIBOSOML_S12; 1.
KM Hypothetical protein.
SQ SEQUENCE 172 AA; 18808 MW; 9F6BD848B95875P5 CRC64;
QY Query Match 92.1%; Score 35; DB 2; Length 172;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 91 LAMSWL 96
QY 1 LAMSWL 6
|:|||||
Db 91 LAMSWL 96

RESULT 9
Q50005 PRELIMINARY; PRT; 196 AA.
ID Q50005
AC Q50005;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE U1764V (Hypothetical protein M1041).
GN M1041.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R., Robison K.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Fellwell T., Fraser A., Hamlin N.,
RA Holtroyd S., Hornby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus";
RL Nature 409:1007-1011(2001).
DR EMBL, U15181; AAM62925.1; -;
DR EMBL, AL583920; CAC31422.1; -;
DR Lepidoma; ML1041; -;
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 196 AA; 21186 MW; 15D4AF7CDF653936 CRC64;
QY Query Match 92.1%; Score 35; DB 16; Length 196;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 109 LAMSWL 114
QY 1 LAMSWL 6
|:|||||
Db 109 LAMSWL 114

RESULT 10
Q8RSV7 PRELIMINARY; PRT; 197 AA.
ID Q8RSV7
AC Q8RSV7;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Maturase (Fragment).
OS Uncultured marine bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=56765;
RN [1]
RP SEQUENCE FROM N.A.
RA Podar M., Mullineux L., Sogin M.L., Perlman P.S.;
RT "Bacterial group II introns in a deep sea hydrothermal vent
RT environment";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF075118; AAL78689.1; -;
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00078; rvc; 1.
KM RNA-directed DNA polymerase; Transferase.
FT NON TER
SQ SEQUENCE 197 AA; 24010 MW; FA76F629B32D836A CRC64;
QY Query Match 92.1%; Score 35; DB 2; Length 197;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAWSWL 6
DB 172 LAWSWL 177

RESULT 11

086317 PRELIMINARY; PRT; 210 AA.

AC 086317
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein RV2680.
GN RV2680 OR MT2754 OR MYV010.04.

OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;

RN
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=9825987; PubMed=9634230;
RA Cole S.T., Broese R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltham D., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean U., Moule S., Murphy L.,
RA Oliver S., Ooborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sultson J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).

RN
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Debey R., Dodson R., Gwin M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Balch W., Uterback T., Weidman J., Knouri H., Gill J., Mikula A.,
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z96072; CAB09496.1; -
DR EMBL; AE007105; AAK47069.1; ALT_INT.
DR TIGR; MT2754; -
DR TubercuList; RV2680; -
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 210 AA; 22573 MW; 2D9429BF1FE0956A CRC64;

Query Match 92.1%; Score 35; DB 16; Length 210;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAWSWL 6
DB 123 LAWSWL 128

RESULT 12

094515 PRELIMINARY; PRT; 321 AA.

AC 094515
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE ITC protein (LD15458P) (Sphingolipid delta 4 desaturase protein DES-
DE 1).
GN ITC OR DES1 OR CG9078.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pennkock C., Baldwin D.,
RA Ballew R.M., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhendari D., Bolshakov S.,
RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlephina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rees M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).

RN
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON R;
RX MEDLINE=97156918; PubMed=9003299;
RA Endo K., Akiyama T., Kobayashi S., Okada M.;
RT "Degenerative spermatocyte, a novel gene encoding a transmembrane
RT protein required for the initiation of meiosis in Drosophila
RT spermatogenesis."
RL Mol. Gen. Genet. 253:157-165(1996).

RN
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Paclet J., Paragas V., Park S., Pounanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RN
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Terns P., Franke S., Zaehring U., Sperling P., Heinz R.;
RT "Identification and Characterization of a Sphingolipid Delta-
RT Desaturase Family."
RL J. Biol. Chem. 277:10000-10006(2002).

RN
RP EMBL; AE003612; AAF52318.1; -
DR EMBL; X94180; CAA63889.1; -
DR EMBL; AY061196; AAL28744.1; -
DR EMBL; AF466379; AAM12535.1; -

DR FlyBase; FBgn0001941; tlc.
 DR InterPro; IPR001064; Crystalin.
 DR InterPro; IPR005804; PA_dsaat.fam.
 DR InterPro; IPR006025; Zn_Mtpeptide.
 DR Pfam; PF00487; PA_dsaaturase.1.
 DR PROSITE; PS00225; CRYSTALLIN_BETNGAMMA.1.
 DR PROSITE; PS00142; ZINC_PROTEASE.1.
 DR Trnemebrane.
 SQ SEQUENCE 321 AA; 37213 MW; B8DB13961BF5F38E CRC64;
 Query Match 92.1%; Score 35; DB 5; Length 321;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAMSWL 6
 Db 64 LAMSWL 69

RESULT 13
 Q9VEY8 PRELIMINARY; PRT; 329 AA.
 AC Q9VEY8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG10148 protein.
 GN CG10148.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NX NCBI_TaxID=7227;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Plannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 RA Burkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foeller C., Gabriellian A.B., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idbegwan C.,
 RA Jalaal M., Kalush F., Karpen G.H., Ke Z., Kesterson J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svyrkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinbeck G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AEO03698; AAF54907.1; -
 DR FlyBase; FBgn0038120; CG10148.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003581; LRR_typ.
 DR Pfam; PF00560; LRR; 4.
 DR PRINTS; PR00019; LEURICRAFT.
 DR SMART; SM00369; LRR_TYP.1.
 DR PROSITE; PS05006; LRR_TYPICAL.1.
 SQ SEQUENCE 329 AA; 37165 MW; C41063485C334DA CRC64;
 Query Match 92.1%; Score 35; DB 5; Length 329;
 Best Local Similarity 83.3%; Pred. No. 6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAMSWL 6
 Db 17 LAMSWL 22

RESULT 14
 Q8FWH6 PRELIMINARY; PRT; 398 AA.
 AC Q8FWH6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Pyridine nucleotide-diaphorase oxidoreductase family protein.
 GN BRA0479.
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 NX NCBI_TaxID=29461;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=2247741; PubMed=12271122;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Bauman M.J.,
 RA Daugherty S.C., Debroy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
 RA Redmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 DR EMBL; AEO14545; AAN33671.1; -
 DR TIGR; BRA0479; -
 KW Complete proteome.
 SQ SEQUENCE 398 AA; 43624 MW; 574D95CA92B98424 CRC64;
 Query Match 92.1%; Score 35; DB 16; Length 398;
 Best Local Similarity 83.3%; Pred. No. 7.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAMSWL 6
 Db 370 VAMSWL 375

RESULT 15
 Q92NU3 PRELIMINARY; PRT; 422 AA.
 AC Q92NU3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative NAADH dehydrogenase transmembrane protein (BC 1.6.99.3).
 GN NH0 OR R02079 OR SMC04452.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium.

OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=2139507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Borhe G., Ampe F., Batut J.,
RA Boisset P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kise E., Lelaure V., Masny D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591789; CAC46658.1; -;
DR InterPro; IPR001327; PAD_pyr_redox.
DR InterPro; IPR001100; Pyr_redox.
DR Pfam; PF00070; Pyr_redox; 1.
DR PRINTS; PR00368; PADPFR.
DR PRINTS; PR00411; PWDPRPASEI.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 422 AA; 46023 MW; 1490D9AC1EA517DB CRC64;

Query Match

92.1%; Score 35; DB 16; Length 422;

Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LANSWL 6

Db 394 VANSWL 399

Search completed: February 18, 2004, 14:35:43
Job time : 19.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(Without alignment)
35.929 Million cell updates/sec

Title: US-09-643-260-7

Sequence: 38
1 LAMSWL 6

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents: AA:*
1: /cgn2_6/ptcdat/1/1aa/5A COMB.pep:*
2: /cgn2_6/ptcdat/1/1aa/5B COMB.pep:*
3: /cgn2_6/ptcdat/1/1aa/6A COMB.pep:*
4: /cgn2_6/ptcdat/1/1aa/6B COMB.pep:*
5: /cgn2_6/ptcdat/1/1aa/PTUS COMB.pep:*
6: /cgn2_6/ptcdat/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	92.1	196	4 US-08-311-731A-69	Sequence 69, Appl
2	35	92.1	198	4 US-08-311-731A-319	Sequence 319, App
3	34	89.5	56	4 US-09-205-258-359	Sequence 359, App
4	34	89.5	63	4 US-08-311-731A-311	Sequence 311, App
5	34	89.5	172	4 US-09-252-991A-17325	Sequence 17325, A
6	34	89.5	260	4 US-09-252-991A-21611	Sequence 21611, A
7	34	89.5	269	4 US-09-252-991A-31792	Sequence 31792, A
8	34	89.5	280	4 US-09-634-238-334	Sequence 334, App
9	34	89.5	313	4 US-09-252-991A-28418	Sequence 28418, A
10	34	89.5	320	4 US-09-339-159B-22	Sequence 22, Appl
11	34	89.5	331	4 US-09-339-159B-12	Sequence 12, Appl
12	34	89.5	335	4 US-09-252-991A-23548	Sequence 23548, A
13	34	89.5	343	4 US-09-252-991A-26240	Sequence 26240, A
14	34	89.5	369	4 US-09-339-159B-16	Sequence 16, Appl
15	34	89.5	468	4 US-09-485-648-4	Sequence 4, Appl
16	34	89.5	468	4 US-09-503-565-4	Sequence 4, Appl
17	34	89.5	468	4 US-09-485-649-4	Sequence 4, Appl
18	34	89.5	476	4 US-09-339-159B-8	Sequence 8, Appl
19	34	89.5	486	4 US-09-339-159B-4	Sequence 2, Appl
20	34	89.5	490	4 US-09-339-159B-2	Sequence 2, Appl
21	34	89.5	493	4 US-09-485-648-2	Sequence 2, Appl
22	34	89.5	493	4 US-09-503-565-2	Sequence 2, Appl
23	34	89.5	493	4 US-09-485-649-2	Sequence 2, Appl
24	34	89.5	493	4 US-09-339-159B-6	Sequence 6, Appl
25	34	89.5	545	4 US-09-252-991A-25304	Sequence 25304, A
26	33	86.8	95	4 US-09-252-991A-19590	Sequence 19590, A
27	33	86.8	355	3 US-08-818-112-79	Sequence 79, Appl

28	33	86.8	355	4 US-08-818-111-80	Sequence 80, Appl
29	33	86.8	355	4 US-09-056-556-79	Sequence 79, Appl
30	33	86.8	355	4 US-09-072-596-80	Sequence 80, Appl
31	33	86.8	454	4 US-09-252-991A-23585	Sequence 23585, A
32	33	86.8	454	4 US-09-252-991A-28780	Sequence 28780, A
33	32	84.2	137	1 US-08-137-117D-31	Sequence 31, Appl
34	32	84.2	137	2 US-08-436-717-31	Sequence 31, Appl
35	32	84.2	187	6 5217891-4	Patent No. 5217891
36	32	84.2	193	4 US-09-252-991A-31699	Sequence 31699, A
37	32	84.2	224	4 US-09-465-901-30	Sequence 30, Appl
38	32	84.2	379	4 US-09-252-991A-26255	Sequence 26255, A
39	32	84.2	745	2 US-08-887-518-3	Sequence 3, Appl
40	32	84.2	745	2 US-09-023-321-3	Sequence 3, Appl
41	32	84.2	745	2 US-08-890-853-4	Sequence 3, Appl
42	32	84.2	745	2 US-09-032-475-3	Sequence 3, Appl
43	32	84.2	745	2 US-09-099-125A-4	Sequence 4, Appl
44	32	84.2	745	2 US-09-099-124A-4	Sequence 4, Appl
45	32	84.2	745	3 US-09-032-476-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-311-731A-69
Sequence 69, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LABRAE FOR
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 196 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LABRAE
US-08-311-731A-69

Query Match 92.1%; Score 35; DB 4; Length 196;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0;

QY 1 LAMSWL 6

Db 109 VAMSWL 114

RESULT 2

US-08-311-731A-319
Sequence 319, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MOO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 319:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Mycobacterium leprae
US-08-311-731A-319

Query Match 92.1%; Score 35; DB 4; Length 198;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
Db 111 VAMSWL 116

RESULT 3
US-09-205-258-359
Sequence 359, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15

```

; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 359
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (56)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-359

Query Match          89.5%; Score 34; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAMSW 5
        |||||
DB      9 LAMSW 13

RESULT 4
US-08-311-731A-311
; Sequence 311, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; NUMBER OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 311:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
US-08-311-731A-311

Query Match          89.5%; Score 34; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AMSWL 6
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DB      43 AMSWL 47

RESULT 5
US-09-252-991A-17325
; Sequence 17325, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17325
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17325

Query Match          89.5%; Score 34; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 2,3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAMSW 5
        |||||
DB      38 LAMSW 42

RESULT 6
US-09-252-991A-21611
; Sequence 21611, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21611
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21611

Query Match          89.5%; Score 34; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 3,3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAMSW 5
        |||||
DB      186 LAMSW 190

RESULT 7
US-09-252-991A-31792
; Sequence 31792, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
```

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; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31792
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31792

Query Match      89.5%; Score 34; DB 4; Length 269;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LAWSWL 6
Db      232 LAWGWL 237

RESULT 8
US-09-634-238-334
; Sequence 334, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensen, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.104311
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(280)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-634-238-334

Query Match      89.5%; Score 34; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAWSW 5
Db      170 LAWSW 174

RESULT 9
US-09-252-991A-28418
; Sequence 28418, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
```

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; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28418
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28418

Query Match      89.5%; Score 34; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAWSW 5
Db      80 LAWSW 84

RESULT 10
US-09-339-159B-22
; Sequence 22, Application US/09339159B
; Patent No. 6566114
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Markus
; APPLICANT: Schuelein, Martin
; APPLICANT: Schmoor, Klink
; APPLICANT: Andersen, Lene
; APPLICANT: Bjornvad, Mads
; TITLE OF INVENTION: No. 6566114e1 Mannanases
; FILE REFERENCE: 5440.204-US
; CURRENT APPLICATION NUMBER: US/09/339,159B
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 22
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-339-159B-22

Query Match      89.5%; Score 34; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAWSW 5
Db      276 LAWSW 280

RESULT 11
US-09-339-159B-12
; Sequence 12, Application US/09339159B
; Patent No. 6566114
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Markus
; APPLICANT: Schuelein, Martin
; APPLICANT: Schmoor, Klink
; APPLICANT: Andersen, Lene
; APPLICANT: Bjornvad, Mads
; TITLE OF INVENTION: No. 6566114e1 Mannanases
; FILE REFERENCE: 5440.204-US
; CURRENT APPLICATION NUMBER: US/09/339,159B
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 331
; TYPE: PRT
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/ ORGANISM: Bacillus sp.AA12
US-09-339-159B-12

Query Match      89.5%; Score 34; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAMSW 5
        |||||
        281 LAMSW 285

RESULT 12
US-09-252-991A-23948
; Sequence 23948, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23948
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23948

Query Match      89.5%; Score 34; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AWSWL 6
        |||||
        247 AWSWL 251

RESULT 13
US-09-252-991A-26240
; Sequence 26240, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26240
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26240

Query Match      89.5%; Score 34; DB 4; Length 343;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAMSW 5
        |||||
        299 LAMSW 303
```

```
RESULT 14
US-09-339-159B-16
; Sequence 16, Application US/09339159B
; Patent No. 6566114
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Markus
; APPLICANT: Schulein, Martin
; APPLICANT: Schmoor, Kirk
; APPLICANT: Andersen, Lene
; APPLICANT: Bjornvad, Mads
; TITLE OF INVENTION: No. 6566114e1 Mannanases
; FILE REFERENCE: 5440.204-US
; CURRENT APPLICATION NUMBER: US/09/339,159B
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-339-159B-16

Query Match      89.5%; Score 34; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAMSW 5
        |||||
        318 LAMSW 322

RESULT 15
US-09-485-648-4
; Sequence 4, Application US/09485648
; Patent No. 6376445
; GENERAL INFORMATION:
; APPLICANT: Bettiol, Jean-Luc P.
; APPLICANT: Showell, Michael S.
; TITLE OF INVENTION: Detergent Compositions Comprising a Mannanase and a
; FILE REFERENCE: Mannanase and protease
; CURRENT APPLICATION NUMBER: US/09/485,648
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: PCT/US98/11996
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-485-648-4

Query Match      89.5%; Score 34; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAMSW 5
        |||||
        280 LAMSW 284

Search completed: February 18, 2004, 14:41:47
Job time : 8.06579 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-7
Perfect score: 38
Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	338	1	GALE MYCPN
2	34	89.5	1239	1	POL5_EEBV
3	34	89.5	1240	1	POL5_EEBV
4	34	89.5	1402	1	NIS0_MOUSE
5	33	86.8	118	1	YEL1_HAELN
6	33	86.8	685	1	ROB1_DROME
7	33	86.8	1053	1	HMDH_SCHPO
8	33	86.8	1564	1	N184_SCHPO
9	32	84.2	60	1	YMRP_ECOLI
10	32	84.2	107	1	YMRP_ECOLI
11	32	84.2	136	1	Y07C_BPT4
12	32	84.2	252	1	Y410_RHISN
13	32	84.2	446	1	N14M_CERCA
14	32	84.2	471	1	MEUB_ENTAE
15	32	84.2	471	1	MEUB_ENTAE
16	32	84.2	586	1	S132_MOUSE
17	32	84.2	587	1	S132_MOUSE
18	32	84.2	592	1	S132_MOUSE
19	32	84.2	745	1	IKKA_HUMAN
20	32	84.2	745	1	IKKA_HUMAN
21	32	84.2	756	1	IKKB_MOUSE
22	32	84.2	757	1	IKKB_MOUSE
23	32	84.2	757	1	IKKB_MOUSE
24	32	84.2	842	1	AMPN_LACDL
25	32	84.2	981	1	RRPO_AHNNV
26	32	84.2	982	1	RRPO_AHNNV
27	31	81.6	51	1	LHB2_ECTHA
28	31	81.6	53	1	LHB1_ECTHA
29	31	81.6	54	1	LHB6_RHOAC
30	31	81.6	54	1	LHB7_RHOAC
31	31	81.6	247	1	YU83_YEAST
32	31	81.6	255	1	UNG_HAYE2
33	31	81.6	262	1	CTE2_MOUSE

34	31	81.6	278	1	CVST_SYNE7
35	31	81.6	300	1	Y223_HAELN
36	31	81.6	326	1	N14M_ASTER
37	31	81.6	343	1	YSC2_THERM
38	31	81.6	367	1	NODX_RHILV
39	31	81.6	443	1	PD6C_BRANA
40	31	81.6	447	1	PD6C_SPIOL
41	31	81.6	448	1	PD6C_ARATH
42	31	81.6	467	1	S115_MOUSE
43	31	81.6	483	1	VE2_HPV14
44	31	81.6	493	1	VE2_HPV19
45	31	81.6	497	1	VE2_HPV20

ALIGNMENTS

RESULT 1

ID	GALE_MYCPN	STANDARD	PRT	338 AA
AC	P75517			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactosyltransferase) (UDP-galactose 4-epimerase)			
GN	GALE OR MPN257 OR MP576.			
OS	Mycoplasma pneumoniae.			
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.			
OX	NCBI_TaxID=2104;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 29342 / M129;			
RX	MEDLINE=97105885; PubMed=8948633;			
RA	Himmelfreich R., Hilbert H., Piagens H., Pirkl E., Li B.-C., Herrmann R.;			
RT	"Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae."			
RL	Nucleic Acids Res. 24:4420-4449(1996).			
CC	-1- CATALYTIC ACTIVITY: UDP-glucose = UDP-galactose.			
CC	-1- COFACTOR: NAD.			
CC	-1- PATHWAY: Galactose metabolism; third step.			
CC	-1- SUBUNIT: Homodimer (By similarity).			
CC	-1- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY.			
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CC	-----			
DR	EMBL; AE000056; AAB96224.1; -			
DR	PIR; S73902; S73902.			
DR	HSSP; P09147; IRVS.			
DR	InterPro; IPR001509; Epimerase_Dh.			
DR	InterPro; IPR005886; GALE.			
DR	Pfam; PF01370; Epimerase; 1.			
DR	TIGRFAMs; TIGR01179; gale; 1.			
KW	Isomerase; NAD; Galactose metabolism; Complete proteome.			
FT	NP_BIND 7			
FT	SEQUENCE 338 AA; 38132 MW; 9C50FF3856E8C03 CRC64;			

QY	1 LAMSWL 6	89.5%; Score 34; DB 1; Length 338;
DB	244 LAMSWL 249	Best Local Similarity 83.3%; Prod. No. 1.2e+02;
		Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 2
ID POLS_EEEV STANDARD; PRT; 1239 AA.
AC P08768;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 40, Last annotation update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Structural polypeptide (P130) [Contains: Coat protein C (EC 3.4.21.-) (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2; 6 kDa peptide; Spike glycoprotein E1].
OS Eastern equine encephalitis virus (Eastern equine encephalomyelitis virus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_Taxid=11021;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=82V-2137;
RX MEDLINE=87282265; PubMed=2886548;
RA Chang G.-J.J., Trent D.W.;
RT "Nucleotide sequence of the genome region encoding the 26S mRNA of eastern equine encephalomyelitis virus and the deduced amino acid sequence of the viral structural proteins.";
RT J. Gen. Virol. 68:2129-2142(1987).
CC -1- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
CC -1- PTM: SPECIFIC ENZYMOLOGICAL CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL HEMAGGLUTININ.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
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CC -----
CC DR EMBL; X05816; CAA29261.1; -
CC DR PIR; A26816; VHWVEE.
CC DR HSSP; P03315; 1VCP.
CC DR MEROPS; S03.001; -
CC DR InterPro; IPR002548; Alpha_E1_glycop.
CC DR InterPro; IPR000936; Alpha_E2_glycop.
CC DR InterPro; IPR002533; Alpha_E3_glycop.
CC DR InterPro; IPR000930; Togavirin.
CC DR Pfam; PF00944; Alpha_core; 1.
CC DR Pfam; PF01589; Alpha_E1_glycop; 1.
CC DR Pfam; PF00943; Alpha_E2_glycop; 1.
CC DR Pfam; PF01563; Alpha_E3_glycop; 1.
CC DR PRINTS; PR00798; TOGAVIRIN.
CC DR Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
CC Serine protease.
CC -----
CC KM CHAIN 1 259 COAT PROTEIN C.
CC FT CHAIN 260 322 SPIKE GLYCOPROTEIN E3.
CC FT CHAIN 323 742 SPIKE GLYCOPROTEIN E2.
CC FT CHAIN 743 798 6 kDa PEPTIDE.
CC FT CHAIN 799 1239 SPIKE GLYCOPROTEIN E1.
CC FT ACT_SITE 136 136 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 142 142 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 210 210 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 210 210 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT TRANSMEM 261 277 POTENTIAL.
CC FT TRANSMEM 684 701 POTENTIAL.
CC FT TRANSMEM 727 737 POTENTIAL.
CC FT TRANSMEM 777 798 POTENTIAL.
CC FT TRANSMEM 1211 1235 POTENTIAL.
CC FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 932 932 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 1239 AA; 137411 MW; 8C764A405D2D41C CRC64;
Query Match 89.54; Score 34; DB 1; Length 1239;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 AWSML 6
Db 1205 AWSML 1209
RESULT 3
ID POLS_EEEV STANDARD; PRT; 1240 AA.
AC P27284;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Structural polypeptide (P130) [Contains: Coat protein C (EC 3.4.21.-) (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2; 6 kDa peptide; Spike glycoprotein E1].
OS Eastern equine encephalitis virus (strain va33(ten broeck)) (Eastern equine encephalomyelitis virus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_Taxid=11022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91220727; PubMed=2024496;
RA Weaver S.C., Scott T.W., Rico-Hesse R.;
RT "Molecular evolution of eastern equine encephalomyelitis virus in North America.";
RT Virology 182:774-784(1991).
CC -1- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
CC -1- PTM: SPECIFIC ENZYMOLOGICAL CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL HEMAGGLUTININ.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
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CC -----
CC DR EMBL; M69094; AAA42980.1; -
CC DR PIR; A39992; VHWVEE.
CC DR HSSP; P03315; 1VCP.
CC DR MEROPS; S03.001; -
CC DR InterPro; IPR002548; Alpha_E1_glycop.
CC DR InterPro; IPR000936; Alpha_E2_glycop.
CC DR InterPro; IPR002533; Alpha_E3_glycop.
CC DR InterPro; IPR000930; Togavirin.
CC DR Pfam; PF00944; Alpha_core; 1.
CC DR Pfam; PF01589; Alpha_E1_glycop; 1.
CC DR Pfam; PF00943; Alpha_E2_glycop; 1.
CC DR Pfam; PF01563; Alpha_E3_glycop; 1.
CC DR PRINTS; PR00798; TOGAVIRIN.
CC DR Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
CC Serine protease.
CC -----
CC KM CHAIN 1 260 COAT PROTEIN C.
CC FT CHAIN 261 323 SPIKE GLYCOPROTEIN E3.
CC FT CHAIN 324 743 SPIKE GLYCOPROTEIN E2.
CC FT CHAIN 744 799 6 kDa PEPTIDE.
CC FT CHAIN 800 1240 SPIKE GLYCOPROTEIN E1.
CC FT ACT_SITE 137 137 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 143 143 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 211 211 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 211 211 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT TRANSMEM 259 276 POTENTIAL.
CC FT TRANSMEM 695 712 POTENTIAL.
CC FT TRANSMEM 722 738 POTENTIAL.
CC FT TRANSMEM 761 799 POTENTIAL.
CC FT TRANSMEM 1212 1236 POTENTIAL.


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FT CAROHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 834 834 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 933 933 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1240 AA; 137290 MW; AEBB1599D083045 CRC64;

Query Match
Best Local Similarity 89.5%; Score 34; DB 1; Length 1240;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AWSWL 6
DB 1206 AWSWL 1210

RESULT 4
N160_MOUSE
ID N160_MOUSE STANDARD; PRT; 1402 AA.
AC Q9Z0W3; Q9CZD9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nuclear pore complex protein Nup160 (Nucleoporin Nup160) (160 kDa
DE nucleoporin) (Gene trap locus N160) (GTL-13).
GN NUP160 OR GTL-13 OR KIA0197.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Van de Putte T., Cozijnsen M., Dewulf N., Tydzanowski P., Lemny O.,
RA Huybrecock D.;
RT KIA0197 gene (D8J781), complete cds.; similar to human
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

[2]
SEQUENCE OF 1151-1402 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Niemi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Glass C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackenbush J.,
RA Schiml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gusninch S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hasehizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

[3]
IDENTIFICATION, SUBUNIT, AND SUBCELLULAR LOCATION.
RX MEDLINE=21448620; PubMed=11564755;
RA Belagere N., Rabut G., Bal S.W., van Overbeek M., Beaudouin J.,
RA Elieberg J., Zatepina O.V., Pasteau F., Labas V., Fromont-Racine M.,
RT "An evolutionarily conserved NPC subcomplex, which redistributes in
RT part to kinetochores in mammalian cells.";
RL J. Cell Biol. 154:1147-1160(2001).

[4]
IDENTIFICATION, FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RX MEDLINE=21541555; PubMed=11684705;

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RA Vasu S., Shah S., Orjalo A., Park M., Fischer W.H., Forbes D.J.;
RT "Novel vertebrate nucleoporins Nup133 and Nup160 play a role in mRNA
RT export.";
RL J. Cell Biol. 155:339-354(2001).
CC -1- FUNCTION: Involved in poly(A)+ RNA transport.
CC -1- SUBUNIT: Forms part of the Nup160 subcomplex in the nuclear pore
CC which is composed of Nup160, Nup133, Nup107 and Nup96. This
CC complex plays a role in RNA export and in tethering Nup8 and
CC Nup153 to the nucleus.
CC -1- SUBCELLULAR LOCATION: Nuclear pore complex.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 1157 and a stop codon in position 1396.
CC -----
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CC -----
DR EMBL; AF104415; AAD1922.2;
DR EMBL; AK012715; BAB28429.1; ALT_FRAME.
DR MGI; MGI:1926227; Nup160.
DR GO; GO:0005643; C:nuclear pore; IDA.
DR GO; GO:0005487; F:nucleocytoplasmic transporter activity; IDA.
DR GO; GO:0006406; P:mRNA-nucleus export; IDA.
KW Nuclear protein; Transport.
FT CONFLICT 1156 1156 A -> T (IN REF. 2).
FT CONFLICT 1314 1314 E -> G (IN REF. 2).
FT CONFLICT 1368 1368 N -> D (IN REF. 2).
SQ SEQUENCE 1402 AA; 158230 MW; 3BF5D9F057D28772 CRC64;

Query Match
Best Local Similarity 89.5%; Score 34; DB 1; Length 1402;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AWSWL 6
DB 1230 AWSWL 1234

RESULT 5
YE16_HAEMIN
ID YE16_HAEMIN STANDARD; PRT; 118 AA.
AC P44188;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein H11416 precursor.
GN H11416.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KM20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fletschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kieravagge A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Wierick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Goodayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodok A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Pine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Genom C.L., McDonald L.A., Small K.V., Frazer C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).

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CC -----
 CC EMBL; U34821; AAC23067.1; -
 CC DR PIR; I64028; I64028.
 CC DR TIGR; H1416; -
 CC DR InterPro; IPR006481; Holin_Lambda.
 CC DR Pfam; PF05106; Phage_holin_3_1.
 CC DR TIGRfam; TIGR01594; holin_lambda; 1.
 CC KW Hypothetical protein; Signal; Complete proteome.
 CC FT SIGNAL 1 27 POTENTIAL.
 CC FT CHAIN 28 118 HYPOTHETICAL PROTEIN H1416.
 CC SO SEQUENCE 118 AA; 13516 MW; 96CE5D469DF8E2B CRC64;

Query Match 86.8%; Score 33; DB 1; Length 118;
 Best Local Similarity 83.3%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OR 1 LAWSWL 6
 DB 11 LINSWL 16

RESULT 6
 ID ROR1 DROME STANDARD; PRT; 685 AA.
 AC Q24486;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transmembrane receptor Ror precursor
 DE (EC 2.7.1.112) (drom).
 GN ROR OR CG4926.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
 RC STRAIN=Canton-S; TISSUE=Larval brain;
 RX MEDLINE=9334822; PubMed=8394009;
 RA Wilson C., Goeberghen D.C.I., Steller H.;
 RT "Ror, a potential neurotrophic receptor gene, encodes a Drosophila
 RT homolog of the vertebrate Ror family of Trk-related receptor tyrosine
 RT kinases.";
 RT Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Peiffer B.D.,
 RA Wan K.H., Doyle C., Bate E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.P., Agbayani A., An H.-U., Andrews-Plannoch C., Baldwin D.,
 RA Bailly R.M., Baer A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Borchan M.R., Bouck J., Brokstein P., Broctier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Cantor A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke S., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fierliera S., Fleischmann W.,
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laspo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Metel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mikhina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paciel J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stappleton M., Strong R., Sun B.,
 RA Svitkeas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of Drosophila melanogaster.";
 RA Science 287:2185-2195(2000).
 RL [3]
 RP SEQUENCE OF 545-597 FROM N.A.
 RX MEDLINE=98401146; PubMed=9731193;
 RA Oates A.C., Kollberg P., Achen M.G., Wilks A.F.;
 RT "Sampling the genomic pool of protein tyrosine kinase genes using the
 RT polymerase chain reaction with genomic DNA."
 RT Biochem. Biophys. Res. Commun. 249:660-667(1998).
 CC -1- FUNCTION: Tyrosine-protein kinase receptor that functions during
 CC early stages of neuronal development.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein.
 CC -1- TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in neurons of the developing nervous
 CC system.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ROR
 CC SUPRANILY.
 CC -1- SIMILARITY: Contains 1 frizzled (FZ) domain.
 CC -1- SIMILARITY: Contains 1 kringle domain.
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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; L20297; AAA28860.1; -
 CC EMBL; AE003628; AAF52885.1; -
 CC EMBL; AJ002908; CAA05743.1; -
 CC DR PIR; A48289; A48289.
 CC DR HSSP; P11362; 1FGK.
 CC DR FLYbase; FBgn0010407; Ror.
 CC GO; GO:0016023; C:integral to membrane; NAS.
 CC DR GO; GO:0004713; P:protein tyrosine kinase activity; NAS.
 CC DR GO; GO:0007417; P:central nervous system development; IEP.
 CC DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
 CC DR InterPro; IPR000024; Pz domain.
 CC DR InterPro; IPR000001; Kringle.
 CC DR InterPro; IPR000719; Prot_kinase.
 CC DR InterPro; IPR002011; RTkinaseII.
 CC DR InterPro; IPR01245; Tyr_kinase.
 CC DR Pfam; PF00051; kringle; 1.
 CC DR Pfam; PF00069; pkinase; 1.
 CC DR PRINTS; PR00109; TYRKINSE.
 CC DR PRINTS; PR000395; TYRKINSE.
 CC DR ProDom; PD000001; Prot_kinase; 1.
 CC DR SMART; SM00130; KR; 1.
 CC DR SMART; SM00219; TYRK; 1.
 CC DR PROSITE; PS50038; FZ; 1.
 CC DR PROSITE; PS50021; KRINGLE_1; 1.
 CC DR PROSITE; PS50070; KRINGLE_2; 1.

50	SEQUENCE	685 AA,	78142 MM,	526162D27D5FD7C7	CRC64;
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FT	CARBOHYD	63	63		(POTENTIAL).
FT	CARBOHYD	129	129		(POTENTIAL).
FT	CARBOHYD	144	144		(POTENTIAL).
FT	CARBOHYD	250	250		(POTENTIAL).
FT	MOD_RES	569	569		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	MOD_RES	570	570		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
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FT	CARBOHYD	63	63		(POTENTIAL).
FT	CARBOHYD	129	129		(POTENTIAL).
FT	CARBOHYD	144	144		(POTENTIAL).
FT	CARBOHYD	250	250		(POTENTIAL).
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FT	DOMAIN	25	317		POTENTIAL.
FT	TRANSMEM	318	338		TYROSINE-PROTEIN KINASE TRANSMEMBRANE RECEPTOR ROR. (POTENTIAL).
FT	DOMAIN	339	685		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	36	225		POTENTIAL.
FT	DOMAIN	236	310		CYTOSOLASMIC (POTENTIAL).
FT	DOMAIN	410	677		P.
FT	NP BIND	416	424		KRINGLE.
FT	BINDING	442	442		PROTEIN KINASE.
FT	ACT_SITE	539	539		ATP (BY SIMILARITY).
FT	MOD_RES	565	565		ATP (BY SIMILARITY).
FT	MOD_RES	569	569		BY SIMILARITY.
FT	MOD_RES	570	570		PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	MOD_RES	569	569		PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	MOD_RES	570	570		PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	CARBOHYD	45	45		(POTENTIAL).
FT	CARBOHYD	63	63		(POTENTIAL).
FT	CARBOHYD	129	129		(POTENTIAL).
FT	CARBOHYD	144	144		(POTENTIAL).
FT	CARBOHYD	250	250		(POTENTIAL).
FT	MOD_RES	569	569		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	MOD_RES	570	570		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	CARBOHYD	45	45		(POTENTIAL).
FT	CARBOHYD	63	63		(POTENTIAL).
FT	CARBOHYD	129	129		(POTENTIAL).
FT	CARBOHYD	144	144		(POTENTIAL).
FT	CARBOHYD	250	250		(POTENTIAL).
FT	MOD_RES	569	569		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	MOD_RES	570	570		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	CARBOHYD	45	45		(POTENTIAL).
FT	CARBOHYD	63	63		(POTENTIAL).
FT	CARBOHYD	129	129		(POTENTIAL).
FT	CARBOHYD	144	144		(POTENTIAL).
FT	CARBOHYD	250	250		(POTENTIAL).
FT	MOD_RES	569	569		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	MOD_RES	570	570		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
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FT	CARBOHYD	63	63		(POTENTIAL).
FT	CARBOHYD	129	129		(POTENTIAL).
FT	CARBOHYD	144	144		(POTENTIAL).
FT	CARBOHYD	250	250		(POTENTIAL).
FT	MOD_RES	569	569		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	MOD_RES	570	570		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
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FT	CARBOHYD	63	63		(POTENTIAL).
FT	CARBOHYD	129	129		(POTENTIAL).
FT	CARBOHYD	144	144		(POTENTIAL).
FT	CARBOHYD	250	250		(POTENTIAL).
FT	MOD_RES	569	569		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	MOD_RES	570	570		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	CARBOHYD	45	45		(POTENTIAL).
FT	CARBOHYD	63	63		(POTENTIAL).
FT	CARBOHYD	129	129		(POTENTIAL).
FT	CARBOHYD	144	144		(POTENTIAL).
FT	CARBOHYD	250	250		(POTENTIAL).
FT	MOD_RES	569	569		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	MOD_RES	570	570		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	CARBOHYD	45	45		(POTENTIAL).
FT	CARBOHYD	63	63		(POTENTIAL).
FT	CARBOHYD	129	129		(POTENTIAL).
FT	CARBOHYD	144	144		(POTENTIAL).
FT	CARBOHYD	250	250		(POTENTIAL).
FT	MOD_RES	569	569		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	MOD_RES	570	570		(BY PHOSPHORYLATION (AUTO-)) (BY SIMILARITY).
FT	CARBOHYD	45</			

Query Match	86.8%	Score 33	DB 1	Length 685
Best Local Similarity	83.3%	Pred. No. 3.1e+02		
Matches 5; Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY	1	LAWSWT	6
Db	259	LRMSWT	264

RESULT 7		
ID	HMHD_SCHPO	STANDARD; PRT; 1053 AA.
AC	010283; 074425;	
DT	01-NOV-1997 (Rel. 35, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34) (HMG-CoA reductase).	
DE		
GN	HMG1 OR SPCCI62.09C.	
OS	Schizosaccharomyces pombe (Pission yeast).	
OC	Eukaryota; Pungi; Ascomycota; Schizosaccharomycetes;	
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;	
OC	Schizosaccharomycetes.	
OX	NCBI_TaxID=4896;	
OX	[1]	
RN		
RP	SEQUENCE FROM N.A.	
RP	MEDLINE=97051601; PubMed=8896278;	
RX	Lim P.Y., Edwards S., Wright R.;	
RT	"Molecular, functional and evolutionary characterization of the gene encoding HMG-CoA reductase in the Pission yeast, Schizosaccharomyces pombe."	
RT		
RL	Yeast 12:1107-1124(1996).	
RL	[2]	
RN		
RP	SEQUENCE FROM N.A.	
RP	STRAIN=972;	
RC	MEDLINE=21844601; PubMed=11859360;	
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne R., Stewart A.,	
RA	Brooke K., Peat N., Hayles J., Baker S., Basham D., Bowman S.,	
RA	Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,	
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,	

R	A	Holtz R.S., Hornsbly T., Howarth S., Huckle E.J., Hunt S., Jagels K.
R	A	Jalmay C., Jones L., Jones M., Leather S., McDonald S., McLean J.
R	A	Kramer D., O'Neill S., Pearson D., Quall M.A., Radbnawtsch E.,
R	A	Olivier K., O'Neill S., Munhall K., Murphy I., Niblett D., Odell C.,
R	A	Rutherford K., Butler S., Saunders D., Seeger K., Sharp S.,
R	A	Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
R	A	Taylor K., Taylor R.G., Tilley A., Walsh S.V., Warren T., Whitehead S.
R	A	Moodward J., Volckreits G., Aert R., Robben J., Grymoperez B.,
R	A	Meltens I., Vanstreets E., Risger W., Schaefer M., Mueller-Auer S.,
R	A	Gabel C., Puche M., Frlenc C., Holzer E., Moestel D., Hilbert H.,
R	A	Borzym K., Langner U., Beck A., Lemach H., Reimhardt R., Pohl T.M.,
R	A	Eder P., Zimmermann W., Wedler H., Wanduth R., Purcellle B.,
R	A	Goffeau A., Cadieu E., Dreano S., Gloux S., Laureau V., Motterl S.,
R	A	Gaillet F., Ayas S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
R	A	Lucas M., Rochet M., Galliardin C., Tallada V.A., Garçon A., Thode G.
R	A	Dugas R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
R	A	Dominguez A., Revuelta J.L., Moreno S., Armerong J., Forsburg S.L.,
R	A	Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
R	A	Shpakovskii G.V., Usseery D., Barrett B.G., Nurse P.;
R	T	"The genome sequence of Schizosaccharomyces pombe.";
RL	Nature	415:871-880(2002).
-I-	FUNCTION:	INVOLVED IN THE CONTROL OF CHOLESTEROL BIOSYNTHESIS. IT
CC	-I-	IS THE RATE-LIMITING ENZYME OF THE STEROL BIOSYNTHEISIS. IT
CC	-I-	HYDROXY-3-METHYLGLUTARYL-COA + 2 NADPH.
CC	-I-	PATWAY: Cholesterol biosynthesis.
CC	-I-	SUBCELLULAR LOCATION: Integral membrane protein; Endoplasmic reticulum.
CC	-I-	SIMILARITY: BELONGS TO THE HMG-CoA REDUCTASE FAMILY.
CC	-I-	This SWISS-PROT entry is copyright. It is produced through a collabor
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CC	-I-	the European Bioinformatics institute. There are no restrictions on
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CC	-I-	modified and this statement is not removed. Usage by and for comme
CC	-I-	entities requires a license agreement (See http://www.tdb-stb.ch/anno
CC	-I-	o send an email to licens@tbd-stb.ch).
CC	-I-	-- -- -- -- --
DR	EMBL	/L76979/, AACB92277.1; -.
DR	EMBL	/AL023860/, CALJ9589.1; -.
DR	PIR	/S72194/, S72194.
DR	GeneDB	Sponme; SPCCI62.09C; -.
DR	InterPro	IPIR002202; HMG_COA_R_NADP.
DR	InterPro	IPIR004554; HMG_COA_R_NADP.
DR	InterPro	IPIR007531; SSD_5TM.
DR	Pfam	/PF00368/, HMG-CoA_red; 1.
DR	PRINTS	/PR00071/, HMGCARDPTAGE.
DR	TIGRFAMs	/TGIR00533/, HMG CoA R_NADP; 1.
DR	PROSITE	/PS00066/, HMG COA REDUCTAS_1_1.
DR	PROSITE	/PS00338/, HMG_COA_REDUCTAS_2_1.
DR	PROSITE	/PS01192/, HMG_COA_REDUCTAS_3_FALSE_NBSG.
DR	PROSITE	/PS50065/, HMG_COA_REDUC_TASE_4_1.
DR	PROSITE	/PS50156/, SSD; 1.
KW	Oxidoreductase; Glycoprotein; Endoplasmic reticulum; Transmembrane;	
KW	Cholesterot biogynthese; NMDP.	
FT	DOMAIN	1 .. 547 MEMBRANE-BOUND.
FT	DOMAIN	548 .. 615 LINKER.
FT	DOMAIN	616 .. 1053 CATALYTIC.
FT	TRANSMEM	9 .. 29 POTENTIAL.
FT	TRANSMEM	204 .. 224 POTENTIAL.
FT	TRANSMEM	233 .. 253 POTENTIAL.
FT	TRANSMEM	259 .. 279 POTENTIAL.
FT	TRANSMEM	321 .. 341 POTENTIAL.
FT	TRANSMEM	342 .. 362 POTENTIAL.
FT	TRANSMEM	418 .. 438 POTENTIAL.
FT	TRANSMEM	527 .. 547 POTENTIAL.
FT	ACT_SITE	712 .. 712 BY SIMILARITY.
FT	ACT_SITE	922 .. 922 BY SIMILARITY.
FT	ACT_SITE	1018 .. 1018 GENERAL BASE (BY SIMILARITY).
FT	CARBONYD	137 .. 137 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBONYD	399 .. 399 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBONYD	518 .. 518 N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBONYD	578 .. 578 N-LINKED (GLCNAC . .) (POTENTIAL).

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FT CARBOHYD 776 776 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1022 1022 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 751 751 N -> D (IN REF. 1).
SQ SEQUENCE 1053 AA; 114876 MW; 335EC236522D238 CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 1; Length 1053;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
DB 177 ISMSWL 182

RESULT 8
ID N184 SCHPO STANDARD; PRT; 1564 AA.
AC 09P7M6; 09Y6G4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nucleoporin nup184 (Nuclear pore protein nup184).
GN NUP184 OR SPAP27G11.10C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
RC STRAIN=972;
RX MEDLINE=99318821; PubMed=10388805;
RA Whalen W.A., Yoon J.H., Shen R., Dhar R.;
RT "Regulation of mRNA export by nutritional status in fission yeast.";
RL Genes 152:827-838(1999).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=1848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Soudous J., Peat N., Hayles J., Baker S., Baaham D., Bowman S.,
RA Brookes K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Frazer A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsle K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Shelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkert G., Aert R., Robben J., Gymnopoulos B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritsch C., Holzer H., Moestl D., Hillbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Beger P., Zimmermann W., Wedler H., Wambutt R., Burnell B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelarge V., Mottier S.,
RA Gallier F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rocher M., Galliard C., Tallada V.A., Garzon A., Thode J.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Sapatnicki L., Lowe T., McCombie W.R., Paulsen I., Poehlein J.,
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- FUNCTION: INTERACTS WITH POM152 IN THE CORE STRUCTURE OF THE
CC NUCLEAR PORE COMPLEX (NPC). INVOLVED IN THE EXPORT OF MRNA.
CC -1- SUBCELLULAR LOCATION: Nuclear pore complex.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 1560
CC ONWARD AND IS LONGER (1628 AA) DUE TO A FRAMESHIFT.
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CC -----
DR EMBL; AF055035; AAD3830.1; ALT_FRAME.
DR EMBL; AL157917; CAB76031.1; -.
DR GeneDB Spombe; SPAP27G11.10C; -.
KW Nuclear protein; Transport.
FT CONFLICT 1219 1219
SQ SEQUENCE 1564 AA; 176962 MW; 248F3A5F38C30B7 CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 1; Length 1564;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
DB 6 LMSWI 11

RESULT 9
ID YMR_ECOLI STANDARD; PRT; 60 AA.
AC P75979;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ymr.
GN YMR OR B1150.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. II, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampedo G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AE000214; AAC74234.1; -.
DR EMBL; D90749; BAA35976.1; -.
DR EMBL; D90750; BAA35988.1; -.
DR PIR; C64860; C64860.
DR EcoGene; BGI4336; ymr.

```

KW Hypothetical protein; Transmembrane; Complete proteome.
 PT TRANSMEM 5 25 POTENTIAL.
 DT 26 46
 SQ SEQUENCE 60 AA; 6381 MW; A41487AAFEED364A CRC64;
 Query Match 84.2%; Score 32; DB 1; Length 60;
 Best Local Similarity 83.3%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6
 DB 39 LFWSWL 44

RESULT 10
 ID YNFA_RH1LO STANDARD; PRT; 107 AA.
 AC 098402;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein ml17841.
 GN ML17841.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC NCBI_TaxId=381;
 OK NCBI_TaxId=381;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFP303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneo T., Nakamura Y., Sato S., Asamiizu E., Kato T., Sasamoto S.,
 Watanabe A., Ideasawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
 RA Takuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti."
 RL DNA Rep. 7:331-338(2000).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE UPF0060 FAMILY.
 CC -----
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 CC -----
 CC EMBL; APO03012; BAB54221.1; -;
 DR HAMAP; MF_00010; -; 1.
 DR InterPro; IPR003844; UPF0060.
 DR Pfam; PF02694; UPF0060; 1.
 DR ProDom; PD015609; UPF0060; 1.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 4 24 POTENTIAL.
 FT TRANSMEM 30 50 POTENTIAL.
 FT TRANSMEM 60 80 POTENTIAL.
 FT TRANSMEM 87 107 POTENTIAL.
 SQ SEQUENCE 107 AA; 11591 MW; 0C666D85212C16C3 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 107;
 Best Local Similarity 83.3%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6
 DB 71 LAMWML 76

RESULT 11
 Y07C_BPT4

ID Y07C_BPT4 STANDARD; PRT; 136 AA.
 AC P13323;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical 16.0 kDa protein in segB-lpt intergenic region (ORF3).
 GN Y07C OR IPT-2 OR TRNA3.
 OS Bacteriophage T4.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC T4-like viruses.
 OK NCBI_TaxId=10665;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86037230; PubMed=4057254;
 RA Broda J., Abelson J.;
 RT "Sequence organization and control of transcription in the
 RT bacteriophage T4 crna region."
 RL J. Mol. Biol. 185:545-563(1985).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Kutter E., Arita F., Kunitawa T., Taugita A., Mosig G.,
 RA Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;
 RT "Bacteriophage T4 genome analysis."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBSJ databases.
 CC -----
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 CC -----
 CC EMBL; X03016; CAA26805.1; -;
 DR EMBL; AF158101; AAP42681.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 136 AA; 16034 MW; 02ED3B4D8D274D9A CRC64;

Query Match 84.2%; Score 32; DB 1; Length 136;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AMSWL 6
 DB 35 AMSWL 39

RESULT 12
 ID Y410_RHISN STANDARD; PRT; 252 AA.
 AC P55498;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 28.6 kDa protein Y410.
 GN Y410.
 OS Rhizobium sp. (strain NGR234).
 OG Plasmid sym pNGR234a.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OK NCBI_TaxId=394;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97305956; PubMed=9163424;
 RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
 RA Perret X.;
 RT "Molecular basis of symbiosis between Rhizobium and legumes."
 RL Nature 387:394-401(1997).
 CC -1- SIMILARITY: LOW SIMILARITY TO THE IS1111A/IS1328/IS1533 FAMILY OF
 CC TRANSPOSASES.
 CC -1- SIMILARITY: HIGH TO F13; SOME, TO Y4PF/Y4SB AND Y4QE.
 CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AEO00079; AAB91710.1; -.
DR InterPro; IPR003346; Transposase_20.
DR Pfam; PF02371; Transposase_20; 1.
KW Hypothetical protein, Plasmid.
SQ SEQUENCE 252 AA; 28552 MW; D993C7DA03E15190 CRC64;

Query Match      84.2%; Score 32; DB 1; Length 252;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6
DB 190 LAWLWL 195

RESULT 13
NM_04M_CERCA STANDARD; PRT; 446 AA.
ID NM_04M_CERCA
AC Q34048; Q34053;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
GN ND4.
OS Ceratitidis capitata (Mediteranean fruit fly).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Tephritidae; Tephritidae; Ceratitidis.
OK NCBI_TaxId=7213;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Guatemala Laboratory colony, and Hawaii Laboratory colony;
RX MEDLINE=95261546; PubMed=7742977;
RA Gasparich G.E., Sheppard W.S., Han H.Y., McPherson B.A., Steck G.J.;
RT "Analysis of mitochondrial DNA and development of PCR-based
RT diagnostic molecular markers for Mediterranean fruit fly (Ceratitidis
RT capitata) populations.";
RL Insect Mol. Biol. 4:61-67(1995).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -----
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CC -----
DR EMBL; U12925; AAA85797.1; -.
DR EMBL; U12924; AAA85796.1; -.
DR InterPro; IPR003918; NADHub_oxred4.
DR InterPro; IPR001750; Oxidored_g1.
DR InterPro; IPR000260; Oxidored_g5_N.
DR Pfam; PF00361; Oxidored_g1; 1.
DR Pfam; PF01059; Oxidored_g5_N; 1.
DR PRINTS; PR01437; NUOXDRDTRASE4.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
KW OXIDOREDUCTASE; NAD; Ubiquinone; E9AACA06796897FD CRC64;
SQ SEQUENCE 446 AA; 50967 MW; E9AACA06796897FD CRC64;

Query Match      84.2%; Score 32; DB 1; Length 446;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
DB 190 LAWLWL 195

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DB 374 VSWSWL 379

RESULT 14
MEIB_ENTAB STANDARD; PRT; 471 AA.
ID MEIB_ENTAB
AC 007366;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melibiose carrier protein (Thiomethylgalactoside permease II)
DE (Melibiose permease) (Na+ (Li+)/melibiose symporter) (Melibiose
DE transporter).
GN MEIB.
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OK NCBI_TaxId=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97332569; PubMed=9188803;
RA Okazaki N., Kuroda M., Shinamoto T., Tsuchiya T.;
RT "Characteristics of the melibiose transporter and its primary
RT structure in Enterobacter aerogenes.";
RL Biochim. Biophys. Acta 1326:83-91(1997).
CC -1- FUNCTION: PROTEIN RESPONSIBLE FOR MELIBIOSE TRANSPORT. IT IS
CC CAPABLE OF USING HYDROGEN AND LITHIUM CATIONS AS COUPLING CATIONS
CC FOR CORTRANSPORT, DEPENDING ON THE PARTICULAR SUGAR TRANSPORTED
CC (SYMPORT SYSTEM).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -1- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
CC (SGP).
CC -----
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CC -----
DR EMBL; D86576; BAA20461.1; -.
DR InterPro; IPR001927; Na/Gal_symport.
DR TIGRFAMs; TIGR00792; gph; 1.
KW PROSITE; PS00872; NA GALACTOSIDE SYMP; 1.
KW Transports; Sugar transport; Transmembrane; Inner membrane; Symport.
FT DOMAIN 1 11
FT TRANSMEM 12 32
FT DOMAIN 33 36
FT TRANSMEM 37 57
FT DOMAIN 58 79
FT TRANSMEM 80 100
FT DOMAIN 101 106
FT TRANSMEM 107 127
FT DOMAIN 128 149
FT TRANSMEM 150 170
FT DOMAIN 171 175
FT TRANSMEM 176 196
FT DOMAIN 197 234
FT TRANSMEM 235 255
FT DOMAIN 256 266
FT TRANSMEM 267 287
FT DOMAIN 288 296
FT TRANSMEM 297 317
FT DOMAIN 318 323
FT TRANSMEM 324 344
FT DOMAIN 345 373
FT TRANSMEM 374 394
FT DOMAIN 395 411
FT TRANSMEM 412 432
FT DOMAIN 433 471
SQ SEQUENCE 471 AA; 52214 MW; 9755D85D91828106 CRC64;

```

Query Match 84.2%; Score 32; DB 1; Length 471;
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LAMSWL 6
 |||
 DB 106 LAMVWL 111

RESULT 15
 MELB_KLEPN STANDARD; PRT; 471 AA.

AC 002581.
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melibiose carrier protein (Thiomethylgalactoside permease II)
 DE (Melibiose permease) (Na+ (L1+)/melibiose symporter) (Melibiose transporter).
 GN MELB.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2002;
 RX MEDLINE=92406738; PubMed=1339436;
 RA Hama H., Wilson T.H.;
 RT "Primary structure and characteristics of the melibiose carrier of
 Klebsiella pneumoniae.";
 RL J. Biol. Chem. 267:18371-18376(1992).
 CC -1- FUNCTION: PROTEIN RESPONSIBLE FOR MELIBIOSE TRANSPORT. IT IS
 CAPABLE OF USING HYDROGEN AND LITHIUM CATIONS AS COUPLING CATIONS
 FOR COTRANSPORT, DEPENDING ON THE PARTICULAR SUGAR TRANSPORTED
 (SYMPORT SYSTEM). IT CATALYZES HYDROGEN CATION-MELIBIOSE, LITHIUM
 CATION-LACTOSE, & HYDROGEN/LITHIUM CATIONS-METHYL-1-THIO-BETA-D-
 GALACTOPYRANOSIDE (TMG) COTRANSPORT. THIS PROTEIN SEEMS TO BE
 LACKING THE ABILITY TO RECOGNIZE SODIUM CATIONS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
 (SGP).
 CC -----
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 CC -----
 CC EMBL; M97257; AAA25067.1; -.
 DR PIR; B44166;
 DR InterPro; IPR001927; Na/Gal_symport.
 DR TIGRfam; TIGR00792; gph; 1.
 DR PROSITE; PS00872; NA_GALACTOSIDE_SYP; 1.
 KW Transport; Sugar transport; Transmembrane; Inner membrane; Symport.
 FT DOMAIN 1 11
 FT TRANSMEM 12 32 POTENTIAL.
 FT DOMAIN 33 36 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 37 57 POTENTIAL.
 FT DOMAIN 58 79 POTENTIAL.
 FT TRANSMEM 80 100 POTENTIAL.
 FT DOMAIN 101 106 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 107 127 POTENTIAL.
 FT DOMAIN 128 149 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 150 170 POTENTIAL.
 FT DOMAIN 171 175 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 176 196 POTENTIAL.
 FT DOMAIN 197 234 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 235 255 POTENTIAL.
 FT DOMAIN 256 266 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 267 287 POTENTIAL.

FT DOMAIN 288 296 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 297 317 POTENTIAL.
 FT DOMAIN 318 323 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 324 344 POTENTIAL.
 FT DOMAIN 345 373 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 374 394 POTENTIAL.
 FT DOMAIN 395 411 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 412 432 POTENTIAL.
 FT DOMAIN 433 471 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 471 AA; 52329 MW; 6D373D098F4BAEC7 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 471;
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LAMSWL 6
 |||
 DB 106 LAMVWL 111

Search completed: February 18, 2004, 14:28:05
 Job time : 4.55263 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignment)
87.531 Million cell updates/sec

Title: US-09-643-260-7

Perfect score: 38
Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	94.7	675	2 H69200	heavy-metal transp
2	35	92.1	116	2 T03472	conserved hypothet
3	35	92.1	172	2 T51122	crtr protein limpo
4	35	92.1	196	2 C87039	conserved hypothet
5	35	92.1	210	2 C70528	hypothetical prote
6	35	92.1	421	2 A12824	NADH dehydrogenase
7	35	92.1	438	2 H97602	probable NADH deny
8	35	92.1	441	2 A13607	NADH2 dehydrogenas
9	34	89.5	136	2 A10124	probable prepillin
10	34	89.5	151	2 AE2249	hypothetical prote
11	34	89.5	162	2 B81635	conserved hypothet
12	34	89.5	207	2 A48608	E1 glycoprotein -
13	34	89.5	224	2 C48652	transfer protein s
14	34	89.5	264	2 H83224	phosphonate transp
15	34	89.5	266	2 C83602	proliporotein dia
16	34	89.5	296	2 E83292	conserved hypothet
17	34	89.5	338	2 S73902	UDP-glucose 4-epim
18	34	89.5	357	2 C97564	hypothetical prote
19	34	89.5	446	2 A83355	hypothetical prote
20	34	89.5	516	2 J80134	mannan endo-1,4-de
21	34	89.5	709	2 F75584	hypothetical prote
22	34	89.5	1147	2 T35781	hypothetical prote
23	34	89.5	1239	1 VHWYBE	structural polypo
24	34	89.5	1240	1 VHWYEV	structural polypo
25	34	89.5	1241	1 S26373	genome polypotein
26	34	89.5	1242	2 S72350	structural polypo
27	34	89.5	1242	2 A56605	structural polypo
28	34	89.5	1315	2 T05300	hypothetical prote
29	34	89.5	1411	2 T48529	hypothetical prote

30	34	89.5	4924	2 T50176	probable peptide s
31	33	86.8	65	2 E83492	hypothetical prote
32	33	86.8	72	2 AD2464	hypothetical prote
33	33	86.8	118	2 I64028	hypothetical prote
34	33	86.8	306	2 G82256	conserved hypothet
35	33	86.8	311	2 A83159	hypothetical prote
36	33	86.8	355	2 F70983	hypothetical prote
37	33	86.8	420	2 E72357	probable serine pr
38	33	86.8	433	2 E70968	sugar ABC transpor
39	33	86.8	440	2 D87076	hypothetical prote
40	33	86.8	661	2 F83342	probable conserved
41	33	86.8	685	1 A48289	probable cation-tr
42	33	86.8	919	2 T37062	neurotrophic recep
43	33	86.8	1053	2 S72194	probable transcrip
44	33	86.8	1628	2 T43682	hydroxymethylgluta
45	33	86.8	2121	2 T27406	nucleoporin - fibs
					hypothetical prote

ALIGNMENTS

RESULT 1

H69200 heavy-metal transporting Cpx-type ATPase - Methanobacterium thermoautotrophicum (strain

C/Species: Methanobacterium thermoautotrophicum
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C/Accession: H69200

R/Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Oliv, D.; Spadefora, R.; Viscare, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, I.
K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func

A/Reference number: A69000; MUID:98037514; PMID:9371463

A/Accession: H69200

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-675 <MT>

A/Cross-References: GB:A6000854; GB:A6000666; NID:G2621839; PIDN:AAB85258.1; PID:G2621E

A/Experimental source: strain Delta H

C/Genetics:

A/Genes: MTH755
C/Superfamily: Enterococcus copper-transporting ATPase codb; ATPase nucleotide-binding

F/76-413/Domain: ATPase transduction domain homology <ATT>

F/484-626/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 94.7% Score 36; DB 2; Length 675;
Best Local Similarity 83.3% Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6

DB 299 IAMSWL 304

RESULT 2

T03472 conserved hypothetical protein - Rhodobacter capsulatus

C/Species: Rhodobacter capsulatus

C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999

C/Accession: T03472

R/Vlack, C.; Paces, V.; Malcev, N.; Paces, J.; Haselkorn, R.; Forststein, M.

Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997

A/Title: Sequence of a 189-Kb segment of the chromosome of Rhodobacter capsulatus SB10C

A/Reference number: Z14955; MUID:97404404; PMID:9256491

A/Accession: T03472

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-116 <VLC>

A/Cross-References: EMBL:AF010496; NID:G3128256; PIDN:AA016125.1; PID:G3128273

C/Genetics:

A/Map position: 1
Query Match 92.1% Score 35; DB 2; Length 116;

Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LAMSWL 6
:|||||
Db 63 LAMSWL 68

RESULT 3
T51122
crck protein [imported] - Brevibacterium linens
C/Species: Brevibacterium linens
C/Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
R/Krubsak, P.; Sandmann, G.
Mol. Gen. Genet. 263, 423-432, 2000
A/Title: A carcinogenic gene cluster from Brevibacterium linens with novel lycopen cyc
A/Reference number: Z25303; MUID:2029196; PMID:10821176
A/Accession: T51122
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-172 <KRU>
A/Cross-references: EMBL:AF139916; PIDN:AP65585.1
A/Experimental source: DSM 20426; ATCC9175
C/Genetics:
A/Gene: crck

Query Match 92.1%; Score 35; DB 2; Length 172;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
:|||||
Db 91 VAMSWL 96

RESULT 4
C87039
conserved hypothetical protein ML1041 [imported] - Mycobacterium leprae
C/Species: Mycobacterium leprae
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C/Accession: C87039
R/Cole, S.T.; Eigemeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Felwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A/Title: Massive gene decay in the leprosy bacillus.
A/Reference number: A86909; MUID:21128732; PMID:11234002
A/Accession: C87039
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-196 <STO>
A/Cross-references: GB:AL450380; NID:G13093055; PIDN:CAC31422.1; GSPDB:GN00147
C/Genetics:
A/Gene: ML1041
C/Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2680

Query Match 92.1%; Score 35; DB 2; Length 196;
Best Local Similarity 83.3%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
:|||||
Db 109 VAMSWL 114

RESULT 5
C70528
hypothetical protein Rv2680 - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2000
C/Accession: C70528

R/Cole, S.T.; Broeck, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
; Ratandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: C70528
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-210 <COL>
A/Cross-references: GB:Z96072; GB:AL123456; NID:G3261793; PIDN:CA809496.1; PID:el30003
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: Rv2680
C/Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2680

Query Match 92.1%; Score 35; DB 2; Length 210;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
:|||||
Db 123 VAMSWL 128

RESULT 6
A12824
NADH dehydrogenase ndh [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C/Accession: A12824
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Genthner, D.; Kulyavin, T.; Levy, R.; Li, M.; McCle
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm
er, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: A12824
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-421 <KIR>
A/Cross-references: GB:AE008688; PIDN:AA143015.1; PID:G17740478; GSPDB:GN00186
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: ndh
A/Map position: circular chromosome
C/Superfamily: NADH dehydrogenase

Query Match 92.1%; Score 35; DB 2; Length 421;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
:|||||
Db 393 VAMSWL 398

RESULT 7
H97602
probable NADH dehydrogenase (Y09899) [imported] - Agrobacterium tumefaciens (strain C5)
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C/Accession: H97602
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium ti
A/Reference number: A97559; MUID:21608551; PMID:11743194
A/Accession: H97602
A/Status: preliminary

A:Molecule type: DNA
A:Residues: 1-438 <KUR>
A:Cross-references: GB:AE007869; PIDN:AA87777.1; PID:g15157148; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_3667
A:Map position: circular chromosome
C:Superfamily: NADH dehydrogenase

Query Match 92.1%; Score 35; DB 2; Length 438;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
DB 410 VAMSWL 415

RESULT 8

A:13607
NADH2 dehydrogenase (EC 1.6.99.3) [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002

C:Accession: A13607
R:DelVecchio, V.G.; Kaparat, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD252; PMID:11756688

A:Cross-references: GB:AE008918; PIDN:AL54028.1; PID:g17964981; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME10786

A:Map position: 11

C:Superfamily: NADH dehydrogenase

C:Keywords: oxidoreductase

Query Match 92.1%; Score 35; DB 2; Length 441;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
DB 413 VAMSWL 418

RESULT 9

A:10124
probable prepilin peptidase dependent protein YPO1017 [imported] - Yersinia pestis (str)

C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C:Accession: A10124
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

11, M.; Rutherford, K.; Simmons, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: A10124

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-136 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC89860.1; PID:g15979085; GSPDB:GN00175

C:Genetics:

A:Gene: YPO1017

Query Match 89.5%; Score 34; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAMSWL 6
DB 68 LAMSWL 72

RESULT 10

A:AE2249
hypothetical protein alr3548 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C:Accession: AE2249

R:Nakano, T.; Nakamura, Y.; Waki, C.P.; Kuritz, T.; Sasamoto, S.; Matsubae, A.; Iritani

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ar

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE2249

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-151 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA875247.1; PID:g17132681; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr3548

Query Match 89.5%; Score 34; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5
DB 18 LAMSW 22

RESULT 11

A:883635

conserved hypothetical protein PA0085 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: B83635

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; E

adman, S.; Yun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lapidis, K.; Lin

., J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A:Reference number: AB2950; MUID:20437337; PMID:10984043

A:Accession: B83635

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-162 <STO>

A:Cross-references: GB:AE004447; GB:AE004091; NID:g9945902; PIDN:AG03475.1; GSPDB:GN00

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0085

Query Match 89.5%; Score 34; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5
DB 28 LAMSW 32

RESULT 12

A:48608

B1 glycoprotein - eastern equine encephalomyelitis virus (fragment)

C:Species: eastern equine encephalomyelitis virus
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999

C:Accession: A48608

R:Weaver, S.C.; Bellett, L.A.; Gousser, L.; Repik, P.M.; Scott, T.W.; Holland, J.J.

Virology 195, 700-709, 1993

Query Match 89.5%; Score 34; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A:Title: Diversity within natural populations of eastern equine encephalomyelitis virus.
 A:Reference number: A48608; MUID:93311728; PMID:8101674
 A:Contents: 215-85; MD5B
 A:Accession: A48608
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-207 <ME>
 A:Cross-references: GB:563996; NID:9400551; PIDN:AA827576.1; PID:9400552
 A:Note: sequence extracted from NCBI backbone (NCBIN:135481, NCBI:P:135482)
 C:Superfamily: togavirus structural polypeptide
 C:Keywords: glycoprotein

Query Match 89.5%; Score 34; DB 2; Length 207;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAMSW 6
 DB 173 LAMSW 177

RESULT 13

C48652
 C:transfer protein epdA - Streptomyces ambofaciens plasmid pSAM2
 C:Species: Streptomyces ambofaciens
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 22-Oct-1999
 C:Accession: C48652; S33428
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; I
 J. Bacteriol. 175, 5529-5536, 1993
 A:Title: Transfer functions of the conjugative integrating element pSAM2 from Streptomy
 A:Reference number: A48652; MUID:93374848; PMID:8366038
 A:Accession: C48652
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-224 <HAG>
 A:Cross-references: EMBL:Z19593; NID:9298051; PIDN:CAA79641.1; PID:9298054
 C:Genetics:
 A:Genome: plasmid

Query Match 89.5%; Score 34; DB 2; Length 224;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5
 DB 66 LAMSW 70

RESULT 14

H83224
 C:phosphonate transport protein phnB PA3382 [Imported] - Pseudomonas aeruginosa (strain PA
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: H83224
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: H83224
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <STO>
 A:Cross-references: GB:AE004759; GB:AE004091; NID:99949500; PIDN:AA06770.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: phnB; PA3382
 C:Superfamily: phnB protein

Query Match 89.5%; Score 34; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5
 DB 31 LAMSW 35

RESULT 15

C83602
 C:polyporetein diacylglycerol transferase PA0341 [Imported] - Pseudomonas aeruginosa (s
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: C83602
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; I
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: C83602
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-266 <STO>
 A:Cross-references: GB:AE004472; GB:AE004091; NID:99946188; PIDN:AA03730.1; GSPDB:GN0
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: lgt; PA0341
 C:Superfamily: polyporetein diacylglycerol transferase

Query Match 89.5%; Score 34; DB 2; Length 266;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSW 6
 DB 229 LAMSW 234

Search completed: February 18, 2004, 14:38:40
 Job time : 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 / Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-6
Perfect score: 40
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	236	3	Q8NUT9
2	37	92.5	274	16	Q8G659
3	37	92.5	437	16	Q92K30
4	37	92.5	548	16	Q92M15
5	37	92.5	581	5	Q8MSH3
6	37	92.5	597	5	Q9VGP2
7	37	92.5	610	16	Q86712
8	37	92.5	885	16	Q91389
9	36	90.0	205	16	Q9ACR5
10	36	90.0	227	4	Q81XK8
11	36	90.0	242	12	Q919X8
12	36	90.0	355	11	Q8B1T9
13	36	90.0	358	10	Q50002
14	36	90.0	374	16	Q9H210
15	36	90.0	433	16	Q8P4A1
16	36	90.0	438	16	Q8P7V8

17	36	90.0	452	4	Q96AB7	Q96AB7 homo sapien
18	36	90.0	463	5	Q8MWJ0	Q8MWJ0 apis cerana
19	36	90.0	477	11	Q9CYU6	Q9CYU6 mus musculu
20	36	90.0	484	4	Q8BTV6	Q8BTV6 homo sapien
21	36	90.0	686	16	Q8FQ29	Q8FQ29 cornebacte
22	36	90.0	889	16	Q9AAZ6	Q9AAZ6 caulobacter
23	36	90.0	1005	10	Q9XGZ2	Q9XGZ2 arabidopsis
24	36	90.0	1535	2	Q9L4X2	Q9L4X2 streptomyce
25	34	85.0	166	4	Q8NBM1	Q8NBM1 homo sapien
26	34	85.0	273	10	Q94JN4	Q94JN4 arabidopsis
27	34	85.0	273	10	Q94JN4	Q94JN4 arabidopsis
28	34	85.0	275	10	Q65710	Q65710 arabidopsis
29	34	85.0	376	3	Q9UVL4	Q9UVL4 penicillium
30	34	85.0	617	10	P93050	P93050 arabidopsis
31	34	85.0	1074	16	Q8PJ70	Q8PJ70 xanthomonas
32	34	85.0	1842	3	Q96WT6	Q96WT6 schizosacch
33	34	85.0	1842	3	Q96WT7	Q96WT7 schizosacch
34	34	85.0	1842	3	Q96WT8	Q96WT8 schizosacch
35	33	82.5	49	6	Q8BPL6	Q8BPL6 equus caball
36	33	82.5	98	5	Q9VB45	Q9VB45 dirosophila
37	33	82.5	136	2	Q8KZ39	Q8KZ39 uncultured
38	33	82.5	154	11	Q8BGD2	Q8BGD2 mus musculu
39	33	82.5	161	6	Q8MUT3	Q8MUT3 oryctolagus
40	33	82.5	161	11	Q9Z1P9	Q9Z1P9 rattus norv
41	33	82.5	198	16	Q9PA54	Q9PA54 xyella fas
42	33	82.5	213	12	Q9E1I7	Q9E1I7 meloegrid h
43	33	82.5	213	12	Q9DP11	Q9DP11 meloegrid h
44	33	82.5	234	3	Q8NUT6	Q8NUT6 hyocrea bc
45	33	82.5	234	3	Q00095	Q00095 trichoderma

ALIGNMENTS

RESULT 1

Q8NUT9 PRELIMINARY; PRT; 236 AA.
AC Q8NUT9
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Endoglucanase.
GN CEL12C.
OS Bionectria ochroleuca.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
CC Hypocreales; Bionectriaceae; Bionectria.
OX NCBI_TaxID=29856;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22067395; PubMed=12073090;
RA Goedegebuur F., Fowler T., Phillips J., van der Kleij P.,
van Solingen P., Dankmeyer L., Power S.D.,
"Cloning and relational analysis of 15 novel fungal endoglucanases
from family 12 glycosyl hydrolase.";
RL Curr. Genet. 41:89-98(2002).
DR EMBL; AF435065; AAM7708.1; -
DR InterPro; IPR002594; Glyco_hydro_12.
DR Pfam; PF01670; Glyco_hydro_12; 1.
DR ProDom; PD004316; Glyco_hydro_12; 1.
SQ SEQUENCE 236 AA; 26024 MW; C3D8A7E33F0C41D8 CRC64;

Query Match 92.5%; Score 37; DB 3; Length 236;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
Db 63 ADMSWS 68

RESULT 2

Q8G659 PRELIMINARY; PRT; 274 AA.

AC Q8659; 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Probable dihydroxycarboxate dehydrogenase electron transfer subunit.
 GN PRK OR BL0790.
 OS Bifidobacterium longum.
 OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
 OC Bifidobacteriaceae; Bifidobacterium.
 OX NCBI_TaxID=216816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCC 2705;
 RX MEDLINE=22294977; PubMed=12381787;
 RA Schell M.A., Kamirantzou M., Snel B., Vilanova D., Berger B.,
 RA Passi G., Zwaenlin M.-C., Desiere F., Bork P., Delley M.,
 RA Priddle R.D., Arisong F.; Bifidobacterium longum reflects its adaptation
 RT to the human gastrointestinal tract."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
 DR EMBL; AEO14701; FAN24605.1; -
 KM Complete proteome.
 SQ SEQUENCE 274 AA; 29978 MW; 971E016E79636DB CRC64;

Query Match 92.5%; Score 37; DB 16; Length 274;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6
 DB 171 ADMSWS 176

RESULT 3
 ID Q92K30 PRELIMINARY; PRT; 437 AA.

AC Q92K30; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein R02283.
 GN R02283 OR SMC01671.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S.,
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Maury D.,
 RA Pohl T., Portetelle D., Puhler A., Purnelle B., Rampersager U.,
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 Sinorhizobium meliloti strain 1021."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 DR EMBL; AL591790; CAC46862.1; -
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 437 AA; 48372 MW; 950E0B3DA963CE78 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 437;
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6
 DB 157 ADMSWA 162

RESULT 4
 Q92M15

ID Q92M15 PRELIMINARY; PRT; 548 AA.

AC Q92M15; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative fatty-acid-CoA ligase protein (EC 6.---).
 GN R02631 OR SMC00741.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S.,
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Maury D.,
 RA Pohl T., Portetelle D., Puhler A., Purnelle B., Rampersager U.,
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 Sinorhizobium meliloti strain 1021."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 DR EMBL; AL591791; CAC47210.1; -
 KM Ligase; Complete proteome.
 SQ SEQUENCE 548 AA; 59383 MW; 659A68C546EA953B CRC64;

Query Match 92.5%; Score 37; DB 16; Length 548;
 Best Local Similarity 83.3%; Pred. No. 4.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6
 DB 235 ADMSWA 240

RESULT 5
 ID Q8MSH3 PRELIMINARY; PRT; 581 AA.

AC Q8MSH3; 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE GH24640p.
 GN CG6728.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Fries B.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo U., Pacled J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AV118818; AAM50678.1; -
 DR EMBL; FBgn0037896; CG6728.
 KM FlyBase; FBgn0037896; CG6728.
 DR InterPro; IPR000172; GMC_oxred.
 DR InterPro; IPR000169; SHProt_acetate.
 DR Pfam; PF00732; GMC_oxred; 3.
 DR PROSITE; PS00639; THIOLE PROTEASE HIS; 1.
 SQ SEQUENCE 581 AA; 63475 MW; A2F13BBBC25A96D CRC64;

Query Match 92.5%; Score 37; DB 5; Length 581;
 Best Local Similarity 83.3%; Pred. No. 4.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
 :|||||
 Db 158 SDMSWA 163

RESULT 6
 Q9VGP2 PRELIMINARY; PRT; 597 AA.
 AC Q9VGP2; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG6728 protein.
 GN CG6728
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Sutcliffe R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutcliffe R.C., Morten U.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Bence P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borovaya D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A.L., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laevo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mantei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nuskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Put V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B.C., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Maasman D.A., Weinstein G.M., Weinstein J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang K., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003691; AAF54634.1; -;
 DR FlyBase; FBgn0037896; CG6728.
 DR InterPro; IPR001172; GNC_oxred.
 DR InterPro; IPR000169; SHPTC_acetate.
 DR Pfam; PF00732; GNC_oxred.1.
 DR PROSITE; PS00624; GNC_oxred.2; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 SQ SEQUENCE 597 AA; 65274 MW; 8C4C362AF8A0902A CRC64;

Query Match 92.5%; Score 37; DB 5; Length 597;
 Best Local Similarity 83.3%; Pred. No. 4.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
 :|||||
 Db 158 SDMSWA 163

RESULT 7
 O86712 PRELIMINARY; PRT; 610 AA.
 AC O86712; 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein SC06530.
 GN SC06530 OR SC5C7.15.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxId=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K.F., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL939128; CAA20627.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 610 AA; 67368 MW; 052C8A90DB589021 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 610;
 Best Local Similarity 83.3%; Pred. No. 4.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
 :|||||
 Db 83 ADMSWA 88

RESULT 8
 Q91389 PRELIMINARY; PRT; 885 AA.
 AC Q91389; 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Two-component sensor KdpD.
 GN KDPD OR PA1636.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxId=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RX Stever C.R., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino B., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kae A., Laidig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an
 RT opportunistic pathogen."
 RL Nature 406:959-964(2000).
 CC -1 - SIMILARITY: TO PROKARYOTE SENSOR TRANSDUCTION PROTEINS.
 DR EMBL: AEO04591; MAG5025.1; -.
 DR HSSP: P02933; IUOY.
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR004358; Bact_sens_pr_C.
 DR InterPro: IPR003018; GAF.
 DR InterPro: IPR003661; His_kinase.
 DR InterPro: IPR005467; His_kinase.
 DR InterPro: IPR003852; KdpD.
 DR Pfam: PF02518; HATPase_c_1.
 DR Pfam: PF00512; HlsKA; 1.
 DR Pfam: PF02702; KdpD; 1.
 DR PRINTS: PR00344; BCTRLSENSOR.
 DR SMART: SM00065; GAF; 1.
 DR SMART: SM00387; HATPase_c; 1.
 DR SMART: SM00388; HlsKA; 1.
 DR PROSITE: PS50109; HIS_KIN; 1.
 KM Kinase; Phosphorylation; Sensory transduction; Transferase;
 KW Complete proteome.
 SQ SEQUENCE 885 AA; 97019 MW; 20FC6E2B2AB876C0 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 885;
 Best Local Similarity 83.3%; Pred. No. 6.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
 |||||
 DB 563 ADMAWA 568

RESULT 9
 ID Q9ACR5 PRELIMINARY; PRT; 205 AA.
 AC Q9ACR5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein SCP1.253.
 GN SCP1.253.
 OS Streptomyces coelicolor.
 OG Bacteri; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomyces; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=21956410; PubMed=12000953;
 RA Bertley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomsen N.R., James K.D., Harris D.E., Quail M.A., Kleeser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Frazer A., Gobie A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleeser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.,
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RT *coelicolor* A3(2)."
 RL Nature 417:141-147(2002).
 DR EMBL: AL590464; CAC36779.1; -.
 KM Hypothetical protein; Plasmid; Complete proteome.
 SQ SEQUENCE 205 AA; 23051 MW; 6602396CF93F2D9 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 205;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
 |||||
 DB 10 ADMSW 14

RESULT 10
 ID Q8IXK8 PRELIMINARY; PRT; 227 AA.
 AC Q8IXK8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to hypothetical protein BC017335.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC040173; AAH40173.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 227 AA; 25487 MW; F1A71EA57062A05 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 227;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
 |||||
 DB 113 ADMSW 117

RESULT 11
 ID Q919X8 PRELIMINARY; PRT; 242 AA.
 AC Q919X8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CUN068 hypothetical protein.
 GN CUN068.
 OS *Culex nigripalpus* baculovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
 OX NCBI_TaxID=130556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Florida1997;
 RX MEDLINE=2148685; PubMed=11602755;
 RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
 RA Becnel J.J., Rock D.L., Kutish G.F.,
 RT "Genome Sequence of a *Baculovirus* Pathogenic for *Culex nigripalpus*."
 RT J. Virol. 75:11157-11165(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Florida1997;
 RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
 RA Becnel J.J., Rock D.L., Kutish G.F.,
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF403738; AA94146.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 242 AA; 27222 MW; 6014967531110B52 CRC64;

Query Match 90.0%; Score 36; DB 12; Length 242;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
 |||||
 DB 80 DMSWA 84

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RESULT 12
ID Q8BIT9 PRELIMINARY; PRT; 355 AA.
AC Q8BIT9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Mitochondrial ribosomal protein L41 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
RA The PANOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK087998; BAC40084.1;
SO SEQUENCE 355 AA; 40183 MW; PEF8546127402D58 CRC64;

Query Match 90.0%; Score 36; DB 11; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 215 ADMSW 219

RESULT 13
ID Q50002 PRELIMINARY; PRT; 358 AA.
AC Q50002;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytochrome protease.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucoside I; Rosales; Rosaceae; Amygdaloidae; Prunus.
OX NCBI_Taxid=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bergeon; TISSUE=Necrocarp, and Exocarpy;
RA Mdegule-A-Mdegule D., Gomez R.-M., Fils-Lycaon B.;
RT "Sequence of APTPI, a Cytochrome Protease From Apricot Fruit
RT (Accession No. U93166). Gene Expression During Fruit Ripening. (PGR97-
RT 179)."
RL Plant Physiol. 115:1730-1730(1997).
DR EMBL; U93166; AAB97142.1;
DR HSRP; P07711; ICDL.
DR MEROPS; C01.041; -.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR000668; SHPoc_acetate.
DR InterPro; IPR000169; SHPoc_acetate.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR PRODOM; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept_C1; 1.
DR PROSITE; PS00038; HLH 1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
DR Hydrolyase; Protease; Thiol protease.
SQ SEQUENCE 358 AA; 39309 MW; C98F78793B002554 CRC64;

Query Match 90.0%; Score 36; DB 10; Length 358;

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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 108 ADMSW 112

RESULT 14
ID Q9H210 PRELIMINARY; PRT; 374 AA.
AC Q9H210;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein PA3230.
GN PA3230.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
MEDLINE=20437337; PubMed=10984043;
RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino B., Westbrock-Adams S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lathig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL; AE004746; AAC06618.1;
RX Hypothetical protein; Complete proteome.
SQ SEQUENCE 374 AA; 42269 MW; 31EF185C4F63884 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWA 6
Db 81 DMSWA 85

RESULT 15
ID Q8P4A1 PRELIMINARY; PRT; 433 AA.
AC Q8P4A1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cationic amino acid transporter.
GN XCC3809.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_Taxid=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
RX da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Canavotte G., Canavan F., Cardozo J., Chambergo F., Clapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Doroty H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fomiglieri E.F., Franco M.C., Greggio C.C., Guiber A.,
RA Katsuyama A.M., Kishii L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

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RA Martins E.C., Melânia J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Secubal J.C., Kitajima J.P.,
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 host specificities."
 RL Nature 417:459-463(2002).
 DR EMBL; AE012502; AAW43483.1; -;
 DR InterPro; IPR002293; AA/rel_permease1.
 DR InterPro; IPR004841; Permease.
 DR Pfam; PF00324; aa_permeases; 1.
 KW Complete proteome.
 SQ SEQUENCE 433 AA; 45128 MW; EF217D2A7C516533 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 433;

Best Local Similarity 100.0%; Pred.No. 4.6e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6

DB 181 DMSWA 185

Search completed: February 18, 2004, 14:35:41
 Job time : 18.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 / Search time 3.55263 Seconds

(Without alignments)
/9.423 Million cell updates/sec

Title: US-09-643-260-6

Sequence: 40
1 ADMSWA 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	470	1 NRAM_IADBU	Q07570 Influenza a
2	36	90.0	470	1 NRAM_IADCH	Q07571 Influenza a
3	36	90.0	470	1 NRAM_IADH2	Q07572 Influenza a
4	36	90.0	470	1 NRAM_IADW2	Q07573 Influenza a
5	36	90.0	470	1 NRAM_IADU3	Q07599 Influenza a
6	36	90.0	470	1 NRAM_IACRN	Q07574 Influenza a
7	36	90.0	470	1 NRAM_IAGHD	Q07577 Influenza a
8	36	90.0	470	1 NRAM_IADH1	Q07578 Influenza a
9	36	90.0	470	1 NRAM_IAMAE	Q07583 Influenza a
10	36	90.0	470	1 NRAM_IATKL	Q07585 Influenza a
11	36	90.0	598	1 MRS5_APMR	Q97432 apis mellif
12	34	85.0	376	1 PGR_PENGR	Q93883 penicillium
13	34	85.0	1842	1 PMS2_SCHPO	Q10889 s fatty aci
14	33	82.5	99	1 NOS3_SHEEP	P79209 ovls arles
15	33	82.5	220	1 Y132_METJA	Q57596 methanococ
16	33	82.5	232	1 C1B2_SHEEP	P80943 ovls arles
17	33	82.5	333	1 C1B2_SHEEP	Q29422 ovls arles
18	33	82.5	410	1 Y801_DEIRA	Q97468 delinococcus
19	33	82.5	421	1 PNT1_SCHPO	Q13511 echizosacch
20	33	82.5	470	1 NRAM_IADIT	Q07584 Influenza a
21	33	82.5	479	1 BG1A_BACSU	P42973 bacillus su
22	33	82.5	492	1 AERA_AERTU	P09166 aeromonas t
23	33	82.5	529	1 YC00_METJA	P46810 mycobacteri
24	33	82.5	578	1 YC12_KLEBN	Q58617 methanococ
25	33	82.5	579	1 YC12_KLEBN	Q48458 klabiella
26	33	82.5	817	1 PNT1_SCHPO	Q86551 streptomyc
27	33	82.5	914	1 PNT1_SCHPO	P09000 clostridium
28	33	82.5	1201	1 NOS3_MOUSE	P70313 mus musculu
29	33	82.5	1202	1 NOS3_MOUSE	P29473 mus musculu
30	33	82.5	1204	1 NOS3_BOVIN	P29473 bos taurus
31	33	82.5	1204	1 NOS3_BOVIN	Q28869 sus scrofa
32	32	80.0	100	1 NOS3_CANVO	P97270 cavia porce
33	32	80.0	107	1 STEL_RHIVE	P00302 rhus vernic

34	32	80.0	125	1 VG61_BPMW2	O64253 mycobacteri
35	32	80.0	272	1 C1L_RHOU	P23135 rhodospirill
36	32	80.0	282	1 3MG2_ECOLI	P04395 escherichia
37	32	80.0	295	1 X769_HUMAN	Q99871 homo sapien
38	32	80.0	339	1 YXGB_ECOLI	P27250 escherichia
39	32	80.0	360	1 WNT2_ECOLI	P34889 caenorhabdi
40	32	80.0	362	1 DCUP_YEAST	P32347 saccharomyc
41	32	80.0	375	1 H1S7_XANCP	P58882 xanthomonas
42	32	80.0	411	1 POLC_BUCAI	P57265 buchera ap
43	32	80.0	418	1 HLT_VIRPA	Q99289 vibrio para
44	32	80.0	453	1 NRAM_IAMIL	P03470 influenza a
45	32	80.0	454	1 NRAM_IAPUE	P03468 influenza a

ALIGNMENTS

RESULT 1	ID	NRAM_IADBU	STANDARD:	PRT:	470 AA.
AC	Q07570;				
DT	01-FEB-1995 (Rel. 31, Created)				
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Neuraminidase (EC 3.2.1.18).				
GN	NA.				
OS	Influenza A virus (strain A/Duck/Burjatta/652/88).				
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;				
OC	Influenza A viruses; Influenzavirus A.				
OX	NCBI_Taxid=38956;				
RY	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93212520; PubMed=8460490;				
RA	Saito T., Kawaka Y., Webster R.G.;				
RT	"Phylogenetic analysis of the N8 neuraminidase gene of Influenza A				
RT	viruses."				
RL	Virology 193:868-876(1993).				
CC	-1- FUNCTION: Removes the terminal sialic acid from carbohydrate side				
CC	chains of the host cell surface proteins and from the viral				
CC	envelope. Such a reaction prevents self-aggregation and facilitates				
CC	the mobility of the virus to and from the site of infection.				
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,				
CC	alpha-(2-8)- glycosidic linkages of terminal sialic residues in				
CC	oligosaccharides, glycoproteins, glycolipids, colominic acid and				
CC	synthetic substrates.				
CC	-1- SUBUNIT: Homotrimer.				
CC	-1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED				
CC	SPIKE ON THE SURFACE OF THE VIRION.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.				
CC	-----				
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CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
CC	EMBL; L06572; AAA3365.1; -				
DR	HSSP; P06820; 2BAT.				
DR	InterPro; IPR001860; Glyco_hydro_34.				
DR	Pfam; PF00064; neur; 1.				
DR	ProDom; PD000431; Glyco_hydro_34; 1.				
KW	Hydrolase; Glycosidase; Glycoprotein; Transmembrane.				
FT	TRANSMEM	7	38		ANCHOR (BY SIMILARITY).
FT	DOMAIN	39	88		HYPERVARIABLE STALK REGION.
FT	DOMAIN	89	470		HEAD OF NEURAMINIDASE.
FT	ACT_SITE	273	273		BY SIMILARITY.
FT	ACT_SITE	275	275		BY SIMILARITY.
FT	CARBOHYD	46	46		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	54	54		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	144	144		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	293	293		N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 51989 MW; DIA6F07460F6F8AD CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 2

NRAM_IADCH STANDARD; PRT; 470 AA.
ID NRAM_IADCH
AC 007571;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Chabarovsk/1610/72).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=39571;
RN SEQUENCE FROM N.A.
RP MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawasaka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RT Virology 193:868-876(1993).

CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitates
the mobility of the virus to and from the site of infection.

CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
alpha-(2-8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
SPIKE ON THE SURFACE OF THE VIRION.

CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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or send an email to license@isb-sib.ch).

CC -----
DR EMBL: L06573; AAA43367.1; -.
DR HSSP: P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KM Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38
FT DOMAIN 39 88
FT ACT_SITE 89 470
FT ACT_SITE 273 273
FT ACT_SITE 275 275
FT CARBOHYD 46 46
FT CARBOHYD 54 54
FT CARBOHYD 84 84
FT CARBOHYD 144 144
FT CARBOHYD 293 293
FT CARBOHYD 398 398
SQ SEQUENCE 470 AA; 52070 MW; 169AB89FB8E806DC CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;

Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 3

NRAM_IADH2 STANDARD; PRT; 470 AA.
ID NRAM_IADH2
AC 007572;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Hokkaido/8/80).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11358;
RN SEQUENCE FROM N.A.
RP MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawasaka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RT Virology 193:868-876(1993).

CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitates
the mobility of the virus to and from the site of infection.

CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
alpha-(2-8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
SPIKE ON THE SURFACE OF THE VIRION.

CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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CC -----
DR EMBL: L06574; AAA43372.1; -.
DR HSSP: P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KM Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38
FT DOMAIN 39 88
FT ACT_SITE 89 470
FT ACT_SITE 273 273
FT ACT_SITE 275 275
FT CARBOHYD 46 46
FT CARBOHYD 54 54
FT CARBOHYD 84 84
FT CARBOHYD 144 144
FT CARBOHYD 293 293
FT CARBOHYD 398 398
SQ SEQUENCE 470 AA; 52015 MW; B1C1D3B2C650B93C CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5

DB 453 ADMSW 457

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|||||
RESULT 4
NRAM_IADW2 STANDARD; PRT; 470 AA.
ID NRAM_IADW2 007573;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Memphis/928/74).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OK NCBI_TaxID=11367;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L06575; AAA3404.1; -.
DR HSP: P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
DR KRM Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
DR TRANSMEM 7 38
FT DOMAIN 39 88 ANCHOR (BY SIMILARITY).
FT DOMAIN 89 470 HYPERVARIABLE STALK REGION.
FT ACT SITE 273 273 HEAD OF NEURAMINIDASE.
FT ACT SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52146 MW; 30F5F9FE364C1F49 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
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DB 453 ADMSW 457

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RESULT 5
NRAM_IADU3 STANDARD; PRT; 470 AA.
ID NRAM_IADU3 007599;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Ukraine/1/63).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OK NCBI_TaxID=11374;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L06576; AAA16234.1; -.
DR HSP: P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
DR KRM Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
DR TRANSMEM 7 37
FT DOMAIN 38 88 ANCHOR (BY SIMILARITY).
FT DOMAIN 89 470 HYPERVARIABLE STALK REGION.
FT ACT SITE 273 273 HEAD OF NEURAMINIDASE.
FT ACT SITE 275 275 PROBABLE.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 51960 MW; B46D54A03AC8C8 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
|||||
DB 453 ADMSW 457

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DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
RT viruses."
RT Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL, L06584; AAA43428.1; -.
DR HSSP, P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur. 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KM Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52348 MW; D3BD2AAC0159FE66 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADM5W 5
DB 453 ADM5W 457

RESULT 7
ID NRAM_IAGHD STANDARD; PRT; 470 AA.
AC Q07577;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.

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```

OS Influenza A virus (strain A/Herring gull/DE/67/88).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38964;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
RT viruses."
RT Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL, L06585; AAA43368.1; -.
DR HSSP, P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur. 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KM Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52265 MW; 2BAF0B75B80539B7 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADM5W 5
DB 453 ADM5W 457

RESULT 8
ID NRAM_IAGHI STANDARD; PRT; 470 AA.
AC Q07578;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Egypt/11/89).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11401;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RT Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RL viruses."
RT Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06579; AAA43374.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
DR Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
KW TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT SITE 273 273 BY SIMILARITY.
FT ACT SITE 273 273 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52234 MW; C50B21050A37668 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 9
NRAM_IATKL STANDARD; PRT; 470 AA.
AC 007583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Mallard/Edmonton/220/90).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38965;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RT Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RL viruses."
RT Virology 193:868-876(1993).

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RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses."
RT Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06586; AAA43369.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
DR Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
KW TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT SITE 273 273 BY SIMILARITY.
FT ACT SITE 273 273 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 557630C3B112765 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 10
NRAM_IATKL STANDARD; PRT; 470 AA.
AC 007583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RT Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RL viruses."
RT Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side

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CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitate
 CC the mobility of the virus to and from the site of infection.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 CC SPIKE ON THE SURFACE OF THE VIRION.
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
 CC -----
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 CC -----
 CC EMBL; L06588; AAA3410.1; -.
 CC DR HSBP; L06820; 2BAT.
 CC DR InterPro: IPR001860; Glyco_hydro_34.
 CC DR Pfam; PF00064; neur; 1.
 CC DR ProDom; PD000431; Glyco_hydro_34; 1.
 CC KM HydroLase; GlycoSibase; Glycoprotein; Transmembrane.
 CC FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 CC FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 CC FT ACT_SITE 273 273 BY SIMILARITY.
 CC FT ACT_SITE 275 275 BY SIMILARITY.
 CC FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 470 AA; 52352 MW; DE573742ABF1E6B CRC64;
 CC -----
 CC Query Match 90.0%; Score 36; DB 1; Length 470;
 CC Best Local Similarity 100.0%; Pred. No. 62;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 1 ADMSW 5
 CC DB 453 ADMSW 457
 CC -----
 CC RESULT 11
 CC MRJ5_APIME STANDARD; PRT; 598 AA.
 CC AC 097432;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DE Major royal jelly protein 5 precursor (MRJP-5) (see-milk protein).
 CC GN MRJP5.
 CC OS Apis mellifera (Honeybee).
 CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygora;
 CC NC Nematoda; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 CC OC Apoidea; Apis.
 CC OK NCBI_TaxID=7460;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Head;
 CC RA MEDLINE=99373663; PubMed=10441680;
 CC RT "Albert S., Bhattacharya D., Khandin J., Schmitzova J., Simuth J.;
 CC "The family of major royal jelly proteins and its evolution.";
 CC J. Mol. Evol. 49:290-297(1999).
 CC RL -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
 CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE
 CC LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG
 CC LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE

CC HONEYBEE QUEEN.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: HYPOPHARYNGEAL GLANDS OF NURSE HONEY BEES.
 CC -1- DEVELOPMENTAL STAGE: PRODUCED BY THE CERPATIC GLANDULAR SYSTEM OF
 CC THE NURSE HONEY BEE.
 CC -1- SIMILARITY: BELONGS TO THE MAJOR ROYAL JELLY PROTEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF004842; AAD01205.1; -.
 CC DR InterPro: IPR003534; RoyalJelly.
 CC DR Pfam; PF03022; MRJP, 2.
 CC DR PRINTS; PR01366; ROYALJELLY.
 CC KM Signal; Repeat; Glycoprotein.
 CC FT SIGNAL 1 17 POTENTIAL.
 CC FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.
 CC FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 598 AA; 70236 MW; 2C603C7B7ACDF63 CRC64;
 CC -----
 CC Query Match 90.0%; Score 36; DB 1; Length 598;
 CC Best Local Similarity 100.0%; Pred. No. 77;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 2 DMSWA 6
 CC DB 113 DMSWA 117
 CC -----
 CC RESULT 12
 CC PGLR_PENGR STANDARD; PRT; 376 AA.
 CC AC 093883;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DE Polygalacturonase precursor (EC 3.2.1.15) (Pc) (Pectinase).
 CC GN PEG1.
 CC OS Penicillium griseoformeum.
 CC OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
 CC OK NCBI_TaxID=84562;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=CCT 6421;
 CC RA Ribon A.B., Coelho J.L.C., Barros B.G., Araujo E.F.;
 CC RT "Cloning and characterization of a gene encoding the
 CC endopolygalacturonase of Penicillium griseoformeum.";
 CC RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
 CC galactosiduronic linkages in pectate and other galacturonans.
 CC -1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
 CC (POLYGALACTURONASES).
 CC -----
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 CC -----
 CC EMBL; AF085238; AAC83692.1; -.
 CC DR InterPro: IPR000743; Glyco_hydro_28.
 CC DR InterPro: IPR006626; Pch1.

DR Pfam; PF00295; Glyco_hydro_28; 1.
 DR SMART; SM00710; PBI1; 5.
 DR PROSITE; PS00502; POLYGALACTURONASE; 1.
 KW Hydrolase; Glycosidase; Cell wall; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 376 POLYGALACTURONASE.
 SO SEQUENCE 376 AA; 38068 MW; 1ED1EC56ED56528 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 376;
 Best local Similarity 66.7%; Pred. No. 1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
 DB 349 SDMSWS 354

RESULT 13
 ID FAS2_SCHPO STANDARD; PRT; 1842 AA.
 AC Q10289; O14163; P78973;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fatty acid synthase subunit alpha (BC 2.3.1.86) [includes:
 DE Acyl carrier; 3-oxoacyl-[acyl-carrier protein] reductase
 DE (EC 1.1.1.100) (Beta-ketoacyl-[acyl-carrier protein] reductase); 3-oxoacyl-[acyl-carrier
 DE protein] synthase (EC 2.3.1.41) (Beta-ketoacyl synthase)].
 GN FAS2 OR LSD1 OR SPAC4A8.11C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96354912; PubMed=8769419;
 RA Saitoh S., Takahashi K., Nabeeshima K., Yamashita Y., Nakaseko Y.,
 RA Hiraoka A., Yanagida M.;
 RT "Aberrant mitosis in fission yeast mutants defective in fatty acid
 RT synthetase and acetyl CoA carboxylase.";
 RL J Cell Biol. 134:949-961(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21363051; PubMed=11470243;
 RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,
 RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Seraka M.;
 RT "Very long-chain fatty-acid-containing phospholipids accumulate in
 RT fatty acid synthase temperature-sensitive mutant strains of the
 RT fission yeast Schizosaccharomyces pombe fas2/lsd1.";
 RL Biochim. Biophys. Acta 1532:223-233(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Scouras K., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks R., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor A., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA Jones K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voicikart G., Aert R., Robben J., Grymprez B.,
 RA Welter G., Vansteelandt B., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gebelens I., Fuchs M., Fritz C., Holzer E., Moesli D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wandt R., Pirmale B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Uebey D., Barrett B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RN Nature 415:871-880(2002).
 RP SEQUENCE OF 1-215 FROM N.A.
 RA Koken M.H.M., de Rooij J.;
 RL Submitted (Feb-1997) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1-20.
 RX MEDLINE=94245730; PubMed=8188691;
 RA Kaeslin E., Heyer W.-D.;
 RT "Schizosaccharomyces pombe fatty acid synthase mediates DNA strand
 RT exchange in vitro.";
 RL J. Biol. Chem. 269:14103-14110(1994).
 CC -1- FUNCTION: FATTY ACID SYNTHETASE. CATALYZES THE FORMATION OF
 CC LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
 CC THE ALPHA SUBUNIT CONTAINS DOMAINS FOR: ACYL-CARRIER PROTEIN,
 CC 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND 3-OXOACYL-[ACYL-
 CC CARRIER-PROTEIN] SYNTHASE. THIS SUBUNIT COORDINATES THE BINDING
 CC OF THE SIX BETA SUBUNITS TO THE ENZYME COMPLEX.
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a
 CC long-chain acyl-CoA + N CoA + N CO(2) + 2N NADP(+).
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-
 CC carrier protein] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +
 CC [acyl-carrier protein].
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- SUBUNIT: [Alpha(6)beta(6)] hexamers of two multifunctional
 CC subunits (alpha and beta).
 CC -1- SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM
 CC OTHER FUNGI.
 CC -----
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 CC -----
 DR EMBL; D83412; BAA11913.1; -;
 DR EMBL; AB013747; BAB62029.1; -;
 DR EMBL; Z98762; CAB11481.1; -;
 DR EMBL; U82216; AAB39943.1; -;
 DR PIR; A54083; A54083.
 DR PIR; T38781; T38781.
 DR PIR; T43409; T43409.
 DR GenDB; Spombe; SPAC4A8.11C; -;
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR InterPro; IPR004568; Pantechm_tnm.
 DR InterPro; IPR006162; Pantechm_attach.
 DR Pfam; PF01648; ACPS; 1.
 DR Pfam; PF02801; ketoacyl-synt_1.
 DR Pfam; PF02801; ketoacyl-synt_C; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRfam; TIGR00556; pantechm_tnm; 1.
 DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
 KW Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase;
 KW Transferase; NADP; Phosphopantetheine.
 FT DOMAIN 1 ?
 FT DOMAIN ? ?
 FT BINDING 180 ? 1842 BETA-KETOACYL REDUCTASE.
 FT BINDING 180 180 PHOSPHOPANTETHEINE (BY SIMILARITY).
 FT ACT SITE 1262 1262 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
 FT CONFLICT 107 107 S -> A (IN REF. 4).
 FT CONFLICT 422 422 K -> R (IN REF. 1).

SQ SEQUENCE 1842 AA; 202168 MW; E4019F2D133EB571 CRC64;
 Query Match 85.0%; Score 34; DB 1; Length 1842;
 Best Local Similarity 66.7%; Pred. No. 4.3e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 6
 :||:|
 DB 400 SDNMA 405

RESULT 14
 NOS3_SHEEP STANDARD; PRT; 99 AA.
 AC P79209;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type II) (NOSII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS) (Fragment).
 GN NOS3 OR NOS.
 OS Ovis aries (Sheep).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
 OC BOV1dae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endothelial cells;
 RA Aguan K., Weiner C.P.;
 RT "Effect of hypoxia on the microvasculature of developing fetal brain of sheep: a studies on the expression pattern of constitutive forms of nitric oxide synthase."
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A cAMP-MEDIATED SIGNAL TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + nitric oxide + N NADP(+).
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE ENZYME (BY SIMILARITY).
 CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY SIMILARITY).
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.
 CC -----
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 CC -----
 CC EMBL: U76738; AAB40705.1; -.
 DR HSSP; P29473; 1D0C.
 DR InterPro; IPR004030; NO_synthase.
 DR Pfam; PF02898; NO_synthase; 1.
 DR PROSITE; PS60001; NOS; PARTIAL.
 KM Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding; KM Heme; Multigene family.
 FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 11034 MW; 82C3C765557031DA CRC64;

Query Match 82.5%; Score 33; DB 1; Length 99;
 Best Local Similarity 80.0%; Pred. No. 43;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
 :||:|
 DB 65 ADMAW 69

RESULT 15
 Y132_METUA STANDARD; PRT; 220 AA.
 ID Y132_METUA
 AC 057596;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein M0132.
 GN M0132.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales; CC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=868087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weissbrock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghegan N.S.M., Feldman J.F., Fuhrmann J.L., Nguyen D., Utermack T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Frazer C.W., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
 RL Science 273:1058-1073 (1996).
 CC -1- SIMILARITY: TO M. JANNASCHII MJ1220 AND MJEC142.
 CC -1- SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES (M SUBUNIT).
 CC -----
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 CC -----
 CC EMBL: U67470; AAB98113.1; -.
 DR PIR; D64316; D64316.
 DR TIGR; M0132; -.
 DR InterPro; IPR003356; N6_DNA_Mtase.
 DR Pfam; PF02384; N6_Mtase; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 220 AA; 25766 MW; 710DDAB4C7A47954 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 220;
 Best Local Similarity 80.0%; Pred. No. 88;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
 :||:|
 DB 33 ADMAW 37

Search completed: February 18, 2004, 14:28:04
 Job time : 3.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds

(without alignment)
87.531 Million cell updates/sec

Title: US-09-643-260-6

Perfect score: 40
Sequence: 1 ADMSNA 6Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	610	2	T35222
2	37	92.5	885	2	C83441
3	36	90.0	374	2	B83241
4	36	90.0	889	2	E87304
5	34	85.0	275	2	T05822
6	34	85.0	617	2	C84922
7	34	85.0	1842	2	T33409
8	34	85.0	1842	2	T38781
9	33	82.5	132	2	S65785
10	33	82.5	198	2	B82531
11	33	82.5	220	2	D64316
12	33	82.5	232	2	S58353
13	33	82.5	239	2	D90470
14	33	82.5	257	2	D87152
15	33	82.5	276	2	B75337
16	33	82.5	304	2	F63632
17	33	82.5	310	2	JC7853
18	33	82.5	324	2	A83548
19	33	82.5	328	2	E72424
20	33	82.5	333	2	S47246
21	33	82.5	350	2	S71923
22	33	82.5	368	2	H90998
23	33	82.5	410	2	D75475
24	33	82.5	415	2	A81844
25	33	82.5	418	2	A81460
26	33	82.5	421	2	A81097
27	33	82.5	421	2	T38242
28	33	82.5	433	2	T31511
29	33	82.5	467	2	G82697

30	33	82.5	478	2	B89790	6-phospho-beta-glu
31	33	82.5	479	2	T39553	6-phospho-beta-glu
32	33	82.5	492	2	S03098	aerolysin precursor
33	33	82.5	529	2	C86958	probable GMP synth
34	33	82.5	539	2	T15256	hypothetical prote
35	33	82.5	578	2	G64452	restriction modifi
36	33	82.5	590	2	S72813	GMP synthase (glut
37	33	82.5	616	2	C69226	type I restriction
38	33	82.5	623	2	B75221	type I restriction
39	33	82.5	765	2	B76795	hypothetical prote
40	33	82.5	836	2	D82177	conserved hypotet
41	33	82.5	1202	2	B71424	nitric-oxide synth
42	33	82.5	1203	1	A47501	nitric-oxide synth
43	33	82.5	1205	1	A48943	nitric-oxide synth
44	33	82.5	1329	2	D87226	conserved hypotet
45	33	82.5	1409	2	B74916	alkaline phosphata

ALIGNMENTS

RESULT 1

T35222

hypothetical protein SC5C7.15 SC5C7.15 - Streptomyces coelicolor

Query Match 92.5%, Score 37, DB 2, Length 610,
Best Local Similarity 83.3%, Pred. No. 1e+02,
Matches 5, Conservative 1, Mismatches 0, Indels 0, Gaps 0,

QY 1 ADMSNA 6
DB 83 ADMSNA 88

RESULT 2

C83441 two-component sensor kdpd PA1636 [imported] - Pseudomonas aeruginosa (strain PAO1)

C1Species: Pseudomonas aeruginosa

C1Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C1Accession: C83441

R1Stover, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warener, P.; Hickey, M.J.; E

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lashig, K.; Lin

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A1Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path

A1Reference number: AB2950; MUID:2043737; PMID:10984043

A1Accession: C83441

A1Status: preliminary

A1Molecule type: DNA

A1Residues: 1885 <STO>

A1Cross-references: GB:AE004591; GB:AE004091; NID:g9947599; PIDN:AA05025.1; GSPDB:GNOC

A1Experimental source: strain PAO1

C1Genetics:

A1Gene: kdpd, PA1636

Query Match 92.5%, Score 37, DB 2, Length 885,
Best Local Similarity 83.3%, Pred. No. 1.5e+02,
Matches 5, Conservative 1, Mismatches 0, Indels 0, Gaps 0,

QY 1 ADMSMA 6
|||||
DB 563 ADMAMA 568

RESULT 3

B83241
conserved hypothetical protein PA3230 [imported] - Pseudomonas aeruginosa (strain PAO1)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Accession: B83241
R/Stover, C.K.; Plam, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latbig, K.; Lim, J.; Loy, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: B83241
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-374 <STO>
A/Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AA06618.1; GSPDB:GN001
A/Experimental source: strain PAO1
C/Genetics:
A/Genes: PA3230

Query Match 90.0%; Score 36; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSMA 6
|||||
DB 81 DMSMA 85

RESULT 4

E87304
TonB-dependent receptor [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C/Accession: E87304
R/Niemann, W.C.; Feldblum, T.V.; Paulsen, I.T.; Neilson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolton, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: E87304
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-889 <STO>
A/Cross-references: GB:AE005673; NID:g13421615; PIDN:AAK22433.1; GSPDB:GN00148
C/Genetics:
A/Genes: CO0446

Query Match 90.0%; Score 36; DB 2; Length 889;
Best Local Similarity 100.0%; Pred. No. 2,2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
|||||
DB 618 ADMSW 622

RESULT 5

T05822
hypothetical protein TSK18.170 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
C/Accession: T05822
R/Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Bevan, M.
Submitted to the Protein Sequence Database, April 1998
A/Reference number: Z15453

A/Accession: T05822
A/Molecule type: DNA
A/Residues: 1-275 <BEV>
A/Cross-references: EMBL:AL022580
A/Experimental source: cultivar Columbia; BAC clone TSK18
C/Genetics:
A/Map position: 4
A/Introns: 103/3; 141/3; 169/1; 206/3
A/Note: TSK18.170

Query Match 85.0%; Score 34; DB 2; Length 275;
Best Local Similarity 66.7%; Pred. No. 1,4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSMA 6
|||||
DB 57 SDMSWS 62

RESULT 6

C84922
probable protein kinase [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C/Accession: C84922
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talton, J.; Eues, D.; Niemann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.; Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: C84922
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-617 <STO>
A/Cross-references: GB:AE002093; NID:g4494908; PIDN:AA013705.1; GSPDB:GN00139
C/Genetics:
A/Genes: AT2g48010
A/Map position: 2

Query Match 85.0%; Score 34; DB 2; Length 617;
Best Local Similarity 66.7%; Pred. No. 3,1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSMA 6
|||||
DB 500 ADMAMS 505

RESULT 7

T43409
probable fatty-acid synthase (EC 2.3.1.85) alpha chain - fission yeast (Schizosaccharomyces pombe)
N/Alternate names: fatty acid synthetase alpha subunit
C/Species: Schizosaccharomyces pombe
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C/Accession: T43409
R/Saitoh, S.; Takahashi, K.; Nabeshima, K.; Yamashita, Y.; Nakaseko, Y.; Hatake, A.; Y. J. Cell Biol. 134, 949-961, 1996
A/Title: Aberrant mitosis in fission yeast mutants defective in fatty acid synthetase
A/Reference number: Z2493; MUID:96354912; PMID:8769419
A/Accession: T43409
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1842 <SAI>
A/Cross-references: EMBL:DB3412; NID:g1199959; PIDN:BA011913.1; PID:g1199960
C/Genetics:
A/Note: Isd1+
C/Superfamily: yeast fatty-acid synthase
C/Keywords: acyltransferase; coenzyme A

Query Match 85.0%; Score 34; DB 2; Length 1842;
Best Local Similarity 66.7%; Pred. No. 9,4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
: : : :
DB 400 SDMNWA 405

RESULT 8

T38781
fatty acid synthase, subunit alpha - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
A:Accession: T38781
R:Skellton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Submitted to the EMBL Data Library, August 1997
A:Reference number: 221751
A:Accession: T38781
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1842 <SKP>
A:Cross-references: EMBL:298762; PIDN:CA11481.1; GSPDB:GN00066; SPDB:SPAC4A8.11c
A:Experimental source: strain 972h-; cosmid c4A8
C:Genetics:
A:Gene: SPDB:SPAC4A8.11c
C:Superfamily: yeast fatty-acid synthase

Query Match 85.0%; Score 34; DB 2; Length 1842;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
: : : :
DB 400 SDMNWA 405

RESULT 9

S65785
mel-13a protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
A:Accession: S65785
R:Teru, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.
Biochim. Biophys. Acta 1305, 109-112, 1996
A>Title: Cloning and characterization of two transcripts generated from the mel-13 gene
A:Reference number: S65785; MUID:96180310; PMID:8597592
A:Accession: S65785
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <TET>
A:Cross-references: EMBL:U35309
C:Genetics:
A:Gene: mel-13
C:Superfamily: mouse mel-13a protein
C:Keywords: alternative splicing

Query Match 82.5%; Score 33; DB 2; Length 132;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
: : : :
DB 57 SDMSW 61

RESULT 10

B82531
conserved hypothetical protein XF2666 [imported] - Xylella fastidiosa (strain 9asc)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C:Accession: B82531
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences
Nature 406, 151-157, 2000
A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: B82531
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-198 <STM>

A:Cross-references: GB:AE004072; GB:AE003849; NID:99107884; PIDN:AAE85463.1; GSPDB:GN01
A:Experimental source: strain 9asc
A:Authors: A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Bijones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre,
as-Neto, E.; Docena, C.; El-Dorzy, H.; Facinani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Frega, J.S.; Franca, S.C.; Franco, M.C.; Frol
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laiz
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,
A:Authors: Martins, E.M.P.; Macukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiter, D.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa, V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva
M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2666
C:Superfamily: conserved hypothetical protein M1677

Query Match 82.5%; Score 33; DB 2; Length 198;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
: : : :
DB 135 DMNWA 139

RESULT 11

D64316
restriction modification enzyme subunit M1 homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2002
A:Accession: D64316
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
R.; Reich, C.T.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodok, A.
ron, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, P.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: D64316
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-220 <BDL>
A:Cross-references: GB:U67470; GB:L77117; NID:92826247; PIDN:AAE98113.1; PID:91592267;
C:Genetics:
A:Map position: REV127472-126810
A:Start codon: TTG
C:Superfamily: type I site-specific deoxyribonuclease chain hsdM (associate member)

Query Match 82.5%; Score 33; DB 2; Length 220;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
: : : :
DB 33 ADMNW 37

RESULT 12

S58353
Cdhb protein - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C:Accession: S58353

R:Ferguson, B.D.; Dutle, B.M.; Hein, W.; Hopkins, J.
submitted to the EMBL Data Library, July 1995
A:Description: The ovine CD1 gene family contains at least four CD1B homologues.
A:Reference number: S59353
A:Accession: S59353
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-232 <FER>
A:Cross-references: EMBL:X90567; NID:g945010; PIDN:CA62187.1; PID:g945011
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:115-180/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 33; DB 2; Length 232;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
|||:|
Db 156 ADMTW 160

RESULT 13
D90470
hypothetical protein cySH [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C/Accession: D90470
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.U.; Chan-
Jong, I.; Ueffing, A.C.; Kozera, C.U.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to Genbank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: D90470
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-239 <RUR>
A:Cross-references: GB:AE006641; NID:g13816282; PIDN:AAK43019.1; GSPDB:GN00155
C:Genetics:
A:Gene: cySH
C:Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase

Query Match 82.5%; Score 33; DB 2; Length 233;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
|||:|
Db 172 ADMTW 176

RESULT 14
D87152
conserved hypothetical protein ML1945 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C/Accession: D87152
R:Coile, S.T.; Egilmeter, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; He-
am, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A>Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: D87152
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <STO>
A:Cross-references: GB:AL450380; NID:g13093601; PIDN:CAC30900.1; GSPDB:GN00147
C:Genetics:
A:Gene: ML1945
C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1100

Query Match 82.5%; Score 33; DB 2; Length 257;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6
|||:|
Db 11 ATMSWA 16

RESULT 15
B75337
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C/Accession: B75337
R:White, O.; Eileen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S.; Shen, M.; Vamathavan, J.T.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; I
Science 286, 1571-1577, 1999
A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: B75337
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <WHI>
A:Cross-references: GB:AE002032; GB:AE000513; NID:g6459715; PIDN:AF11479.1; PID:g6459
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1923
A:Map position: 1

Query Match 82.5%; Score 33; DB 2; Length 276;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
|||:|
Db 84 ADMAW 88

Search completed: February 18, 2004, 14:38:39
Job time : 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-6
Perfect score: 40
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfileal.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	938	4	US-09-252-991A-23882
2	36	90.0	68	4	US-09-252-991A-18367
3	36	90.0	142	4	US-09-252-991A-31533
4	36	90.0	174	4	US-09-325-932A-163
5	36	90.0	225	4	US-09-325-932A-162
6	36	90.0	242	4	US-09-345-936B-3
7	36	90.0	378	4	US-09-325-932A-158
8	36	90.0	445	4	US-09-252-991A-22368
9	36	90.0	462	4	US-09-252-991A-21704
10	34	85.0	44	3	US-08-905-223-274
11	33	82.5	74	1	US-08-379-538-2
12	33	82.5	136	2	US-08-774-065-2
13	33	82.5	164	4	US-09-252-991A-23817
14	33	82.5	218	1	US-08-032-848C-10
15	33	82.5	218	1	US-08-438-870-10
16	33	82.5	218	2	US-08-169-948B-34
17	33	82.5	218	2	US-08-448-873-34
18	33	82.5	218	3	US-08-362-452D-34
19	33	82.5	218	3	US-09-216-295-1
20	33	82.5	218	4	US-08-507-362A-18
21	33	82.5	232	3	US-09-146-770-1
22	33	82.5	232	4	US-09-633-084-1
23	33	82.5	232	4	US-10-075-872-1
24	33	82.5	232	4	US-10-261-997-1
25	33	82.5	234	1	US-08-032-848C-9
26	33	82.5	234	1	US-08-438-870-9
27	33	82.5	234	3	US-09-146-770-3

28	33	82.5	234	3	US-09-146-770-4	Sequence 4, App11
29	33	82.5	234	3	US-09-216-295-3	Sequence 3, App11
30	33	82.5	234	3	US-09-216-295-4	Sequence 4, App11
31	33	82.5	234	4	US-09-633-084-3	Sequence 3, App11
32	33	82.5	234	4	US-09-633-084-4	Sequence 4, App11
33	33	82.5	234	4	US-10-075-872-3	Sequence 3, App11
34	33	82.5	234	4	US-10-075-872-4	Sequence 4, App11
35	33	82.5	234	4	US-10-261-997-3	Sequence 3, App11
36	33	82.5	234	4	US-10-261-997-4	Sequence 4, App11
37	33	82.5	239	3	US-09-216-295-15	Sequence 15, App1
38	33	82.5	316	4	US-09-252-991A-17312	Sequence 17312, A
39	33	82.5	467	4	US-08-140-104A-2	Sequence 2, App11
40	33	82.5	670	4	US-09-252-991A-22079	Sequence 22079, A
41	33	82.5	1205	2	US-07-908-245-2	Sequence 2, App11
42	33	82.5	1205	2	US-08-319-866-10	Sequence 10, App1
43	33	82.5	1205	3	US-09-123-708-6	Sequence 6, App11
44	33	82.5	1205	3	US-09-123-624-6	Sequence 6, App11
45	32	80.0	5	6	5217869-75	Patent No. 5217869

ALIGNMENTS

```
RESULT 1
US-09-252-991A-23882
; Sequence 23882, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23882
; LENGTH: 938
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23882

Query Match          92.5%; Score 37; DB 4; Length 938;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADMSWA 6
Db      581 ADMSWA 586

RESULT 2
US-09-252-991A-18367
; Sequence 18367, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18367
; LENGTH: 68
; TYPE: PRT
```

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18367

Query Match 90.0%; Score 36; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
DB 2 DMSWA 6

RESULT 3
US-09-252-991A-31533
Sequence 31533, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31533
LENGTH: 142
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31533

Query Match 90.0%; Score 36; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 94 ADMSW 98

RESULT 4
US-09-325-932A-163
Sequence 163, Application US/09325932A
Patent No. 6451604
GENERAL INFORMATION:
APPLICANT: Plim, Barry
APPLICANT: Laebam, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 163
LENGTH: 174
TYPE: PRT
ORGANISM: Bucalypus grandis
US-09-325-932A-163

Query Match 90.0%; Score 36; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 109 ADMSW 113

RESULT 5

US-09-325-932A-162
Sequence 162, Application US/09325932A
Patent No. 6451604

GENERAL INFORMATION:
APPLICANT: Plim, Barry
APPLICANT: Laebam, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 162
LENGTH: 225
TYPE: PRT
ORGANISM: Bucalypus grandis
US-09-325-932A-162

Query Match 90.0%; Score 36; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 100 ADMSW 104

RESULT 6
US-09-345-236B-3
Sequence 3, Application US/09345236B
Patent No. 6521454
GENERAL INFORMATION:
APPLICANT: Becnel, James J.
APPLICANT: Tuku, Fukuda
APPLICANT: Moser, Bettina
APPLICANT: Cockburn, Andrew
APPLICANT: White, Susan R.
APPLICANT: Under, Albert H.
TITLE OF INVENTION: No. 6521454e1 Baculoviruses, Insecticidal
FILE REFERENCE: 21042.0004
CURRENT APPLICATION NUMBER: US/09/345,236B
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 242
TYPE: PRT
ORGANISM: mosquito baculovirus
US-09-345-236B-3

Query Match 90.0%; Score 36; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
DB 80 DMSWA 84

RESULT 7
US-09-325-932A-158
Sequence 158, Application US/09325932A
Patent No. 6451604
GENERAL INFORMATION:
APPLICANT: Plim, Barry
APPLICANT: Laebam, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 158
LENGTH: 378
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-325-932A-158

Query Match 90.0%; Score 36; DB 4; Length 378;
Best Local Similarity: 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 128 ADMSW 132

RESULT 8
US-09-252-991A-22368
Sequence 22368, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22368

LENGTH: 445

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22368

Query Match 90.0%; Score 36; DB 4; Length 445;
Best Local Similarity: 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
DB 304 DMSWA 308

RESULT 9

US-09-252-991A-21704

Sequence 21704, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21704

LENGTH: 462

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21704

Query Match 90.0%; Score 36; DB 4; Length 462;
Best Local Similarity: 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
DB 169 DMSWA 173

RESULT 10

US-08-905-223-274

Sequence 274, Application US/08905223

Patent No. 6222029

GENERAL INFORMATION:

APPLICANT: Edwards, Jean-Baptiste D.

APPLICANT: Lacroix, Bruno

TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS

NUMBER OF SEQUENCES: 503

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 501 West Broadway

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-3505

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

OPERATING SYSTEM: Win95

SOFTWARE: Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/905,223

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Israel, Ned A.

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 274:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 amino acids

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

ORIGINAL SOURCE:

ORGANISM: Homo Sapiens

TISSUE TYPE: Brain

FEATURE:

NAME/KEY: sig_peptide

LOCATION: -26...-1

IDENTIFICATION METHOD: Von Heljne matrix

OTHER INFORMATION: score 9.6

US-08-905-223-274

RESULT 11

US-08-379-538-2

Sequence 2, Application US/08379538

Patent No. 5804554

GENERAL INFORMATION:

APPLICANT: Volkman, Robert A.

APPLICANT: Saccomano, Nicholas A.

APPLICANT: Nason II, Deane M.

Query Match 85.0%; Score 34; DB 3; Length 44;
Best Local Similarity: 83.3%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSW 6
DB 19 ADMSW 24

APPLICANT: Heck, Steven D.
APPLICANT: Ronau, Robert T.
TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES
TITLE OF INVENTION: FROM FILISTATA HIBERNALIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pfizer Inc
STREET: 235 East 42nd Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,538
FILING DATE: 3-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/887073
FILING DATE: 21-MAY-1992
APPLICATION NUMBER: PCT/US93/03921
FILING DATE: 30-APRIL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ziehlnekt, Bryan
REGISTRATION NUMBER: 34,462
REFERENCE/DOCKET NUMBER: PC8175A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 573-4585
TELEFAX: (212) 573-1939
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: No
ANTI-SENSE: No
ORIGINAL SOURCE:
ORGANISM: Filistata hibernalis
TISSUE TYPE: venom
US-08-379-538-2

Query Match 82.5%; Score 33; DB 1; Length 74;
Best Local Similarity 80.0%; Pred. No. 95;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
Db 52 DMSWS 56

RESULT 12
US-08-774-065-2
Sequence 2, Application US/08774065
Patent No. 5989899
GENERAL INFORMATION:
APPLICANT: Bower, Benjamin
APPLICANT: Clarkson, Kathleen
APPLICANT: Larens, Edmund
APPLICANT: Ward, Michael
TITLE OF INVENTION: NOVEL OVERSIZED CELLULASE COMPOSITIONS
TITLE OF INVENTION: FOR USE IN DETERGENT COMPOSITIONS AND
TITLE OF INVENTION: IN THE TREATMENT OF TEXTILES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENENCOR INTERNATIONAL
STREET: 925 PAGE MILL ROAD
CITY: PALO ALTO

STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,065
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Glasster, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-846-7620
TELEFAX: 415-845-6504
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-774-065-2

Query Match 82.5%; Score 33; DB 2; Length 136;
Best Local Similarity 66.7%; Pred. No. 1,76+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6
Db 62 ADMWS 67

RESULT 13
US-09-252-991A-23817
Sequence 23817, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23817
LENGTH: 164
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23817

Query Match 82.5%; Score 33; DB 4; Length 164;
Best Local Similarity 83.3%; Pred. No. 2,16+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6
Db 132 AGMSWA 137

RESULT 14
US-08-032-848C-10
Sequence 10, Application US/08032848C
Patent No. 5475101

GENERAL INFORMATION:
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Weiss, Geoffrey L.
APPLICANT: Larenaas, Edward
APPLICANT: Lorch, Jeffrey D.
TITLE OF INVENTION: Purification and Molecular Cloning of
TITLE OF INVENTION: EG III Cellulase
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/032,848C
FILING DATE: MAR 17 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Horn, Margaret A.
REGISTRATION NUMBER: 33,401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 742-7356
TELEFAX: 415 742-7217
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-032-848C-10

Query Match 82.5%; Score 33; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6
|||
|:
DB 46 ADWQMS 51

RESULT 15
US-08-438-870-10
Sequence 10, Application US/08438870
Patent No. 5753484
GENERAL INFORMATION:
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Weiss, Geoffrey L.
APPLICANT: Larenaas, Edward
APPLICANT: Lorch, Jeffrey D.
TITLE OF INVENTION: Purification and Molecular Cloning of EG
TITLE OF INVENTION: III Cellulase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,870
FILING DATE: May 10, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Christopher L. Stone
REGISTRATION NUMBER: 35,696
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 742-7555
TELEFAX: 415 742-7217
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-438-870-10

Query Match 82.5%; Score 33; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6
|||
|:
DB 46 ADWQMS 51

Search completed: February 18, 2004, 14:41:46
Job time : 7.06579 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-5
Perfect score: 40
Sequence: 1 LDMSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	362	1	DCUP_YEAST
2	36	90.0	598	1	MRJ5_APIME
3	36	90.0	745	1	IKKA_HUMAN
4	36	90.0	745	1	IKKA_MOUSE
5	36	90.0	756	1	IKKB_HUMAN
6	36	90.0	757	1	IKKB_MOUSE
7	36	90.0	757	1	IKKB_RAT
8	36	90.0	983	1	EPB3_CHICK
9	36	90.0	983	1	EPB3_HUMAN
10	36	90.0	983	1	EPB3_MOUSE
11	36	90.0	984	1	EPB3_RAT
12	34	85.0	411	1	FOLC_BUCAL
13	33	82.5	376	1	PGLR_BENGR
14	33	82.5	453	1	NRAM_IAMWL
15	33	82.5	454	1	NRAM_IAPUE
16	33	82.5	492	1	AERA_ABRTR
17	33	82.5	524	1	CP72_CATRO
18	33	82.5	656	1	VEKE_SALTI
19	33	82.5	840	1	VPH1_YEAST
20	33	82.5	1842	1	PAG2_SCHPO
21	32	80.0	86	1	YZXS_HUMAN
22	32	80.0	107	1	STEL_RHUVZ
23	32	80.0	191	1	GDIR_CAEEL
24	32	80.0	210	1	KTHV_SCHPO
25	32	80.0	272	1	CYL_RHORU
26	32	80.0	282	1	3MG2_ECOLI
27	32	80.0	295	1	X7G9_HUMAN
28	32	80.0	296	1	CYOA_BUCAL
29	32	80.0	307	1	QOX2_ACEAC
30	32	80.0	314	1	CYOA_PSEPU
31	32	80.0	360	1	MNT2_CAEEL
32	32	80.0	375	1	H1S7_XANCP
33	32	80.0	418	1	HLT_VTBPA

34	32	80.0	470	1	NRAM_IADBU	Q07570 Influenza a
35	32	80.0	470	1	NRAM_IADCH	Q07571 Influenza a
36	32	80.0	470	1	NRAM_IADH2	Q07572 Influenza a
37	32	80.0	470	1	NRAM_IADW2	Q07573 Influenza a
38	32	80.0	470	1	NRAM_IADU3	Q07574 Influenza a
39	32	80.0	470	1	NRAM_IAGEN	Q07575 Influenza a
40	32	80.0	470	1	NRAM_IAGHD	Q07577 Influenza a
41	32	80.0	470	1	NRAM_IAMHI	Q07578 Influenza a
42	32	80.0	470	1	NRAM_IAMAE	Q07583 Influenza a
43	32	80.0	470	1	NRAM_IATKL	Q07585 Influenza a
44	32	80.0	479	1	BGLA_BACSU	P42973 bacillus su
45	32	80.0	500	1	PROP_ECOLI	P30848 escherichia

ALIGNMENTS

RESULT 1
ID DCUP_YEAST STANDARD, PRT, 362 AA.
AC P32347;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UDP).
GN HEM12 OR HEM6 OR POP3 OR YD9609.03.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92249304; PubMed=1576986;
RA Garey J.R., Labbe-Bois R., Chelstowska A., Rycka J., Harrison L.,
RA Kushner J., Labbe P.;
RT "Uroporphyrinogen decarboxylase in Saccharomyces cerevisiae, HEM12
RT gene sequence and evidence for two conserved glycines essential for
RT enzymatic activity.";
RL Eur. J. Biochem. 205:1011-1016 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93348774; PubMed=8346678;
RA Dittmer C., Larocque R., Keng T.;
RT "Molecular analysis of HEM6 (HEM12) in Saccharomyces cerevisiae, the
RT gene for uroporphyrinogen decarboxylase.";
RL Yeast 9:613-623 (1993).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=8286C / AB972;
RA Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP MEDLINE=93111946; PubMed=1471989;
RA Chelstowska A., Zoadek T., Garey J.R., Kushner J., Rycka J.,
RA Labbe-Bois R.;
RT "Identification of amino acid changes affecting yeast
RT uroporphyrinogen decarboxylase activity by sequence analysis of hem12
RT mutant alleles.";
RL Biochem. J. 288:753-757 (1992).
RN [5]
RP BIOCHEMICAL ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4
CO(2).
CC -1- PATHWAY: Porphyrin and heme biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.ebi.ac.uk/announce/>
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CC EMBL: X63721; CAA45253.1; -
DR EMBL: Z19089; CAA79514.1; -
DR EMBL: Z49209; CAA89078.1; -
DR PIR: S23471; S23471.
DR HSSP: P06133; IURO.
DR SGD: S0002454; HEM12.
DR GO: GO:0004853; F:uroporphyrinogen decarboxylase activity; IMP.
DR GO: GO:0006783; P:heme biosynthesis; IMP.
DR InterPro: IPR006361; Heme.
DR InterPro: IPR000257; Uro_decboxyls.
DR Pfam: PF01208; URO-D; 1.
DR Prodom: PD003225; Uro_decboxyls; 1.
DR Trigram: TIGR01464; Heme; 1.
DR PROSITE: PS00906; UROD_1; 1.
DR PROSITE: PS00907; UROD_2; 1.
DR Lyase: Decarboxylase; Forphyrin biosynthesis; Heme biosynthesis.
FT VARIANT 59 S -> F (IN HEM12-14).
FT VARIANT 62 S -> I (IN HEM12-14).
FT VARIANT 107 L -> S (IN HEM12-3 AND HEM12-13).
FT VARIANT 215 S -> N (IN HEM12-2 AND HEM12-11).
FT MUTAGEN 33 G->D: INACTIVATION.
FT MUTAGEN 300 G->D: INACTIVATION.
SQ SEQUENCE 362 AA; 41349 MW; E9CB3A48E62BC277 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMSW 5
Db 279 LDMSW 283

RESULT 2
MRJ5 APIME STANDARD; PRT; 598 AA.
ID MRJ5 APIME
AC 09743;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein).
GN MRJP5.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apoidea; Apis.
OC NCBI_TaxId=7460;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=99373663; PubMed=10441680;
RA Albert S., Bhattacharya D., Kluding J., Schmitzova J., Slomuch J.;
RT "The family of major royal jelly proteins and its evolution.";
J. Mol. Evol. 49:290-297(1999).
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE
CC LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG
CC LARVA AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE
CC HONEYBEE QUEEN.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: HYPOPHARYNGEAL GLANDS OF NURSE HONEY BEES.
CC -1- DEVELOPMENTAL STAGE: PRODUCED BY THE CEPHALIC GLANDULAR SYSTEM OF
CC THE NURSE HONEY BEE.
CC -1- SIMILARITY: BELONGS TO THE MAJOR ROYAL JELLY PROTEIN FAMILY.
CC -----
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CC or send an email to license@ebi.ac.uk).

CC EMBL: AF048442; AAD01205.1; -
DR InterPro: IPR003534; RoyalJelly.
DR Pfam: PF03022; MRJP_2.
DR PRINTS: PR01366; ROYALJELLY.
KW SIGNAL; Repeat; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 598 AA; 70236 MW; 2C603C7B7ACD63 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DMSWA 6
Db 113 DMSWA 117

RESULT 3
IKKA HUMAN STANDARD; PRT; 745 AA.
ID IKKA HUMAN
AC 01511; 014666; Q13132; Q92467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase subunit (IC 2.7.1.1-)
DE (I kappa-B kinase alpha) (IKBA) (IKK-alpha) (IKKAPB kinase)
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
GN CHUK OR IKKA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RC TISSUE=T-cell;
RX MEDLINE=97386461; PubMed=9244310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Roche M.;
RT Identification and characterization of an IkappaB kinase.";
Cell 90:373-383(1997).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97394468; PubMed=9252186;
RA Didonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
RT "A cytokine-responsive IkappaB kinase that activates the transcription
RT factor NF-kappaB.";
Nature 388:548-554(1997).
RN [3]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
RP SER-176.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cyclo-oxygenase-activated IkappaB kinases essential for
RT NF-kappaB activation.";
Science 278:860-866(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
Gene 222:31-40(1998).
RN [5]
RP SEQUENCE OF 32-745 FROM N.A.

RC TISSUE-cervical carcinoma;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connelly M.A., Marcu K.B.;
 RT "CHK1, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain";
 RT Cell. Biol. Res. 41:537-549 (1995).
 RN [6]
 RP PHOSPHORYLATION BY MAPK14/NIK, AND MUTAGENESIS OF SER-176, THR-179
 RP AND SER-180.
 RX MEDLINE=98188283; PubMed=9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
 RT Ser-176";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797 (1998).
 RN [7]
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RX MEDLINE=99413720; PubMed=10485710;
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
 RA Donner D.B.;
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt
 RT serine-threonine kinase";
 RT Nature 401:82-85 (1999).
 RN [8]
 RP IKKA-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delnase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation";
 RT Science 284:309-313 (1999).
 RN [9]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Iln A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase";
 RT Mol. Cell. Biol. 18:7336-7343 (1998).
 RN [10]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection";
 RT Am. J. Physiol. 278:C451-C462 (2000).
 RN [11]
 RP SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKKB AND IKKG.
 RX MEDLINE=21968797; PubMed=11971985;
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 RA O'Malley B.W.;
 RT "Regulation of SRC-3 (pCTP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
 RT activity by I kappa B kinase";
 RT Mol. Cell. Biol. 22:3549-3561 (2002).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-GAMMA/MEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAPK14/NIK, MEK1, IKAP and IKB-alpha-P65-550
 CC complex. A weak interaction with IRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- PTM: Phosphorylated by MAPK14/NIK, AKT and to a lesser extent by
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
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 CC or send an email to license@sib.ch).
 CC -----
 DR EMBL, AF012890; AAC51662.1; -
 DR EMBL, AF009225; AAC51671.1; -
 DR EMBL, AF080157; AAD08996.1; -
 DR EMBL, U22512; AAC50713.1; -
 DR HSSP; Q63450; 1A06.
 DR Genew; HGNC:1974; CHUK.
 DR MIM; 600664; -
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0008384; P:IkappaB kinase activity; TAS.
 DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
 DR GO; GO:0007252; P:I-kappaB phosphorylation; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR Prodom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC_1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding,
 DR Phosphorylation.
 FT DOMAIN 15 302
 FT DOMAIN 455 476
 FT NP_BIND 21 29
 FT BINDING 44 44
 FT ACT_SITE 23 23
 FT MOD_RES 176 176
 FT MOD_RES 23 23
 FT MUTAGEN 44 44
 FT MUTAGEN 44 44
 FT MUTAGEN 176 176
 FT MUTAGEN 176 176
 FT MUTAGEN 179 179
 FT MUTAGEN 180 180
 FT CONFLICT 543 543
 FT CONFLICT 604 604
 FT CONFLICT 679 680
 FT CONFLICT 684 684
 FT CONFLICT 686 687
 FT SEQUENCE 745 AA; 84653 MM; 79A0B59BC98A56C2 C6C64;
 Query Match 90.0%; Score 36; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDMSW 5
 Db 738 LDMSW 742
 RESULT 4
 ID IKKA_MOUSE STANDARD; PRT; 745 AA.
 AC 060680; G9D2X3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
 DE (I kappa-B kinase alpha) (IKK-A) (Ikappab kinase)
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous

DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NF-kappaB).
 GN CHUK OR IKK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10099;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/c;
 RX MEDLINE=9604444; PubMed=7558004;
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 RT chromosome 10 and mouse chromosome 19.";
 RL Genomics 27:348-351(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/c;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connolly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi Y., Fukuda S.,
 RA Aizawa T., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito K., Okazaki Y., Gotohori T., Bono H., Kanakawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Knehl P., Lewis S., Matsuo Y., Nakai K., Pesole G., Quackenbush J.,
 RA Sakai L.M., Stauber P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sekai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfield D., Boujars N., Carninci P., de Bonaldo M.P.,
 RA Brownstein M.J., But C., Fletcher C., Fujita M., Gaitanaris M.,
 RA Guelincich S., Hill D., Hofmann M., Hume D.A., Kamiiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Norasaka H., Saito K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Konturki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=20198447; PubMed=10733566;
 RA McKensie P.R., Connolly M.A., Balzarano D., Mueller J.R.,
 RA Gelezunas R., Marcu K.B.;
 RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
 RT IKKbeta have different activation requirements.";
 RL Mol. Cell. Biol. 20:2635-2649(2000).
 RN [5]
 RP PHOSPHORYLATION BY MAPK14/NIK.
 RX MEDLINE=96188236; PubMed=5520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Minara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RP IKK-ALPHA BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delnase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [7]

RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [8]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAPK14/NIK, MEK1, IKAP and IKK-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKK, IKKG and CREBBP (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC IsoId=Q60680-1; Sequence=Displayed;
 CC Name=2; Synonyms=Delta LH;
 CC IsoId=Q60680-2; Sequence=VSP_004866; VSP_004867;
 CC Name=3; Synonyms=Delta H;
 CC IsoId=Q60680-3; Sequence=VSP_004868; VSP_004869;
 CC -1- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
 CC 3 are expressed predominantly in brain and T-lymphocytes.
 CC -1- DEVELOPMENTAL STAGES: Maximally expressed at E7 day followed by
 CC E11, E15 and E17 days. In the limb development, its expression
 CC predominates in the limb buds at E12.5 day.
 CC -1- PTM: Phosphorylated by MAPK14/NIK, AKT and to a lesser extent by
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: U12473; AAC52589.1; -
 CC EMBL: AK018671; BAB31335.1; -
 CC DR ETR; 149101; 149101.
 CC DR HSSP; G63450; 1A06.
 CC DR MGD; MG1:99484; Chuk.
 CC DR InterPro; IPR000719; Prot. Kinase.
 CC DR InterPro; IPR002290; Ser Thr kinase.
 CC DR InterPro; IPR001245; Tyr_kinase.
 CC DR Pfam; PF00069; pkinase; 1.
 CC DR PRINTS; PR00109; TYRKINASE.
 CC DR PRODOM; PD000001; Prot. Kinase; 1.
 CC DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 CC DR PROSITE; PS00011; PROTEIN KINASE DOW; 1.
 CC KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 CC Phosphorylation; Alternative splicing.
 CC FT DOMAIN 15 300
 CC FT DOMAIN 455 476
 CC FT DOMAIN 738 743
 CC FT NP_BIND 21 29
 CC ATP (BY SIMILARITY).

FT	BINDING	44	44		ATP(BY SIMILARITY)..
FT	ACT_SITE	144	144		BY SIMILARITY.
FT	MOD_RES	23	23		PHOSPHORYLATION (BY PRG/AKT1)
FT	MOD_RES	23	23		(BY SIMILARITY).
FT	MOD_RES	176	176		PHOSPHORYLATION (BY MAP3K14)
FT	VASPPLOC	452	471		(BY SIMILARITY).
FT	VASPPLOC				MUSLRVYANILRKMTKLIS -> IFRKNVKSMENGRKGH
FT	VASPPLOC	472	745		SIP (In isoform 2).
FT	VASPPLOC				/FTID=VSP_004866.
FT	VASPPLOC	577	584		Missing (In isoform 2).
FT	VASPPLOC				/FTID=VSP_004867.
FT	VASPPLOC	585	745		DLYSDST -> GKTLQSGY (in isoform 3).
FT	VASPPLOC				/FTID=VSP_004868.
FT	VASPPLOC	585	745		/FTID=VSP_004869.
FT	VASPPLOC				Missing (In isoform 3).
FT	CONFLICT	236	236		K -> E (IN REF. 3).
FT	CONFLICT	400	400		S -> Y (IN REF. 3).
FT	CONFLICT	400	400		S -> Y (IN REF. 3).
SO	SEQUENCE	745 AA;	84728 MW;		3PERF582AERF92233 CRC64;

Query Match Best Local Similarity 90.0%; Score 36; DB 1; Length 745;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Oy      1 LDMSW 5
          |||||
Db       738 LDMSW 742
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RESULT 5

ID IKKB HUMAN STANDARD; PRT; 756 AA.

IKKB_HUMAN OI4920;O75327;
16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (IC 2.7.1.-)
DE 2) (IKKAP-B kinase beta) (IKK-beta) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1NS).
GN IKKB or IKKB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=96008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.,
RT "IKK-1 and IKK-2: cytokine-activated Ikappab kinases essential for
RT NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX MEDLINE=96008814; PubMed=9346485;
RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
RT "Ikappab kinase-beta: NF-kappaB activation and complex formation with
RT Ikappab kinase-alpha and NIK.";
RL Science 278:866-869(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-J.;
RT "Ikappab kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40(1998).
RN [4]
RP SEQUENCE FROM N.A., AND GENE MAPPING.
RX MEDLINE=98438415; PubMed=9763654;
RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
RT "Assignment of Ikappab kinase beta (IKKB) to human chromosome band
RT p12-p11 by in situ hybridization."

Cytogenet. Cell Genet. 82:32-33(1998).

[5]

SEQUENCE OF 1-256 FROM N.A.

RC TISSUE=Lung;

RX MEDLINE=22386257; PubMed=12477932;

RA Strausberg R.D., Collins F.S., Wagner L.H., Shenman C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Helel F.,

RA Diachenko L., Marziani K., Farmer A.A., Rubin G.M., Hong L.,

RA Stepien M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toishivski S., Garinetti P., Prange C.,

RA Raza S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Roark S.A., McGowan P.O., McKernan K.U., Malek J.A., Gundaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holys S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butcherfield J.S.N., Krzywinski M.T., Skaleja S., Smallie D.E.,

RA Scherker A., Schein J.B., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RL human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).

[6]

IKK PHOSPHORYLATION:

RX MEDLINE=99036238; PubMed=9819420;

RA Nemoto S., Didonato J.A., Lin A.;

RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein

RL kinase kinase kinase 1 and NF-kappaB-inducing kinase.";

Mol. Cell. Biol. 18:7336-7343(1998).

[7]

REVIEW.

RX MEDLINE=20178139; PubMed=10712233;

RA Jobin C., Sartor R.B.;

RT "The I kappa B/NF-kappa B system: a key determinant of mucosal

RL inflammation and protection.";

Am. J. Physiol. 278:C451-C462(2000).

[8]

IDENTIFICATION IN A COMPLEX WITH CREBBP, NCOA2, NCOA3, IKKA AND IKKBG.

RX MEDLINE=21968797; PubMed=11971985;

RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,

RA O'Malley B.W.;

RT "Regulation of SRC-3 (GC1F/ACTR/AIB-1/RAC-3/TRAM-1) coactivator

RL activity by I kappa B kinase.";

Mol. Cell. Biol. 22:3549-3561(2002).

-1 FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to

CC the dissociation of the inhibitor/NF-kappa-B complex and

CC ultimately the degradation of the inhibitor. Also phosphorylates

CC NCOA3 (By similarity).;

CC SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but

CC also as a homodimer. Directly interacts with IKK-gamma/MEMO.

CC Heterodimers form the active complex. The tripartite complex can

CC also bind to MEKK1, MAP3K14/NIK, IRAK and IKK-alpha-p65-P50

CC complex. Phosphorylated IKK-alpha is further released from the

CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG

CC and CREBBP.

-1 SUBCELLULAR LOCATION: Cytoplasmic.

CC -1 TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal

CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and

CC periphereal blood.

CC -1 PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.

CC weakly autophosphorylated.

CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC IRAKAPB KINASE SUBFAMILY.

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or send an email to license@lsb-sib.ch.

CC -----
 DR EMBL; AF029684; AAC51860.1; -
 DR EMBL; AF080158; MAD08997.1; -
 DR EMBL; AF031416; AAC64675.1; -
 DR EMBL; BC006231; AAH06231.1; -
 DR HSSP; Q63450; 1A06.
 DR Genew; HGNC:5960; IKKB.
 DR MIM; 603258; -
 DR GO; GO:0005737; C:cytoplasm; NAS.
 DR GO; GO:0005524; F:ATP binding activity; NAS.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
 DR GO; GO:0016563; F:transcriptional activator activity; NAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
 DR InterPro; IPR000715; Prot_Kinase.
 DR InterPro; IPR002290; Ser_Thr_Kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00240; Ubiquitin; 1.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT SITE 145 145 BY SIMILARITY.
 FT MOD RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD RES 177 177 PHOSPHORYLATION.
 FT MOD RES 181 181 PHOSPHORYLATION.
 FT MURGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO
 FT EFFECT ON BINDING OF NIK.
 FT MURGEN 177 177 S->A: DECREASE OF ACTIVITY.
 FT MURGEN 177 177 S->E: FULL ACTIVATION.
 FT MURGEN 181 181 S->A: DECREASE OF ACTIVITY.
 FT MURGEN 181 181 S->E: FULL ACTIVATION.
 FT CONFLICT 231 255 WSKRQSEVDIVSEDLNATYK -> CYRMPGTVVHS
 FT CNPSTLGRGRMI (IN REF. 5).
 FT CONFLICT 425 425 Q -> H (IN REF. 1).
 FT SEQUENCE 756 AA; 86563 MW; P9CDBP671ABE14E CRC4;
 Query Match 90.0%; Score 36; DB 1; Length 756;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSW 5
 DB 737 LDMSW 741
 RESULT 6
 ID IKKB MOUSE STANDARD; PRT; 757 AA.
 AC 088351, Q8RI16; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase subunit (BC 2.7.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1B).
 GN IKKB OR IKK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKK1.
 RC STRAIN=C57BL/6; TISSUE=Spleen;
 RX MEDLINE=96186238; PubMed=9520401;
 RA Nakano H., Shindo W., Sakon S., Nishinaka S., Mihara M., Yagita H.,

RA Okumura K.;
 RT "Differential regulation of Ikkapab kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
 RT constitutively phosphorylates serine residues of Ikb.";
 RL submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE=99455228; PubMed=10523828;
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates Ikkapab kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=9908238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of Ikkapab kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [5]
 RP REVIEW.
 RA MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P65-P50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
 CC and CREBP (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
 CC -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
 CC the mouse embryo, at E9.5 day its expression begins to be
 CC localized to the brain, neural ganglia, neural tube, and in liver
 CC at E12.5 day. At E15.5 day, the expression is further restricted
 CC to specific tissues of the embryo.
 CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; AF026524; AAC23557.1; -
 DR EMBL; AF088910; AAD52095.1; -
 DR HSSP; Q63450; 1A06.
 DR MGD; MGI:1338071; Ikdkb.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR002290; Ser_Thr_Kinase.
 DR InterPro; IPR001245; Tyr_Kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.

DR Prodom: PD000001; Prot kinase: 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP, FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW transferase; Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 K -> B (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 757 TLDMSW/LQMEDERCSLEQACD -> VTA (IN REF. 2).
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSW 5
 Db 737 LDMSW 741
 RESULT 7
 IKKB RAT STANDARD; PRT; 757 AA.
 AC 09078; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 2) (IKK) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1K2).
 GN IKKB OR IKKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Rayld K.;
 RT "IKK beta in megakaryocyte differentiation."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RA MEDLINE=9038238; PubMed=9819420;
 RX Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of I-kappaB kinases by mitogen-activated protein
 kinase kinase kinase 1 and NF-kappaB-inducing kinase."
 RL Mol. Cell. Biol. 18:7336-7343 (1998).
 RN [3]
 RP REVIEW.
 RA MEDLINE=20178139; PubMed=10712233;
 RX Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 inflammation and protection."
 RL Am. J. Physiol. 278:C451-C462 (2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 the dissociation of the inhibitor/NF-kappa-B complex and
 ultimately the degradation of the inhibitor. Also phosphorylates
 NCOA3.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but

CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-p65-p50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKRA, IKKGB
 CC and CREBBP (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
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 CC or send an email to license@itsb-sib.ch).
 CC -----
 CC EMBL; AF115282; AAF21978.1; -.
 CC HSSP; O63450; 1A06.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR Prodom; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP, FALSE_NEG.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW transferase; Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 757 AA; 8666 MW; 3AF6A67DF91F9C CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSW 5
 Db 737 LDMSW 741
 RESULT 8
 EPB3_CHICK STANDARD; PRT; 983 AA.
 AC P29318; 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (BC 2.7.1.112) (Tyrosine-protein
 DE EphA3 receptor ETK) (CEK4).
 DE EPB3 OR ETK OR CEK4.
 GN EPB3 OR ETK OR CEK4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92031278; PubMed=1657122;
 RX Sajjadi F.G., Pasquale B.B., Subramani S.;
 RT "Identification of a new eph-related receptor tyrosine kinase gene

RT from mouse and chicken that is developmentally regulated and encodes
 RT at least two forms of the receptor."
 RL New Biol. 3:769-778(1991).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING BRAIN AND
 CC EMBRYONIC TISSUES. IN ADULT, THE GREATEST LEVELS OF EXPRESSION
 CC OCCURS IN THE BRAIN. IT IS EXPRESSED IN A GRADED MANNER ACROSS THE
 CC RETINA WITH THE HIGHEST EXPRESSION AT ITS TEMPORAL POLE.
 CC DETECTABLE IN ALL OTHER ADULT TISSUES EXAMINED, EXCEPT THE LIVER.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domain.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, M68514, AAA48666.1, -.
 CC PIR, B45583, B45583.
 CC HSPB, P00523, 2PTK.
 CC InterPro: IPR006209, BGF_1like.
 CC InterPro: IPR001090, Ephrin_receptor.
 CC InterPro: IPR003961, FN_III.
 CC InterPro: IPR003962, FNIII_subd.
 CC InterPro: IPR000719, Prot_Kinase.
 CC InterPro: IPR001660, SAM.
 CC InterPro: IPR001245, Tyr_Kinase.
 CC InterPro: IPR001426, YKase_receptor.
 CC Pfam: PF01404, Eph_1bd, 1.
 CC Pfam: PF00041, FN3, 2.
 CC Pfam: PF00069, Kinase, 1.
 CC Pfam: PF00536, SAM, 1.
 CC PRINTS: PRO0014, FNTYPEIII.
 CC PRINTS: PRO0109, TYRKINASE.
 CC PRODOM: PD001495, Ephrin_receptor, 1.
 CC PRODOM: PD000001, Prot_Kinase, 1.
 CC SMART: SM00615, Eph_1bd, 1.
 CC SMART: SM00060, FN3, 2.
 CC SMART: SM00454, SAM, 1.
 CC SMART: SM00219, Tyrc, 1.
 CC PROSITE: PS01186, BGF_2, UNKNOWN 1.
 CC PROSITE: PS01017, PROTEIN KINASE_ATP, 1.
 CC PROSITE: PS05011, PROTEIN KINASE_DOM, 1.
 CC PROSITE: PS00109, PROTEIN KINASE_TYR, 1.
 CC PROSITE: PS00790, RECEPTOR_TYR_KIN_V_1, 1.
 CC PROSITE: PS00791, RECEPTOR_TYR_KIN_V_2, 1.
 CC PROSITE: PS01051, SAM_DOMAIN, 1.
 CC Transferrase, Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 CC SIGNAL 1 19
 CC CHAIN 20 983
 CC DOMAIN 20 540
 CC TRANSFERRASE 541 564
 CC DOMAIN 565 583
 CC DOMAIN 188 321
 CC DOMAIN 322 431
 CC DOMAIN 432 529
 CC DOMAIN 621 882
 CC DOMAIN 911 975
 CC SITE 981 983
 CC NP_BIND 627 635
 CC BINDING 653 653
 CC ACT_SITE 746 746
 CC MOD_RES 596 596
 CC PHOSPHORYLATION (AUTO-) (POTENTIAL).

PT MOD_RES 602 602 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 PT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 492 492 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 983 AA, 109910 MW, E8895F0BDF77651B CRC64,
 Query Match 90.0%; Score 36; DA 1; Length 983;
 Best local similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSW 5
 DB 342 LDMSW 346
 RESULT 9
 ID EPB3_HUMAN STANDARD; PRT; 983 AA.
 AC P29330; Q9H2V3; Q9H2V4;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (BC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor ETK1) (HEK) (HEK4).
 GN EPHA3 OR ETK1 OR ETK OR HEK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=92179233; PubMed=1311845;
 RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.,
 RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine
 RT kinase expressed by human lymphoid tumor cell lines."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Melanoma;
 RA Chari R., Hames G., Stroobant V., Maille B., Texier C., Mach B.,
 RA Boon T., Coulle P.G.,
 RT "Identification of a tumor specific shared antigen derived from an
 RT Eph-receptor and presented to CD4 T cells on HLA class II
 RT molecules."
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBD databases.
 RN [3]
 RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
 RX MEDLINE=92147681; PubMed=1737782;
 RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wicks A.,
 RA Welch K., Loudovaris M., Rockman S., Bumanns I.,
 RT "Isolation and characterization of a novel receptor-type protein
 RT tyrosine kinase (hek) from a human pre-B cell line."
 RL J. Biol. Chem. 267:3262-3267(1992).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID
 CC FUNCTION.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1);
 CC SECRETED (ISOFORM 2).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P29320-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P29320-2; Sequence=VSP_002995, VSP_002996;
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVEL IN PLACENTA.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domain.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN

DR InterPro; IPR006209; BGF_like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR001426; YKase_receptorV.
 DR Pfam; PF01404; EPH_1bd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_1bd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS50105; SAM_DOMAIN; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Alternative splicing.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 983 EPHRIN TYPE-A RECEPTOR 3.
 FT DOMAIN 21 540 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 541 564 POTENTIAL.
 FT DOMAIN 565 983 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 188 321 CYS-RICH.
 FT DOMAIN 322 431 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 432 529 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 621 882 PROTEIN KINASE.
 FT DOMAIN 911 975 SAM.
 FT SITE 981 983 PDZ-BINDING MOTIF (POTENTIAL).
 FT NP_BIND 627 635 ATP (BY SIMILARITY).
 FT BINDING 653 653 ATP (BY SIMILARITY).
 FT ACT_SITE 746 746 BY SIMILARITY.
 FT MOD_RES 596 596 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 602 602 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 729 729 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 492 492 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSELIC 530 983 Missing (in isoform short).
 FT SEQUENCE 983 AA; 109955 MW; BE44A655D8107A2 CRC64;
 /FTIDA_VSP_002997.
 Query Match 90.0%; Score 36; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR kinase receptor REK4 (TYRO-4).
 GN EPHA3 OR REK4 OR TYRO4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=98120505; PubMed=9458884;
 RA Li Y.Y., McTernan C.F., Feldman A.M.;
 RT "IL-1 beta alters the expression of the receptor tyrosine kinase gene
 r-EphA3 in neonatal rat cardiomyocytes";
 RL Am. J. Physiol. 274:H331-H341(1998).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN THE HEART, BRAIN AND LUNG.
 CC -1- INDUCTION: DOWN-REGULATED BY IL1-BETA IN NEONATAL CARDIAC
 CC MYOCYTES.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC
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 CC
 CC EMBL; U69278; AAC06273.1; -.
 CC HSSP; P00523; 2PTK.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR001426; YKase_receptorV.
 DR Pfam; PF01404; EPH_1bd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; Kinase; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_1bd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS50105; SAM_DOMAIN; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Alternative splicing.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 984 EPHRIN TYPE-A RECEPTOR 3.
 FT DOMAIN 21 541 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 542 565 POTENTIAL.
 FT DOMAIN 566 984 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 189 322 CYS-RICH.
 FT DOMAIN 328 431 FIBRONECTIN TYPE-III 1.

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FT DOMAIN 436 528 FIBRONECTIN TYPE-III 2.
FT PROTEIN KINASE.
FT DOMAIN 622 883 SAM.
FT SITE 912 976 PD2-BINDING MOTIF (POTENTIAL).
FT NP_BIND 984 984 ATP (BY SIMILARITY).
FT BINDING 628 636 ATP (BY SIMILARITY).
FT ACT_SITE 654 654 BY SIMILARITY.
FT MOD_RES 597 597 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 603 603 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 780 780 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 493 493 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 984 AA; 110227 MW; F170C49312F7A0AB CRC64;

Query Match 90.0%; Score 36; DB 1; Length 984;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
Db .343 LDMSW 347

RESULT 12
POLC_BUCAI STANDARD; PRT; 411 AA.
AC P57255;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE POLC bifunctional protein [includes: Poly(1)polyglutamate synthase
DE (EC 6.3.2.17) (Poly(1)poly-gamma-glutamate synthetase) (PPGS);
DE dihydrofolate synthase (EC 6.3.2.12)].
GN POLC OR Bu167
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. ABS."
RL Nature 407:81-86(2000).
CC -1- FUNCTION: CONVERSION OF FOLATES TO POLYGLUTAMATE DERIVATIVES.
CC -1- CATALYTIC ACTIVITY: ATP + (tetrahydrofolyl-[Glu]) (N) + L-glutamate
CC = ADP + phosphate + {tetrahydrofolyl-[Glu]} (N+1).
CC -1- CATALYTIC ACTIVITY: ATP + dihydropterate + L-glutamate = ADP +
CC phosphate + dihydrofolate.
CC -1- PATHWAY: BACTERIA REQUIRE FOLATE FOR THE BIOSYNTHESIS OF GLYCINE,
CC METHIONINE, FORMYL-MET-TRNA, THYMIDYLATES, PURINES, AND
CC PANTOTHENATE.
CC -1- SIMILARITY: Belongs to the folylpolyglutamate synthase family.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF001118; BAB12885.1; -.
CC DR HSSP: P15925; IFGS.
CC DR InterPro: IPR001645; Fpolylgl_synthase.
CC DR InterPro: IPR000713; Mur_ligase.
CC Pfam: PF01225; Mur_ligase; 1.

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DR TIGRPM6; TIGR01499; folC; 1.
DR PROSITE; PS01011; FOLYLPOLYGLU SYNT_1; 1.
DR PROSITE; PS01012; FOLYLPOLYGLU SYNT_2; FALSE NEG.
KM Multifunctional enzyme; Ligase; One-carbon metabolism; ATP-binding;
KW Folate biosynthesis; Complete proteome.
FT NP_BIND 50 56 ATP (BY SIMILARITY).
SQ SEQUENCE 411 AA; 46970 MW; 5DDC2DC653935A CRC64;

Query Match 85.0%; Score 34; DB 1; Length 411;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
Db 219 LDMSW 223

RESULT 13
PGLR_PENGR STANDARD; PRT; 376 AA.
AC O93883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).
GN PGG1.
OS Penicillium griseoformeum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocommataceae; mitosporic Trichocommataceae; Penicillium.
OX NCBI_TaxID=64562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CCT 6421;
RA Ribon A.B., Coelho J.L.C., Barros E.G., Araujo E.F.;
RT "Cloning and characterization of a gene encoding the
RT endopolygalacturonase of Penicillium griseoformeum";
RT Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
CC (POLYGLACTURONASES).
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF085238; AAC83692.1; -.
CC DR InterPro: IPR000743; GLYCO_hydro_28.
CC DR InterPro: IPR006626; Pbh1.
CC DR Pfam: PF00295; GLYCO_hydro_28; 1.
CC DR SMART; SM00710; Pbh1; 5.
CC DR PROSITE; PS00502; POLYGLACTURONASE; 1.
CC DR HYDROLASE; Glycosidase; Cell wall, Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 376 POLYGLACTURONASE.
SQ SEQUENCE 376 AA; 38068 MW; 1EDB1C56D56928 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 376;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
Db 350 DMSWA 354

RESULT 14
NRAM_IAMWL STANDARD; PRT; 453 AA.
ID_NRAM_IAMWL

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AC P03470;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Wilson-Smith/33).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxId=11487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82192605; PubMed=7077751;
RA Hilt A.L., Nayak D.P.;
RT "Complete nucleotide sequence of the neuraminidase gene of human
RT Influenza virus A/WSN/33."
RT J. Virol. 41:730-734 (1982).
RL
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitates
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J02177; AAA43397.1; ALT_SEQ.
DR HSSP: P03472; 20WC.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur. 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT DOMAIN 36 75 ANCHOR.
FT TRANSMEM 7 35 HYPERVARIABLE STALK REGION.
FT ACT_SITE 259 259 HEAD OF NEURAMINIDASE.
FT ACT_SITE 261 261 PROBABLE.
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 453 AA; 49623 MW; 7DC56A4416A47B8 CRC64;
Query Match 82.5%; Score 33; DB 1; Length 453;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 LDMSW 5
DB 437 VDMSW 441

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OS Influenza A virus (strain A/Puerto Rico/8/34).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxId=11455;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81148841; PubMed=7010182;
RA Fields S., Winter G., Brownlee G.G.;
RT "Structure of the neuraminidase gene in human influenza virus
RT A/PR/8/34."
RT Nature 290:213-217 (1981).
RL
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitates
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J02146; AAA43412.1; -.
DR HSSP: P03472; 20WC.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur. 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT DOMAIN 36 75 ANCHOR.
FT TRANSMEM 7 35 HYPERVARIABLE STALK REGION.
FT ACT_SITE 260 260 HEAD OF NEURAMINIDASE.
FT ACT_SITE 262 262 PROBABLE.
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 454 AA; 50143 MW; A0DC4C08A2B53705 CRC64;
Query Match 82.5%; Score 33; DB 1; Length 454;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 LDMSW 5
DB 438 VDMSW 442

```

Search completed: February 18, 2004, 14:28:04
Job time : 4.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39, Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDMWA 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTRMBL.23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioplasmid:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	242	12 Q919K8	Q919K8 culex nigri
2	37	92.5	304	16 Q91719	Q91719 pseudomonas
3	37	92.5	433	16 Q8P4A1	Q8P4A1 xanthomonas
4	37	92.5	438	16 Q8P4V8	Q8P4V8 xanthomonas
5	36	90.0	258	5 Q45498	Q45498 caenorhabditis
6	36	90.0	361	16 Q8P955	Q8P955 xanthomonas
7	36	90.0	374	16 Q9H210	Q9H210 pseudomonas
8	36	90.0	409	10 Q9M3F6	Q9M3F6 arabidopsis
9	36	90.0	463	5 Q8MMJ0	Q8MMJ0 apis cerana
10	36	90.0	538	11 Q8C9K6	Q8C9K6 mus musculus
11	36	90.0	581	5 Q8MSH3	Q8MSH3 drosophila
12	36	90.0	597	5 Q9VGP2	Q9VGP2 drosophila
13	36	90.0	740	6 Q95KV1	Q95KV1 bos taurus
14	36	90.0	745	11 Q8CBT3	Q8CBT3 mus musculus
15	36	90.0	756	6 Q95KV0	Q95KV0 bos taurus
16	36	90.0	984	11 Q8C3U1	Q8C3U1 mus musculus

17	36	90.0	984	11 Q8BRB1	Q8BRB1 mus musculus
18	34	85.0	85	16 Q8PBL8	Q8PBL8 escherichia
19	34	85.0	211	9 Q80148	Q80148 bacterioph
20	34	85.0	211	9 Q21903	Q21903 bacterioph
21	34	85.0	237	10 Q8H2P9	Q8H2P9 cryza sativ
22	34	85.0	245	4 Q8N241	Q8N241 homo sapien
23	34	85.0	297	11 Q8BGS0	Q8BGS0 mus musculus
24	34	85.0	309	2 Q9P163	Q9P163 amycolatops
25	34	85.0	323	12 Q9QTR2	Q9QTR2 marek's dis
26	34	85.0	328	2 Q8KPM8	Q8KPM8 saccharopol
27	34	85.0	394	5 Q9U2T2	Q9U2T2 caenorhabdi
28	34	85.0	611	16 Q8DKF5	Q8DKF5 synchococc
29	34	85.0	616	2 Q33749	Q33749 synchococc
30	34	85.0	1139	16 Q8ZC91	Q8ZC91 yeastinda pe
31	34	85.0	1941	16 Q8G751	Q8G751 bifidobacte
32	33	82.5	97	12 Q9Q7I1	Q9Q7I1 svcs2 plect
33	33	82.5	110	16 Q8DY14	Q8DY14 streptococc
34	33	82.5	173	16 Q8E5U2	Q8E5U2 streptococc
35	33	82.5	173	16 Q8E065	Q8E065 streptococc
36	33	82.5	178	10 Q8LHU6	Q8LHU6 cryza sativ
37	33	82.5	198	16 Q9PA54	Q9PA54 xylella fas
38	33	82.5	232	17 Q8ZSR8	Q8ZSR8 pyrobaculum
39	33	82.5	234	16 Q9X897	Q9X897 streptomyce
40	33	82.5	236	3 Q9E527	Q9E527 neurospora
41	33	82.5	236	3 Q8NUT9	Q8NUT9 biocaccia
42	33	82.5	240	3 Q8NUT1	Q8NUT1 biocaccia
43	33	82.5	246	16 Q8CWD6	Q8CWD6 escherichia
44	33	82.5	270	4 Q8NCJ2	Q8NCJ2 homo sapien
45	33	82.5	273	10 Q94JW4	Q94JW4 arabidopsis

ALIGNMENTS

RESULT 1

Q919K8 PRELIMINARY, PRT, 242 AA.

AC Q919K8
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CUN068 hypothetical protein.
GN CUN068.
OS Culex nigripalpus baculovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
OX NCBI_Taxid=130556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Florida1997;
RX MEDLINE=2148685; PubMed=11602755;
RA Afonso C.L., Tulman B.R., Lu Z., Balinsky C.A., Moser B.A.,
RA Becnel J.J., Rock D.L., Kutish G.F.;
RT "Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus";
RL J. Virol. 75:11157-11165(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Florida1997;
RA Afonso C.L., Tulman B.R., Lu Z., Balinsky C.A., Moser B.A.,
RA Becnel J.J., Rock D.L., Kutish G.F.;
RT Submitted (Jun-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF403738; AKK94146.1; -;
KW Hypothetical protein.
SQ SEQUENCE 242 AA; 27222 MW; 6014967531110852 CRC64;

Query Match 100.0%; Score 40; DB 12; Length 242;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMWA 6
|||||
Db 79 LDMWA 84


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RESULT 2
ID 091719 PRELIMINARY; PRT; 304 AA.
AC 091719/
RT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DE 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
GN Probable cytochrome c oxidase assembly factor.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
MEDLINE=2043737; PubMed=10964043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.R., Coulter S.N., Folger K.R., Kas A., Larbig K., Lam R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL; AE004449; AAC03503.1; -.
DR InterPro; IPR006369; CyoE_Ctab.
DR InterPro; IPR000537; UblA.
DR Pfam; PF01040; UblA; 1.
DR TIGRFAMs; TIGR01473; cyoE_cTab; 1.
DR PROSITE; PS00943; UblA; 1.
KM Complete proteome.
SQ SEQUENCE 304 AA; 33430 MW; DC278071764B671C CRC64;

Query Match 92.5%; Score 37; DB 16; Length 304;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ID 1 LDMSWA 6
Db 259 LDMSWA 264

RESULT 3
ID 08P41 PRELIMINARY; PRT; 433 AA.
AC 08P41/
RT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DE 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
GN Cationic amino acid transporter.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavan F., Cardoso J., Chamberg F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madela A.M.B.N., Martinez-Rossi N.M.,
RA Locali E.C., Machado M.A., Madela A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A.F., Takita M.A., Teyura R.E., Teixeira B.C., Tezza R.I.D.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012036; AAM38706.1; -.
DR InterPro; IPR002293; AA/reI_permease1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KM Complete proteome.
SQ SEQUENCE 433 AA; 45795 MW; 921AC5AC60A545E2 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 438;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ID 1 LDMSWA 6
Db 182 VDMSWA 187

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RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012036; AAM38706.1; -.
DR InterPro; IPR002293; AA/reI_permease1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KM Complete proteome.
SQ SEQUENCE 433 AA; 45128 MW; EF217D2A7C516533 CRC64;

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Query Match 92.5%; Score 37; DB 16; Length 433;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ID 1 LDMSWA 6
Db 180 VDMSWA 185

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RESULT 4
ID 08P48 PRELIMINARY; PRT; 438 AA.
AC 08P48/
RT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DE 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
GN Cationic amino acid transporter.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavan F., Cardoso J., Chamberg F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madela A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A.F., Takita M.A., Teyura R.E., Teixeira B.C., Tezza R.I.D.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012036; AAM38706.1; -.
DR InterPro; IPR002293; AA/reI_permease1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KM Complete proteome.
SQ SEQUENCE 438 AA; 45795 MW; 921AC5AC60A545E2 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 438;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ID 1 LDMSWA 6
Db 182 VDMSWA 187

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RESULT 5
O45498      PRELIMINARY;      PRT;      258 AA.
ID O45498;
AC O45498;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
GN F39B2.5 protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Polidoridae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=951916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z92834; CAB07386.1; -.
DR WormRep; F39B2.5; CE16011.
DR InterPro; IPR000980; SH2.
DR Pfam; PF00017; SH2; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00253; SOCS; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50225; SOCS; 1.
SQ SEQUENCE 258 AA; 30897 MW; 820D4D73DC5C8060 CRC64;

Query Match      90.0%; Score 36; DB 5; Length 258;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDMSWA 6
Db 21 LDMSWA 26

RESULT 6
O8P955      PRELIMINARY;      PRT;      361 AA.
ID O8P955;
AC O8P955;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Exopolysaccharide biosynthesis protein.
GN XCC2011.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxId=340;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 33913 / NCPPB 528;
RC MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Purlan L.R.,
RA Queiroz R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
RA Caramonte G., Canhamar F., Cardozo J., Chamberg F., Clapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Porri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Mendes J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

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RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Teal S.M., White P.F.,
RA Setubal J.C., Kikajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012305; NAM41300.1; -.
DR InterPro; IPR002656; ACY1_transf_3.
DR Pfam; PF01757; ACY1_transf_3; 1.
KW Complete proteome.
SQ SEQUENCE 361 AA; 39147 MW; 37AB21791BE0393F CRC64;

Query Match      90.0%; Score 36; DB 16; Length 361;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSW 5
Db 117 LDMSW 121

RESULT 7
O9H210      PRELIMINARY;      PRT;      374 AA.
ID O9H210;
AC O9H210;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DE 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
DE Hypothetical protein PA3230.
GN PA3230.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxId=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PA01;
RC MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino B., Westbrook-Wedman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Rolger K.R., Kas A., Lathig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004746; AAC06618.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;

Query Match      90.0%; Score 36; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6
Db 81 DMSWA 85

RESULT 8
O9M3F6      PRELIMINARY;      PRT;      409 AA.
ID O9M3F6;
AC O9M3F6;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Putative replication protein.
GN T14K23_110.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nyakatura G., Fartmann B., Dauner D., Steer W., Holland R.,
 RA Weichselgartner M., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,
 RA Queller F., Salanoubat M.,
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL132909; CAB87732.1;
 DR InterPro; IPR003871; DUF223.
 DR Pfam; PF02721; DUF223;
 SQ SEQUENCE 409 AA; 45738 MW; ADDC4EF5597B4EB4 CRC64;

Query Match 90.0%; Score 36; DB 10; Length 409;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSW 5
 DB 190 LDMSW 194

RESULT 9

OBMMJ0 PRELIMINARY; PRT; 463 AA.
 AC OBMMJ0;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Major royal jelly protein MRJP2 precursor.
 GN MRJP2.
 OS Apis cerana (indian honeybee).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Apidae; Apis.
 OX NCBI_TaxID=7461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Horse heads;
 RA Sittler-Reed S., Imjongjirak C.;
 RT "Molecular Cloning of Major Royal Jelly Protein (MRJP2) cDNA from Apis
 cerana in Thailand."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF525777; AAM88282.1;
 DR InterPro; IPR003534; RoyalJelly.
 DR Pfam; PR03022; MRJP.1
 DR PRINTS; PR01366; ROYALJELLY.
 KW SIGNAL.
 FT SIGNAL
 SQ SEQUENCE 463 AA; 52412 MW; D648AE2BAF1EDDE9 CRC64;

Query Match 90.0%; Score 36; DB 5; Length 463;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6
 DB 110 DMSWA 114

RESULT 10

OBCK96 PRELIMINARY; PRT; 538 AA.
 AC OBCK96;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Eph receptor A3.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; Tissue=Thymus;
 RC MEDLINE=22354683; PubMed=124466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK041935; BAC31104.1;
 SQ SEQUENCE 538 AA; 60659 MW; EEDAB12E0369EA19 CRC64;

Query Match 90.0%; Score 36; DB 11; Length 538;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSW 5
 DB 343 LDMSW 347

RESULT 11

OBMSH3 PRELIMINARY; PRT; 581 AA.
 AC OBMSH3;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE GH24640p.
 GN CG6728.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Fries B.,
 RA George R., Gonzalez M., Guarin H., Krommler B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nuno J., Paclob J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceolnter S.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY118818; AAM50678.1;
 DR FLYBase; FBgn0037896; CG6728.
 DR InterPro; IPR000172; SHPox_oxite.
 DR InterPro; IPR000169; SHPox_oxite.
 DR Pfam; PF00732; GMC_oxred_3.
 DR PROSITE; PS00639; THIOX_PROTEASE_HIS_1.
 SQ SEQUENCE 581 AA; 63475 MW; A2F13B8BC25E496D CRC64;

Query Match 90.0%; Score 36; DB 5; Length 581;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6
 DB 159 DMSWA 163

RESULT 12

OQVGP2 PRELIMINARY; PRT; 597 AA.
 AC OQVGP2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE CG6728 protein.

GN CG6728.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731122;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle J.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abri J.P., Adayant A., An H.-J., Andrews-Pennnoch C., Baldwin D.,
 RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., May A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
 RA Fosløe A., Garg N.S., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Goddek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Houtin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003691; AAP54634.1; -;
 DR FlyBase: FBgn0037886; CG6728.
 DR InterPro: IPR000172; GMC_oxred.
 DR InterPro: IPR000169; SHProt_acatle.
 DR Pfam: PF00732; GMC_oxred; 1.
 DR PROSITE: PS00624; GMC_OXRED 2; 1.
 DR PROSITE: PS00639; THIOL_PROTEASE_HTS; 1.
 SQ SEQUENCE 597 AA; 65274 MW; 8C4C362AFPA0902A CRC64;

Query Match 90.0%; Score 36; DB 5; Length 597;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
 DB 159 DMSWA 163

DE 1kb kinase-alpha.
 GN BIKKALPHA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCB1_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
 RT "Identification and characterisation of the bovine 1kb kinases (1Kk)
 RT alpha, beta and gamma.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AJ41455; CAC93686.1; -;
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 740 AA; 84343 MW; 01903BE1F44D176 CRC64;

Query Match 90.0%; Score 36; DB 6; Length 740;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
 DB 733 LDMSW 737

RESULT 14
 ID 08CBT3 PRELIMINARY; PRT; 745 AA.
 AC 08CBT3;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Conserved helix-loop-helix ubiquitous kinase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclugonathi; Muridae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=22354683; PubMed=14466851;
 RA The FANTOM Consortium,
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL: AK035326; BAC29034.1; -;
 SQ SEQUENCE 745 AA; 84770 MW; 48C9E01C17A61184 CRC64;

Query Match 90.0%; Score 36; DB 11; Length 745;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
 DB 738 LDMSW 742

RESULT 15
 ID 095KV0 PRELIMINARY; PRT; 756 AA.
 AC 095KV0;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
 DE IKB kinase-beta.
 GN BIKBETA.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rottenberg S., Dobbelaere D.A.E., Heusler V.T.;
 RT "Identification and characterisation of the bovine IKB kinases (IKBs)
 RT alpha, beta and gamma."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AJ14556; CAC93687.1; -
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR02290; Ser_thr_kinase.
 DR InterPro; IPR01245; Tyr_kinase.
 DR Pfam; PF00069; kinase; 1.
 DR PRINTS; PRO0109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;

Query March 90.0%; Score 36; DB 6; Length 756;
 Best Local Similarity 100.0%; Pred. NO. 7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
 |||||
 Db 737 LDMSW 741

Search completed: February 18, 2004, 14:35:40
 Job time : 19.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDMSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76:*
2: PIR:*
3: PIR:*
4: PIR:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	304	2 F83632	probable cytochrome
2	36	90.0	258	2 T21987	hypothetical prote
3	36	90.0	362	2 S23471	uroporphyrinogen d
4	36	90.0	374	2 B83241	conserved hypothet
5	36	90.0	409	2 T47298	probable replicati
6	36	90.0	745	1 I49101	conserved helix-lo
7	36	90.0	983	2 B45583	receptor tyrosine
8	36	90.0	983	2 A38224	protein-tyrosine k
9	36	90.0	983	2 A45583	receptor tyrosine
10	34	85.0	211	2 T03355	gene e12 protein -
11	34	85.0	411	2 B84949	tetrahydrofolylpol
12	34	85.0	433	2 T31511	hypothetical prote
13	34	85.0	616	2 T14235	NADH2 dehydrogenas
14	34	85.0	1139	2 A10379	probable potassium
15	33	82.5	198	2 B82531	conserved hypothet
16	33	82.5	234	2 T36162	probable integral
17	33	82.5	275	2 T05822	hypothetical prote
18	33	82.5	316	2 AB2931	hypothetical prote
19	33	82.5	316	2 D98351	dipterite ABC tran
20	33	82.5	322	2 A13395	NADH2 dehydrogenas
21	33	82.5	324	2 AB3548	vegetarble incomp
22	33	82.5	360	2 S60888	ferric exochelin b
23	33	82.5	415	2 AB1844	hypothetical prote
24	33	82.5	421	2 T31787	hypothetical prote
25	33	82.5	436	2 E69371	bile acid-inducibl
26	33	82.5	453	1 NMIV3	exo-alpha-sialidas
27	33	82.5	454	1 NMIV	exo-alpha-sialidas
28	33	82.5	464	1 S75362	hypothetical prote
29	33	82.5	492	2 S03098	aerolysin precuro

30	33	82.5	516	2 T10000	cytochrome P450 (C
31	33	82.5	524	2 T09999	cytochrome P450 -
32	33	82.5	524	2 T09944	probable cytochrom
33	33	82.5	539	2 T15256	hypothetical prote
34	33	82.5	610	2 T35222	hypothetical prote
35	33	82.5	656	2 A56975	VI polysaccharide
36	33	82.5	656	2 ARI040	VI polysaccharide
37	33	82.5	836	2 DB2177	conserved hypothet
38	33	82.5	840	1 A42970	H+-exporting ATPas
39	33	82.5	885	2 C83441	two-component sens
40	33	82.5	1334	2 T50568	probable multi-dom
41	33	82.5	1575	2 T18545	lysacotin synthet
42	33	82.5	1842	2 T43409	probable fatty-acid
43	33	82.5	1842	2 T38781	fatty acid synthas
44	33	82.5	53	2 T11353	H+-transporting tw
45	32	80.0	83	2 S24712	Ig alpha chain - h

ALIGNMENTS

RESULT 1

F83632

probable cytochrome c oxidase assembly factor PA0113 [Imported] - Pseudomonas aeruginosa

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C/Accession: F83632

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warener, P.; Hickey, M.J.; L

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lir

ry, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: F83632

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-304 <STO>

A/Cross-references: GB:AE004449; GB:AE004091; NID:G9945928; PIDN:AAG03503.1; GSPDB:GNC

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA0113

C/Superfamily: heme O synthase

Query Match

Best Local Similarity 92.5%; Score 37; DB 2; Length 304;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
Db 259 LDMAWA 264

RESULT 2

T21987

hypothetical protein F39B2.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T21987

R/Dobson, R.

submitted to the EMBL Data Library, March 1997

A/Reference number: Z19498

A/Accession: T21987

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-258 <WIL>

A/Cross-references: EMBL:Z92834; PIDN:CA807386.1; GSPDB:GN00019; CESP:F39B2.5

A/Experimental source: clone F39B2

C/Genetics:

A/Gene: CESP:F39B2.5

A/Map position: 1

A/Introns: 16/2; 58/1; 97/3

Query Match 90.0%; Score 36; DB 2; Length 258;

Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWA 6
|||
21 LDMSWA 26

RESULT 3

urophosphorylase decarboxylase (EC 4.1.1.37) - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein YD9609.03; protein YDR047w
C:Species: *Saccharomyces cerevisiae*

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C/Accession: S23471; S33965; S54033; S20190; S27348; S3312
R:Garey, J.R.; Labbe-Bois, R.; Chelstowska, A.; Rytke, J.; Harrison, L.; Kushner, J.; La
Bur, J. *Biochem.* 205, 1011-1016, 1992
A>Title: uroporphyrinogen decarboxylase in *Saccharomyces cerevisiae*. HEM12 gene sequence
A/Reference number: S23471; MUID:92249304; PMID:1576986
A/Accession: S23471

A/Molecule type: DNA
A/Residues: 1-362 <GAR>
A/Cross-references: EMBL:X63721; NID:G3766; PIDN:CAA45253.1; PID:G3767
R:Difflumer, C.; Laroque, R.; Keng, T.
Yeast 9, 613-623, 1993
A>Title: Molecular analysis of HEM6 (HEM12) in *Saccharomyces cerevisiae*, the gene for ur
A/Reference number: S33965; MUID:93348774; PMID:8346678
A/Accession: S33965

A/Molecule type: DNA
A/Residues: 1-362 <DI>
A/Cross-references: EMBL:Z19089; NID:G4775; PIDN:CAA79514.1; PID:G4776
R:Hunt, S.; Bowman, S.; Harris, D.
Submitted to the EMBL Data Library, May 1995
A/Reference number: S54031

A/Accession: S54033
A/Molecule type: DNA
A/Residues: 1-362 <HUN>
A/Cross-references: EMBL:Z49209; NID:G798897; PIDN:CAA89078.1; PID:G798900; MIPS:YDR047w
C/Genetics:
A/Gene: HEM12; HEM6; POP3
A/Cross-references: MIPS:YDR047w; SGD:S0002454
A/Map position: 4R
C/Superfamily: uroporphyrinogen decarboxylase

C/Keywords: carbon-carbon lyase; carboxy-lyase; porphyrin biosynthesis

Query Match 90.0%; Score 36; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
|||
279 LDMSW 283

RESULT 4

conserved hypothetical protein PA3230 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C/Species: *Pseudomonas aeruginosa*

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Accession: B83241
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Ladbis, K.; Lim,
L.O.; S., Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: B83241

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-374 <STO>
A/Cross-references: GB:AE004746; GB:AE004091; NID:G9949350; PIDN:AA06618.1; GSPDB:GN001
A/Experimental source: strain PA01
C/Genetics:

A:Gene: PA3230

Query Match 90.0%; Score 36; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
|||
81 DMSWA 85

RESULT 5

probable replication protein - *Arabidopsis thaliana*
N:Alternate names: protein T14K23.110
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C/Accession: T47298
R:Nyakatura, G.; Faltmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.
Mayer, K.F.X.
Submitted to the Protein Sequence Database, April 2000
A/Reference number: Z24458
A/Accession: T47298

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-409 <NYA>
A/Cross-references: EMBL:AL132909
A/Experimental source: cultivar Columbia; BAC clone T14K23
C/Genetics:
A/Map position: 3
A/Insertions: 47/3; 95/3; 131/2; 175/3; 240/2; 281/3; 304/1; 336/3
A/Note: T14K23.110

Query Match 90.0%; Score 36; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
|||
190 LDMSW 194

RESULT 6

conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse
149101
C/Species: *Mus musculus* (house mouse)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: I49101
R:Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Genomics 27, 348-351, 1995
A>Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosom
A/Reference number: I49101; MUID:96044444; PMID:7558004
A/Accession: I49101

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-745 <HBS>
A/Cross-references: EMBL:U12473; NID:G1079492; PIDN:AAC52589.1; PID:G1079493
C/Genetics:
A/Gene: CHUK
C/Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homo.
C/Keywords: ATP; phosphotransferase
F:13-283/Domain: protein kinase homology <KIN>

Query Match 90.0%; Score 36; DB 1; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
|||
738 LDMSW 742

RESULT 7

B45583
 receptor tyrosine kinase Cck4 - chicken
 C.Species: Gallus gallus (chicken)
 C.Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
 C.Accession: B45583
 R.Sajjadi, F.G.; Paeguale, E.B.; Subramani, S.
 New Biol. 3, 769-778, 1991
 A>Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse and man
 A.Reference number: A45583; MUID:92031278; PMID:1657122
 A.Accession: B45583
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 1-983 <SRJ>
 A.Cross-references: GB:M68514; NID:9454809; PIDN:AAA48666.1; PID:9211447
 A.Note: Sequence extracted from NCBI Backbone (NCBIN:62405; NCBI:62411)
 C.Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C.Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
 F:619-885/Domain: protein kinase homology <KIN>
 F:627-635/Region: protein kinase ATP-binding motif

Query Match
 Best Local Similarity 90.0%; Score 36; DB 2; Length 983;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
 |||||
 Db 342 LDMSW 346

RESULT 8
 A88224
 protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human
 C.Species: Homo sapiens (man)
 C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
 C.Accession: A38224; B38224
 R.Wicks, L.P.; Wilkinson, D.; Salvaris, E.; Boyd, A.W.
 Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
 A>Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed in HEK293 cells
 A.Reference number: A38224; MUID:92179233; PMID:1311845
 A.Accession: A38224
 A.Molecule type: mRNA
 A.Residues: 1-983 <WIC>
 A.Cross-references: GB:M83941; NID:9183931; PIDN:AAA56633.1; PID:9183932
 A.Experimental source: pre-B-cell leukemia cell line LK63
 A.Note: Sequence extracted from NCBI Backbone (NCBI:86627)
 A.Accession: B38224
 A.Molecule type: Protein
 A.Residues: 21-39,810-860 <WIC>
 C.Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C.Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-983/Product: protein-tyrosine kinase hek #status experimental <MAT>
 F:542-565/Domain: transmembrane #status predicted <TM>
 F:619-885/Domain: protein kinase homology <KIN>
 F:627-635/Region: protein kinase ATP-binding motif
 F:233,337,391,404,493/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match
 Best Local Similarity 90.0%; Score 36; DB 2; Length 983;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
 |||||
 Db 343 LDMSW 347

RESULT 9
 A45583
 receptor tyrosine kinase Nek4 - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
 C.Accession: A45583
 R.Sajjadi, F.G.; Paeguale, E.B.; Subramani, S.

New Biol. 3, 769-778, 1991
 A>Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse and man
 A.Reference number: A45583; MUID:92031278; PMID:1657122
 A.Accession: A45583
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 1-983 <SRJ>
 A.Cross-references: GB:M68513; NID:9199119; PIDN:AAA39521.1; PID:9199120
 A.Note: Sequence extracted from NCBI Backbone (NCBIN:62398; NCBI:62401)
 C.Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C.Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
 F:619-885/Domain: protein kinase homology <KIN>
 F:627-635/Region: protein kinase ATP-binding motif

Query Match
 Best Local Similarity 90.0%; Score 36; DB 2; Length 983;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
 |||||
 Db 342 LDMSW 346

RESULT 10
 T03355
 gene e12 protein - Lactococcus phage b11170
 C.Species: Lactococcus phage b11170
 C.Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 04-Mar-2000
 C.Accession: T03355
 R.Cruz-Le Coq, A.M.; Gesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopin, J.
 Submitted to the EMBL Data Library, June 1997
 A.Description: Sequence and organization of the lactococcal isometric b11170 phage gene
 A.Reference number: Z14903
 A.Accession: T03355
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-211 <CRU>
 A.Cross-references: EMBL:AF009630; NID:93282260; PIDN:ACC27226.1; PID:93282307
 C.Genetics:
 A:Gene: e12
 C.Superfamily: Lactococcus phage b11170 gene e12 protein

Query Match
 Best Local Similarity 85.0%; Score 34; DB 2; Length 211;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSW 6
 |||||
 Db 29 LDMSW 34

RESULT 11
 B84949
 tetrahydrofolylpolyglutamate synthase (EC 6.3.2.17) [imported] - Buchnera sp. (strain ?
 C.Species: Buchnera sp.
 C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C.Accession: B84949
 R.Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
 Nature 407, 81-86, 2000
 A>Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
 A.Reference number: B84930; MUID:20445173; PMID:10993077
 A.Accession: B84949
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-411 <STO>
 A.Cross-references: GB:AP000398; GSPDB:GN00144
 A.Experimental source: strain ABS
 C.Genetics:
 A:Gene: folC; BUI67
 C.Superfamily: folylpolyglutamate synthase
 C.Keywords: ligase

Query Match
 Best Local Similarity 85.0%; Score 34; DB 2; Length 411;

Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSW 5
: : : :
Db 219 LDMSW 223

RESULT 12

TJ1511
hypothetical protein Y116A8C.9 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000

C/Accession: TJ1511

submitted to the EMBL Data Library, October 1999

A/Reference number: Z21041

A/Accession: TJ1511

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-433 <WIL>

A/Cross-references: EMBL:AL117204; PIDN:CA55145.1; CESP:Y116A8C.9

A/Experimental source: clone Y116A8C

C/Genetics:

A/Genes: CESP:Y116A8C.9

A/Introns: 16/2; 42/2; 75/2; 107/3; 173/3; 230/3; 262/3; 318/3; 373/1; 398/1

C/Superfamily: *Caenorhabditis elegans* hypothetical protein Y116A8C.9

Query Match 85.0%; Score 34; DB 2; Length 433;

Best Local Similarity 66.7%; Pred. No. 2.2e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 6

: : : :
Db 174 VDMTWA 179

RESULT 13

T14235
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - *Synechococcus* sp. (strain PCC 70

C/Species: *Synechococcus* sp.

A/Variety: strain PCC 7002

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002

C/Accession: T14235

R/Klughammer, B.; Sultemeyer, D.; Badger, M.R.; Price, G.D.

submitted to the EMBL Data Library, April 1997

A/Description: Involvement of ndh3, ndh3 and ORF427 genes in high affinity CO2 uptake

A/Reference number: Z17936

A/Accession: T14235

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-616 <KLU>

A/Cross-references: EMBL:U97516; NID:G2232044; PIDN:AA62184.1

A/Experimental source: strain PCC 7002

C/Genetics:

A/Note: ndh3

C/Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C/Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match 85.0%; Score 34; DB 2; Length 616;

Best Local Similarity 66.7%; Pred. No. 3.1e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSW 6

: : : :
Db 115 MDMSWA 120

RESULT 14

AI0379

probable potassium efflux system YPO3129 [imported] - *Yersinia pestis* (strain CO92)

C/Species: *Yersinia pestis*

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C/Accession: AI0379
R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tiddell, R.W.; Holden, M.T.G.; Prentice, M.J.
demo-Tarrage, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
11. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett.
Nature 413, 523-527, 2001

A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AI0379

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1139 <KUR>

A/Cross-references: GB:AL590842; PIDN:CA92364.1; PID:G15981067; GSPDB:GN00175

C/Genetics:

A/Genes: YPO3129

Query Match 85.0%; Score 34; DB 2; Length 1139;

Best Local Similarity 80.0%; Pred. No. 5.8e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5

: : : :
Db 480 MDMSW 484

RESULT 15

B82531
conserved hypothetical protein XF2666 [imported] - *Xylella fastidiosa* (strain 9a5c)

C/Species: *Xylella fastidiosa*

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000

C/Accession: B82531

R.anonymous. The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequ

Nature 406, 151-157, 2000

A/Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A/Reference number: B82531; MUID:20365717; PMID:10910347

A/Note: for a complete list of authors see reference number A59328 below

A/Accession: B82531

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-198 <SLM>

A/Cross-references: GB:AE004072; GB:AE003849; NID:9107884; PIDN:AA65463.1; GSPDB:GN01

A/Experimental source: strain 9a5c

R.Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrero, D.M.; Carrer,

de-Neco, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferrelia, A.U.S.

submitted to GenBank, June 2000

A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froi

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laiz

Chado, M.A.; Medeira, A.M.B.N.; Medeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins,

A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiter, D

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva

M.; Tuhko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;

A/Reference number: A59328

A/Contents: annotation

C/Genetics:

A/Genes: XF2666

C/Superfamily: conserved hypothetical protein WD1677

Query Match 82.5%; Score 33; DB 2; Length 198;

Best Local Similarity 80.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6

: : : :
Db 135 DMMSWA 139

Search completed: February 18, 2004, 14:38:38
Job time : 8.5921 secs

GenCore version 5.1.6
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OM proteain - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-5
Perfect score: 40
Sequence: 1 LDMSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	6	10 US-09-847-946A-5	Sequence 5, Appli
2	40	100.0	6	11 US-09-847-946A-5	Sequence 5, Appli
3	40	100.0	6	11 US-09-847-946A-10	Sequence 40, Appli
4	40	100.0	6	11 US-09-847-946A-62	Sequence 62, Appli
5	40	100.0	7	11 US-09-847-946A-66	Sequence 66, Appli
6	40	100.0	8	11 US-09-847-946A-59	Sequence 59, Appli
7	40	100.0	8	11 US-09-847-946A-67	Sequence 67, Appli
8	40	100.0	9	11 US-09-847-946A-58	Sequence 58, Appli
9	40	100.0	9	11 US-09-847-946A-61	Sequence 61, Appli
10	40	100.0	9	11 US-09-847-946A-64	Sequence 64, Appli
11	40	100.0	9	11 US-09-847-946A-65	Sequence 65, Appli
12	40	100.0	10	11 US-09-847-946A-57	Sequence 57, Appli
13	40	100.0	10	11 US-09-847-946A-60	Sequence 60, Appli
14	40	100.0	10	11 US-09-847-946A-63	Sequence 63, Appli
15	36	90.0	6	10 US-09-847-946A-2	Sequence 2, Appli

16	36	90.0	6	11 US-09-847-946A-2	Sequence 2, Appli
17	36	90.0	6	11 US-09-847-946A-33	Sequence 33, Appli
18	36	90.0	6	11 US-09-847-946A-41	Sequence 41, Appli
19	36	90.0	6	11 US-09-847-946A-73	Sequence 73, Appli
20	36	90.0	7	11 US-09-847-946A-37	Sequence 37, Appli
21	36	90.0	7	11 US-09-847-946A-77	Sequence 77, Appli
22	36	90.0	8	11 US-09-847-946A-30	Sequence 30, Appli
23	36	90.0	8	11 US-09-847-946A-38	Sequence 38, Appli
24	36	90.0	8	11 US-09-847-946A-78	Sequence 78, Appli
25	36	90.0	8	11 US-09-847-946A-70	Sequence 70, Appli
26	36	90.0	9	11 US-09-847-946A-29	Sequence 29, Appli
27	36	90.0	9	11 US-09-847-946A-32	Sequence 32, Appli
28	36	90.0	9	11 US-09-847-946A-35	Sequence 35, Appli
29	36	90.0	9	11 US-09-847-946A-36	Sequence 36, Appli
30	36	90.0	9	11 US-09-847-946A-69	Sequence 69, Appli
31	36	90.0	9	11 US-09-847-946A-72	Sequence 72, Appli
32	36	90.0	9	11 US-09-847-946A-75	Sequence 75, Appli
33	36	90.0	9	11 US-09-847-946A-76	Sequence 76, Appli
34	36	90.0	10	11 US-09-847-946A-31	Sequence 31, Appli
35	36	90.0	10	11 US-09-847-946A-34	Sequence 34, Appli
36	36	90.0	10	11 US-09-847-946A-71	Sequence 71, Appli
37	36	90.0	10	11 US-09-847-946A-74	Sequence 74, Appli
38	36	90.0	11	11 US-09-847-946A-28	Sequence 28, Appli
39	36	90.0	11	11 US-09-847-946A-68	Sequence 68, Appli
40	36	90.0	11	11 US-09-847-946A-132	Sequence 132, Appli
41	36	90.0	11	11 US-09-847-946A-140	Sequence 140, Appli
42	36	90.0	12	11 US-09-847-946A-43	Sequence 43, Appli
43	36	90.0	13	11 US-09-847-946A-143	Sequence 143, Appli
44	36	90.0	13	11 US-09-847-946A-144	Sequence 144, Appli
45	36	90.0	13	11 US-09-847-946A-145	Sequence 145, Appli

ALIGNMENTS

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RESULT 1
US-09-847-946A-5
; Sequence 5, Application US/09847946B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847, 940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643, 260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-946A-5

Query Match      100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. NO. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0,

QY      1 LDMSWA 6
DB      1 LDMSWA 6

RESULT 2
US-09-847-946A-5
; Sequence 5, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

```

```

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-5
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```

Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 LDMSWA 6
        |||||
Db       1 LDMSWA 6
```

```

RESULT 3
US-09-847-946A-40
; Sequence 40, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-40
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```

Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 LDMSWA 6
        |||||
Db       1 LDMSWA 6
```

```

RESULT 4
US-09-847-946A-62
; Sequence 62, Application US/09847946A
; Publication No. US20030054999A1
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```

; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-62
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```

Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 LDMSWA 6
        |||||
Db       1 LDMSWA 6
```

```

RESULT 5
US-09-847-946A-66
; Sequence 66, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-66
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Query Match          100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 LDMSWA 6
        |||||
Db       1 LDMSWA 6
```

```
RESULT 6
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US-09-847-946A-59
; Sequence 59, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-59

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
Db 3 LDMSWA 8

RESULT 7
US-09-847-946A-67
; Sequence 67, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-67

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
Db 1 LDMSWA 6

RESULT 8
US-09-847-946A-58
; Sequence 58, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-58

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
Db 1 LDMSWA 6

RESULT 9
US-09-847-946A-61
; Sequence 61, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-61

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
|
|
|
|
|
Db 1 LDMSWA 6

RESULT 10
US-09-847-946A-64

/ Sequence 64, Application US/09847946A
/ Publication No. US20030054999A1
/ GENERAL INFORMATION:
/ APPLICANT: May, Michael J
/ APPLICANT: Ghosh, Sankar
/ APPLICANT: Findeis, Mark A
/ APPLICANT: Phillips, Kathryn
/ APPLICANT: Hannig, Gerhard
/ TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
/ FILE REFERENCE: PPI-119
/ CURRENT APPLICATION NUMBER: US/09/847,946A
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: 60/201,261
/ PRIOR FILING DATE: 2000-05-02
/ PRIOR APPLICATION NUMBER: 09/643,260
/ PRIOR FILING DATE: 2000-08-22
/ NUMBER OF SEQ ID NOS: 160
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 64
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-64

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
|
|
|
|
|
Db 3 LDMSWA 8

RESULT 11
US-09-847-946A-65

/ Sequence 65, Application US/09847946A
/ Publication No. US20030054999A1
/ GENERAL INFORMATION:
/ APPLICANT: May, Michael J
/ APPLICANT: Ghosh, Sankar
/ APPLICANT: Findeis, Mark A
/ APPLICANT: Phillips, Kathryn
/ APPLICANT: Hannig, Gerhard
/ TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
/ FILE REFERENCE: PPI-119
/ CURRENT APPLICATION NUMBER: US/09/847,946A
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: 60/201,261
/ PRIOR FILING DATE: 2000-05-02
/ PRIOR APPLICATION NUMBER: 09/643,260
/ PRIOR FILING DATE: 2000-08-22
/ NUMBER OF SEQ ID NOS: 160
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 65
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-65

Query Match 100.0%; Score 40; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
|
|
|
|
|
Db 2 LDMSWA 7

RESULT 12
US-09-847-946A-57

/ Sequence 57, Application US/09847946A
/ Publication No. US20030054999A1
/ GENERAL INFORMATION:
/ APPLICANT: May, Michael J
/ APPLICANT: Ghosh, Sankar
/ APPLICANT: Findeis, Mark A
/ APPLICANT: Phillips, Kathryn
/ APPLICANT: Hannig, Gerhard
/ TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
/ FILE REFERENCE: PPI-119
/ CURRENT APPLICATION NUMBER: US/09/847,946A
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: 60/201,261
/ PRIOR FILING DATE: 2000-05-02
/ PRIOR APPLICATION NUMBER: 09/643,260
/ PRIOR FILING DATE: 2000-08-22
/ NUMBER OF SEQ ID NOS: 160
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 57
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-57

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
|
|
|
|
|
Db 2 LDMSWA 7

RESULT 13
US-09-847-946A-60

/ Sequence 60, Application US/09847946A
/ Publication No. US20030054999A1
/ GENERAL INFORMATION:
/ APPLICANT: May, Michael J
/ APPLICANT: Ghosh, Sankar
/ APPLICANT: Findeis, Mark A
/ APPLICANT: Phillips, Kathryn
/ APPLICANT: Hannig, Gerhard
/ TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
/ FILE REFERENCE: PPI-119
/ CURRENT APPLICATION NUMBER: US/09/847,946A
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: 60/201,261
/ PRIOR FILING DATE: 2000-05-02
/ PRIOR APPLICATION NUMBER: 09/643,260
/ PRIOR FILING DATE: 2000-08-22
/ NUMBER OF SEQ ID NOS: 160
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 60
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-60

US-09-847-946A-60

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
DB 2 LDMSWA 7

RESULT 14

US-09-847-946A-63
; Sequence 63, Application US/09847946A
; Publication No. US2003054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Flindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-63

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
DB 3 LDMSWA 8

RESULT 15

US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2

Query Match 90.0%; Score 36; DB 10; Length 6;

Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
DB 1 LDMSW 5

Search completed: February 18, 2004, 15:41:55
Job time : 16.7529 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-4
Perfect score: 40
Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL.23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteria:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	40	100.0	227	4	Q8IXK8
3	40	100.0	355	11	Q8BIT9
4	40	100.0	452	4	Q96AB7
5	40	100.0	477	11	Q9CTU6
6	40	100.0	484	4	Q9BTU6
7	37	92.5	154	11	Q8BBD2
8	37	92.5	1083	13	Q9OMQ8
9	37	92.5	1083	13	Q8AXU2
10	37	92.5	1100	13	Q9OMQ9
11	37	92.5	1329	16	Q9CD30
12	36	90.0	48	16	Q8VXB2
13	36	90.0	236	3	Q8NVY9
14	36	90.0	261	2	Q9AQ37
15	36	90.0	273	16	Q8NS79
16	36	90.0	274	16	Q8G659

17	36	90.0	310	2	Q9XB87	Q9XB87 zymomonas m
18	36	90.0	310	16	Q8RF1	Q8RF1 corynebacte
19	36	90.0	358	10	Q50002	Q50002 prunus arne
20	36	90.0	703	10	Q9FIS0	Q9FIS0 arabidopsis
21	36	90.0	703	10	Q8GYG3	Q8GYG3 arabidopsis
22	36	90.0	740	6	Q9SKV1	Q9SKV1 bos taurus
23	36	90.0	745	11	Q8CBT3	Q8CBT3 mus musculu
24	36	90.0	747	16	Q69735	Q69735 mycobacteri
25	36	90.0	756	6	Q9SKV0	Q9SKV0 bos taurus
26	36	90.0	803	17	Q97UH8	Q97UH8 sulfolobus
27	36	90.0	889	16	Q9AAZ6	Q9AAZ6 caulobacter
28	36	90.0	896	2	Q9A0H0	Q9A0H0 caldicellul
29	36	90.0	1005	10	Q9XGZ2	Q9XGZ2 arabidopsis
30	36	90.0	1139	16	Q82C91	Q82C91 yeastina pe
31	36	90.0	1345	16	Q91060	Q91060 streptomyce
32	36	90.0	1426	2	Q9X3P6	Q9X3P6 caldicellul
33	36	90.0	1751	2	Q9A0G4	Q9A0G4 caldicellul
34	36	90.0	1770	2	Q9X3P5	Q9X3P5 caldicellul
35	36	90.0	5435	2	Q914X2	Q914X2 streptomyce
36	35	87.5	49	6	Q8SP16	Q8SP16 equus caball
37	35	87.5	161	6	Q8MJT3	Q8MJT3 oryctolagus
38	35	87.5	161	11	Q921P9	Q921P9 rattus norv
39	35	87.5	200	16	Q8NS33	Q8NS33 corynebacte
40	35	87.5	241	16	Q8PR42	Q8PR42 corynebacte
41	35	87.5	323	6	Q9TT79	Q9TT79 ovib aries
42	35	87.5	562	16	Q98AG0	Q98AG0 rhizobium 1
43	35	87.5	565	2	Q9XJ20	Q9XJ20 actinopolys
44	35	87.5	596	5	Q8SSN6	Q8SSN6 dictyosell
45	35	87.5	616	17	Q27025	Q27025 methanobact

ALIGNMENTS

ID	Q9ACRS	PRELIMINARY;	PRT;	205 AA.
AC	Q9ACRS			
DT	01-JUN-2001 (TRMBLrel. 17, Created)			
DT	01-JUN-2001 (TRMBLrel. 17, Last sequence update)			
DT	01-OCT-2002 (TRMBLrel. 22, Last annotation update)			
DE	Hypothetical protein SCPl.253.			
GN	SCPl.253.			
OS	Streptomyces coelicolor.			
OG	Plasmid SCPl.			
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Streptomycinae; Streptomycetaceae; Streptomyces.			
OX	NCBI_TaxID=1902;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=A3(2);			
RX	MEDLINE=21996410; PubMed=12000953;			
RA	Bentley S.D., Charer K.F., Cerdano-Tarraga A.-M., Challis G.L.,			
RA	Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieffer H.,			
RA	Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,			
RA	Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,			
RA	Huang C.-H., Kieffer T., Larke L., Murphy L., Oliver K., O'Neill S.,			
RA	Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,			
RA	Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,			
RA	Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,			
RA	Hopwood D.A.;			
RT	"Complete genome sequence of the model actinomycete Streptomyces			
RT	coelicolor A3(2)."			
RL	Nature 417:141-147(2002).			
DR	EMBL; AL590464; CAC36779.1;			
KW	Hypothetical protein; Plasmid; Complete proteome.			
SO	SEQUENCE 205 AA; 23051 MW; 6602396CF933F2D9 CRC64;			
QY	Query Match	100.0%;	Score 40;	DB 16; Length 205;
	Best Local Similarity	100.0%;	Pred. No. 75;	
	Matches	6; Conservative	0; Mismatches	0; Indels
			0; Gaps	0;

Db 10 ADMSWL 15

RESULT 2

081XK8 PRELIMINARY; PRT; 227 AA.

AC 081XK8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Similar to hypothetical protein BC017335.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK NCBI_TexID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Struhsberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
KW Hypothetical protein.
SQ SEQUENCE 227 AA; 25487 MW; F1A71EA57062A05 CRC64;

Query Match 100.0%; Score 40; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
Db 113 ADMSWL 118

RESULT 3

08BIT9 PRELIMINARY; PRT; 355 AA.

AC 08BIT9;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Mitochondrial ribosomal protein L41 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TexID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002)
DR EMBL; AK087998; BAC40084.1; -
SQ SEQUENCE 355 AA; 40183 MW; FEP8546127402D58 CRC64;

Query Match 100.0%; Score 40; DB 11; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
Db 215 ADMSWL 220

RESULT 4

096AB7 PRELIMINARY; PRT; 452 AA.

AC 096AB7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein FLJ90634.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK NCBI_TexID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Struhsberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Iocag T., Oca T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hito Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aoeoka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Minomiyu K.;
RT "NEDO human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017335; AA017335.1; -
DR EMBL; AK075115; BAC11411.1; -
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 452 AA; 50575 MW; B79D25EB38096733 CRC64;

Query Match 100.0%; Score 40; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
Db 338 ADMSWL 343

RESULT 5

09CYU6 PRELIMINARY; PRT; 477 AA.

AC 09CYU6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE 2810443J12RLK protein (Mitochondrial ribosomal protein L41
DE homolog).
GN 2810443J12RLK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TexID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=1217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Araiawa T., Hara A., Fukumitsu Y., Konno H., Aichi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesl C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Steadl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baren G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Guestinch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Monbarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
 RA Hashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RL EMBL; AK013297; BAB28775.1; -;
 DR EMBL; AK078448; BAC37279.1; -;
 DR MGD; MGI:1914478; 2810443J12R1k.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 3.
 DR SMART; SM00320; WD40; 4.
 DR PROSITE; PS00678; WD_REPEATS_1; 2.
 DR PROSITE; PS50082; WD_REPEATS_2; 1.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KM Repeat; WD repeat.
 SQ SEQUENCE 477 AA; 53201 MW; 26555735244BA9C CRC64;

Query Match 100.0%; Score 40; DB 11; Length 477;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
 DB 337 ADMSWL 342

RESULT 6
 Q9BTV6 PRELIMINARY; PRT; 484 AA.
 ID Q9BTV6;
 AC Q9BTV6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Brain;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003123; AAH03123.1; -;
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 2.
 DR SMART; SM00320; WD40; 3.
 DR PROSITE; PS00678; WD_REPEATS_1; 2.
 DR PROSITE; PS50082; WD_REPEATS_2; 1.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KM Hypothetical protein; Repeat; WD repeat.
 FT NON_TER
 SQ SEQUENCE 484 AA; 54088 MW; 1A2CA3237CB7358E CRC64;

Query Match 100.0%; Score 40; DB 4; Length 484;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
 DB 370 ADMSWL 375

RESULT 7

Q9BGD2 PRELIMINARY; PRT; 154 AA.
 ID Q9BGD2;
 AC Q9BGD2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RL EMBL; AK043157; BAC31480.1; -;
 DR EMBL; AK049078; BAC33535.1; -;
 KM Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 154 AA; 16524 MW; A526724D4074D88 CRC64;

Query Match 92.5%; Score 37; DB 11; Length 154;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
 DB 9 ADMSWL 14

RESULT 8
 Q9OWQ8 PRELIMINARY; PRT; 1083 AA.
 ID Q9OWQ8;
 AC Q9OWQ8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Inducible nitric oxide synthase (EC 1.14.13.39).
 GN iNOS.
 OS Oncomyrchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Proactinopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 NC NCB1_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=gonad;
 RA Wang T., Ward M., Grabowski P.S., Secombes C.J.;
 RT "Molecular cloning, gene organization and expression of rainbow trout
 RT (Oncorhynchus mykiss) inducible nitric oxide synthase (iNOS) gene."
 RL J. Biochem. 358:747-755(2001).
 DR EMBL; AJ300555; CAC83069.1; -;
 DR InterPro; IPR003097; FAD binding.
 DR InterPro; IPR001094; Flavodoxin like.
 DR InterPro; IPR001226; Flavodoxin.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR004030; NO_synthase.
 DR Pfam; PF00667; FAD binding_1; 1.
 DR Pfam; PF00258; Flavodoxin_1; 1.
 DR Pfam; PF00175; NAD binding_1; 1.
 DR Pfam; PF02898; NO_synthase; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 DR PROSITE; PS60001; NOS; 1.
 KM Oxidoreductase.
 SQ SEQUENCE 1083 AA; 123060 MW; 53E4DFD2FA5A8B5D CRC64;

Query Match 92.5%; Score 37; DB 13; Length 1083;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6
 Db 402 ADMAWL 407

RESULT 9

08AXU2 PRELIMINARY; PRT; 1083 AA.
 AC 08AXU2; (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Inducible nitric oxide synthase (EC 1.14.13.39).
 GN INOS.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Proteoanchopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 NX NCBI_TaxID=8022;
 RN [1]

RE SEQUENCE FROM N.A.
 RA Wang T., Bole N., Secombes C.J.;
 RT "Two promoters of inducible nitric oxide synthase gene exist in rainbow trout evidenced by studies with RTs-11 and RTG-2 cell lines."
 RL Submitted (INCV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ295230; CAC82807.1; -.
 KM Oxidoreductase.
 SQ SEQUENCE 1083 AA; 123033 MW; B0F95C3F033AF249 CRC64;

Query Match 92.5%; Score 37; DB 13; Length 1083;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6
 Db 402 ADMAWL 407

RESULT 10

090W09 PRELIMINARY; PRT; 1100 AA.
 AC 090W09;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Inducible nitric oxide synthase (EC 1.14.13.39).
 GN INOS.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Proteoanchopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 NX NCBI_TaxID=8022;
 RN [1]

RE SEQUENCE FROM N.A.
 RA Wang T., Ward M., Grabowski P.S., Secombes C.J.;
 RT "Molecular cloning, gene organization and expression of rainbow trout (Oncorhynchus mykiss) inducible nitric oxide synthase (INOS) gene."
 RL J. Biochem. 358:747-755(2001).
 DR EMBL; AJ295231; CAC82808.1; -.
 DR InterPro; IPR003097; PAD binding.
 DR InterPro; IPR001264; Flavodoxin like.
 DR InterPro; IPR001709; FPN_cyc_redctase.
 DR InterPro; IPR004030; NO synthase.
 DR Pfam; PF00667; PAD binding_1.
 DR Pfam; PF00258; Flavodoxin_1.
 DR Pfam; PF00175; NAD_binding_1; 1.

DR Pfam; PF02898; NO synthase; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PROSITE; PS60001; NOS; 1.
 KM Oxidoreductase.
 SQ SEQUENCE 1100 AA; 125079 MW; E4763388C97D608F CRC64;

Query Match 92.5%; Score 37; DB 13; Length 1100;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6
 Db 419 ADMAWL 424

RESULT 11

09CD30 PRELIMINARY; PRT; 1329 AA.
 AC 09CD30;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein ML2535.
 GN ML2535.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 NX NCBI_TaxID=1769;
 RN [1]

RE SEQUENCE FROM N.A.
 RA STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eigemeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagsi K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrall B.G.;
 RA "Massive gene decay in the leprosy bacillus."
 RT Nature 409:1007-1011(2001).
 RL Nature 409:1007-1011(2001).
 DR EMBL; AL583926; CAC32066.1; -.
 DR Lepitoma; ML2535;
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR002543; FtsK_SpoIIIE.
 DR Pfam; PF01580; FtsK_SpoIIIE; 2.
 DR SMART; SM00382; AAA; 3.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1329 AA; 146129 MW; F9A85758D60E7D8 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 1329;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6
 Db 260 SDMSWL 265

RESULT 12

08VXB2 PRELIMINARY; PRT; 48 AA.
 AC 08VXB2;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DE Hypothetical protein MT0946.
 GN MT0946.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J.F., Deboy R., Dodson R., Geim M.L., Hatt D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF006980; AAK45193.1; -
 DR TIGR; MT0946; -
 KM Hypothetical protein.
 SQ SEQUENCE 48 AA; 5265 MW; C0BFA9D6AA2EF8DF CRC64;

Query Match 90.0%; Score 36; DB 16; Length 48;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
 |||||
 DB 13 ADMSWL 18

RESULT 13

OBNTY9 PRELIMINARY; PRT; 236 AA.

ID OBNTY9
 AC OBNTY9;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Endoglucanase.
 GN CEL12C.
 OS Bionectria ochroleuca.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Bionectriaceae; Bionectria.
 OX NCBI_TaxID=29856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22067395; PubMed=12073090;
 RA Gedegebur F., Fowler T., Phillips J., van der Kley P.,
 RA van Solingen P., Dankmeyer L., Power S.D.;
 RT "Cloning and relational analysis of 15 novel fungal endoglucanases
 RT from family 12 glycosyl hydrolase";
 RL Curr. Genet. 41:89-98(2002).
 DR EMBL; AF435065; AAM77708.1; -
 DR InterPro; IPR002594; Glyco_hydro.12.
 DR Pfam; PF01670; Glyco_hydro.12; 1.
 DR ProDom; PD004316; Glyco_hydro.12; 1.
 SQ SEQUENCE 236 AA; 26024 MW; C3DBA7E33F0C41D8 CRC64;

Query Match 90.0%; Score 36; DB 3; Length 236;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 5
 |||||
 DB 63 ADMSWL 67

RESULT 14

OBNTY9 PRELIMINARY; PRT; 261 AA.

ID OBNTY9
 AC OBNTY9;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Glycosyl hydrolase 6 (Fragment).
 OS Caldicellulosiraptor sp. Tok7B.1.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;

OC Caldicellulosiraptor.
 OX NCBI_TaxID=80339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tok7B.1;
 RX MEDLINE=20171169; PubMed=10706665;
 RA Gibbs M.D., Reeves R.A., Farrington G.K., Anderson P., Williams D.P.,
 RA Bergquist P.L.;
 RT "Multidomain and multifunctional glycosyl hydrolases from the extreme
 RT thermophile Caldicellulosiraptor isolate Tok7B.1";
 RL Curr. Microbiol. 40:333-340(2000).
 DR EMBL; AF078040; AAK06391.1; -
 DR HSSP; Q06851; INBC.
 DR InterPro; IPR001956; CBD_3.
 DR Pfam; PF00942; CBM_3; 1.
 DR ProDom; PD001947; CBD_3; 1.
 KM Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 261 261
 SQ SEQUENCE 261 AA; 28759 MW; 4771744A26A6E04 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 261;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
 |||||
 DB 237 DMSWL 241

RESULT 15

OBNTY9 PRELIMINARY; PRT; 273 AA.

ID OBNTY9
 AC OBNTY9;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol
 DE monophosphatase family.
 GN CGL0800.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032";
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF005276; BAB98193.1; -
 DR InterPro; IPR000760; Inositol_P.
 DR Pfam; PF00459; Inositol_P; 1.
 KM Complete proteome.
 SQ SEQUENCE 273 AA; 29072 MW; C132E2C67E0BBA4D CRC64;

Query Match 90.0%; Score 36; DB 16; Length 273;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWL 6
 |||||
 DB 225 ADMSWL 230

Search completed: February 18, 2004, 14:35:38
 Job time : 18.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-4
Perfect score: 40
Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	470	1 NOS2_ONCMY	Q92091 oncorhynchu
2	36	90.0	470	1 NRAM_IADBU	Q07570 influenza a
3	36	90.0	470	1 NRAM_IADCH	Q07571 influenza a
4	36	90.0	470	1 NRAM_IADH2	Q07572 influenza a
5	36	90.0	470	1 NRAM_IADH2	Q07573 influenza a
6	36	90.0	470	1 NRAM_IADJ3	Q07599 influenza a
7	36	90.0	470	1 NRAM_IAGFN	Q07574 influenza a
8	36	90.0	470	1 NRAM_IAGFD	Q07577 influenza a
9	36	90.0	470	1 NRAM_IAGHI	Q07578 influenza a
10	36	90.0	470	1 NRAM_IAGAB	Q07583 influenza a
11	36	90.0	470	1 NRAM_IATYL	Q07585 influenza a
12	36	90.0	745	1 IKKA_HUMAN	O15111 h inhibitor
13	36	90.0	745	1 IKKA_MOUSE	Q06680 m inhibitor
14	36	90.0	756	1 IKKB_MOUSE	O14920 homo sapien
15	36	90.0	757	1 IKKB_MOUSE	O08351 mus musculu
16	36	90.0	757	1 IKKB_RAT	Q96778 rattus norv
17	36	90.0	1039	1 GUNB_CALSA	P10474 c endogluc
18	36	90.0	1275	1 RFBC_MYXXA	Q05864 myxococcu
19	35	87.5	99	1 NOS3_SHEEP	P73209 ovis arie
20	35	87.5	914	1 GUX2_CLOSR	P50900 clostridum
21	35	87.5	1201	1 NOS3_MOUSE	P73313 mus musculu
22	35	87.5	1202	1 NOS3_HUMAN	P23474 homo sapien
23	35	87.5	1204	1 NOS3_BOVIN	P23473 bos taurus
24	35	87.5	1204	1 NOS3_PIG	Q28969 sus scrofa
25	34	85.0	220	1 Y132_METVA	Q27596 methanococ
26	34	85.0	282	1 3MG2_ECOLI	P04395 escherichia
27	34	85.0	410	1 Y801_DEIRA	Q92468 delnoccocu
28	34	85.0	529	1 GUNA_MYCLE	P48810 mycobacteri
29	34	85.0	578	1 YC20_METPA	Q56617 methanococ
30	34	85.0	578	1 YC12_MLEPN	Q48458 klebsiella
31	34	85.0	591	1 NOS2_CANPA	Q62699 canis fami
32	34	85.0	1144	1 NOS2_MOUSE	P23477 mus musculu
33	34	85.0	1147	1 NOS2_RAT	Q06518 rattus norv

34	34	85.0	1147	1 NOS2_HUMAN	O60591 homo sapien
35	34	85.0	1149	1 NOS2_CAVPO	O54705 cavia porce
36	34	85.0	1153	1 NOS2_HUMAN	P35228 homo sapien
37	34	85.0	1331	1 MANB_CALSA	P22533 caldocellum
38	34	85.0	1742	1 GUNA_CALSA	P22533 caldocellum
39	33	82.5	232	1 C1B3_SHEEP	P80943 ovib arie
40	33	82.5	333	1 C1B2_SHEEP	Q29422 ovib arie
41	33	82.5	336	1 NOS2_BACSU	O34453 bacillus su
42	33	82.5	339	1 YJGB_ECOLI	P27250 escherichia
43	33	82.5	376	1 PGJR_PENGR	O93883 penicillium
44	33	82.5	421	1 PNK1_SCHPO	O13911 schizosach
45	33	82.5	470	1 NRAM_IAGIT	Q07584 influenza a

ALIGNMENTS

RESULT 1
ID NOS2_ONCMY STANDARD; PRT; 470 AA.
AC Q92091;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nitric oxide synthase, Inducible (EC 1.14.13.39) (NOS, type II)
DE (Inducible NOS) (NOS) (Fragment).
GN NOS2.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Grabowski P.S., Laling K.J., Hardie L., Macgilligan F., Ralston S.,
RA Seemee C.J.;
RT "Detection of mRNA for a nitric oxide synthase in macrophages and
RT gill of rainbow trout challenged with an attenuated bacterial
RT pathogen."
RL (in) Moncada S., Stamler J., Higgs B.A. (eds.);
RL 4th International meeting on the biology of nitric oxide, Amelia
RL Island, Florida, Sep. 1995, pp.10:48-48, Portland Press,
RL Brookfield (1996).
CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO
CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + H⁺ = citrulline +
CC nitric oxide + N NADP⁺;
CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME (BY SIMILARITY).
CC -!- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY
CC SIMILARITY).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.
CC -!- SIMILARITY: Contains 1 Flavodoxin-like domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: X97013; CAA65736.1; -.
CC HSP: P29477; INOS.
DR InterPro: IPR003037; FAD binding.
DR InterPro: IPR001094; Flavodoxin-like.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR004030; NO synthase.
DR Pfam: PF00667; FAD binding 1; 1.
DR Pfam: PF00258; Flavodoxin; 1.

DR Pfam; PF02898; NO_gynthase; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
 DR PROSITE; PS60001; NOS; PARTIAL.
 KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme.
 FT NON_TER 1
 FT DOMAIN 139 159 CALMODULIN-BINDING (POTENTIAL).
 FT BIND 169 307 FLAVODOXIN-LIKE.
 FT NP_BIND 253 284 FMN (PYRIMIDINE PART) (BY SIMILARITY).
 FT NP_BIND 398 409 FAD (ADP PART) (BY SIMILARITY).
 FT NON_TER 470 470
 SQ SEQUENCE 470 AA; 53329 MW; 40B6717BE500B64D CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 83.3%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ADMSW 6
 DB 89 ADMWDL 94

RESULT 2
 NRAM_IADBU STANDARD; PRT; 470 AA.
 ID NRAM_IADBU
 AC 007570;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Duck/Burjatia/552/88).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=38957;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93212520; PubMed=8460490;
 RA Saito T., Kawoka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A virus."
 RL Virology 193:868-876(1993).
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitates the mobility of the virus to and from the site of infection.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
 CC -----
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 CC -----
 DR EMBL; L06572; AAA43365.1; -
 DR HSSP; P06820; 2BAT.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 KW Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
 FT ACT_SITE 273 273 BY SIMILARITY.

FT ACT_SITE 275 275 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 470 AA; 51989 MW; DIA6F07460F68AD CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5
 DB 453 ADMSW 457

RESULT 3
 NRAM_IADCH STANDARD; PRT; 470 AA.
 ID NRAM_IADCH
 AC 007571;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Duck/Chabarovsk/1610/72).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=38957;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93212520; PubMed=8460490;
 RA Saito T., Kawoka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A virus."
 RL Virology 193:868-876(1993).
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitates the mobility of the virus to and from the site of infection.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
 CC -----
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 CC -----
 DR EMBL; L06573; AAA43367.1; -
 DR HSSP; P06820; 2BAT.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 KW Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 FT ACT_SITE 273 273 BY SIMILARITY.
 FT ACT_SITE 275 275 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 470 AA; 52070 MW; 169AB89FEB8006DC CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADM5W 5
 DB 453 ADM5W 457

RESULT 4
 ID NRAM_IADH2 STANDARD; PRT; 470 AA.
 AC 007573;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Duck/Hokkaido/8/80).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=11358;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212520; PubMed=8460490;
 RA Saito T., Kawoka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
 RT viruses."
 RT Virology 193:868-876(1993).
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitates
 CC the mobility of the virus to and from the site of infection.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 CC SPIKE ON THE SURFACE OF THE VIRION.
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
 CC -----
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 CC -----
 CC EMBL: L06574; AAA43372.1; -.
 DR HSBP; P06820; 2BRT.
 DR InterPro: IPR001860; Glyco_hydro_34.
 DR Pfam: PF00064; neu; 1.
 DR ProDom: PD000431; Glyco_hydro_34; 1.
 DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
 KM TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 FT ACT SITE 273 273 BY SIMILARITY.
 FT ACT SITE 275 275 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 470 AA; 52015 MW; E1C1D3E2C650B93C CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADM5W 5
 DB 453 ADM5W 457

RESULT 5
 ID NRAM_IADH2 STANDARD; PRT; 470 AA.
 AC 007573;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Duck/Memphis/928/74).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=11367;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212520; PubMed=8460490;
 RA Saito T., Kawoka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
 RT viruses."
 RT Virology 193:868-876(1993).
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitates
 CC the mobility of the virus to and from the site of infection.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 CC SPIKE ON THE SURFACE OF THE VIRION.
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
 CC -----
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 CC -----
 CC EMBL: L06575; AAA43404.1; -.
 DR HSBP; P06820; 2BRT.
 DR InterPro: IPR001860; Glyco_hydro_34.
 DR Pfam: PF00064; neu; 1.
 DR ProDom: PD000431; Glyco_hydro_34; 1.
 DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
 KM TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 FT ACT SITE 273 273 BY SIMILARITY.
 FT ACT SITE 275 275 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 470 AA; 52146 MW; 30F5F9F3E364C1F49 CRC64;

QY 1 ADMSW 5
 DB 453 ADMSW 457

RESULT 6
 NRAM_IADU3
 ID NRAM_IADU3 STANDARD; PRT; 470 AA.

AC 007574;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).

GN NA.
 OS Influenza A virus (strain A/Duck/Ukraine/1/53).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 RX MEDLINE=93212520; PubMed=8460490;
 RN NCB1_Taxid=11374;
 RP SEQUENCE FROM N.A.
 RA Saito T., Kawasaka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
 RT viruses.";
 RL Virology 193:868-876(1993).
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitate
 CC the mobility of the virus to and from the site of infection.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 CC SPIKE ON THE SURFACE OF THE VIRION.
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.

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CC EMBL; L06576; AAA16234.1; -
 CC HSSP; P06820; 28AT.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 KW Hydroxylase; Glycoprotein; Transmembrane.
 FT TRANSMEM 37 ANCHOR (BY SIMILARITY).
 FT DOMAIN 7 HEAD OF NEURAMINIDASE.
 FT CARBOHYD 38
 FT CARBOHYD 88
 FT ACT_SITE 273 PROBABLE.
 FT ACT_SITE 275
 FT CARBOHYD 46 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 54 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 84 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 144 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 398 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 470 AA; 51960 MW; B46D54A03AC84CCE CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
 DB 453 ADMSW 457

RESULT 7
 NRAM_IAGFN
 ID NRAM_IAGFN STANDARD; PRT; 470 AA.

AC 007574;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).

GN NA.
 OS Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 RX MEDLINE=93212520; PubMed=8460490;
 RN NCB1_Taxid=38963;
 RP SEQUENCE FROM N.A.
 RA Saito T., Kawasaka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
 RT viruses.";
 RL Virology 193:868-876(1993).
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitate
 CC the mobility of the virus to and from the site of infection.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 CC SPIKE ON THE SURFACE OF THE VIRION.
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.

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CC EMBL; L06584; AAA43428.1; -
 CC HSSP; P06820; 28AT.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 KW Hydroxylase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 HEAD OF NEURAMINIDASE.
 FT CARBOHYD 38
 FT CARBOHYD 88
 FT ACT_SITE 273 BY SIMILARITY.
 FT ACT_SITE 275
 FT CARBOHYD 46 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 54 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 84 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 144 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 293 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 398 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 470 AA; 52348 MW; D3B2AAC0159FB66 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
 DB 453 ADMSW 457

RESULT 8
 NRAM_IAGHD
 ID NRAM_IAGHD STANDARD; PRT; 470 AA.
 AC 007577;

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DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DN Neuraminidase (EC 3.2.1.18).
OS Influenza A virus (strain A/Herring gull/DE/677/88).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38964;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawacka Y., Webster R.G.;
RT "Phylogenetic analysis of the NA neuraminidase gene of Influenza A
RT viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: L06585; AAA3368.1; -
DR HSSP: P06820; 2B4T.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KM Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52265 MW; 28AF0B75EB0539B7 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 9
NRAM_IAMJI STANDARD; PRT; 470 AA.
AC 007578;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).

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GN NA.
OS Influenza A virus (strain A/Equine/J111n/1/89).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11401;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawacka Y., Webster R.G.;
RT "Phylogenetic analysis of the NA neuraminidase gene of Influenza A
RT viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: L06579; AAA3374.1; -
DR HSSP: P06820; 2B4T.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KM Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52234 MW; CES0B21050A37668 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 10
NRAM_IAMAE STANDARD; PRT; 470 AA.
AC 007583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DN Neuraminidase (EC 3.2.1.18).
OS Influenza A virus (strain A/Mallard/Edmonton/220/90).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.

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OX NCBI_TaxID=38965;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawakita Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
   virus."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
   chains of the host cell surface proteins and from the viral
   envelope. Such a reaction prevents self-aggregation and facilitate
   the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
   alpha-(2-8)-glycosidic linkages of terminal sialic residues in
   oligosaccharides, glycoproteins, glycolipids, colominic acid and
   synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
   SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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   or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06586; AAA4369.1; -
DR HSRP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
FT DOMAIN 7 38 ANCHOR (BY SIMILARITY).
FT 39 88 HYPERVARIABLE STALK REGION.
FT 89 470 HEAD OF NEURAMINIDASE.
FT 273 273 BY SIMILARITY.
FT ACT_SITE 273 273
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 557630C3E1F2765 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 11
NRAM_IATKL STANDARD; PRT; 470 AA.
ID NRAM_IATKL
AC Q07585;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minnesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;

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RA Saito T., Kawakita Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
   virus."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
   chains of the host cell surface proteins and from the viral
   envelope. Such a reaction prevents self-aggregation and facilitate
   the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
   alpha-(2-8)-glycosidic linkages of terminal sialic residues in
   oligosaccharides, glycoproteins, glycolipids, colominic acid and
   synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
   SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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CC -----
DR EMBL; L06588; AAA43410.1; -
DR HSRP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
FT DOMAIN 7 38 ANCHOR (BY SIMILARITY).
FT 39 88 HYPERVARIABLE STALK REGION.
FT 89 470 HEAD OF NEURAMINIDASE.
FT 273 273 BY SIMILARITY.
FT ACT_SITE 273 273
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52352 MW; D8573742ABF1868 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 12
IKKA_HUMAN STANDARD; PRT; 745 AA.
ID IKKA_HUMAN
AC O15111; Q14666; Q13132; Q92467.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
DE (I-kappa-B kinase alpha) (IKBA) (IKK-alpha) (IKK-A) (I-kappa-B kinase)
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitin
   kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
GN CHUK OR IKKA.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RC TISSUE=T-cell;
RX MEDLINE=97386461; PubMed=9244310;

```


FT MUTAGEN 176 176 ACTIVITY.
 FT MUTAGEN 179 179 S->E: FULL ACTIVATION.
 FT MUTAGEN 180 180 T->A: NO CHANGE IN PHOSPHORYLATION.
 FT CONFLICT 543 543 S->A: NO CHANGE IN PHOSPHORYLATION.
 FT CONFLICT 604 604 E->G (IN REF. 2).
 FT CONFLICT 604 604 L->R (IN REF. 5).
 FT CONFLICT 679 680 TS->AY (IN REF. 5).
 FT CONFLICT 684 684 P->A (IN REF. 3 AND 5).
 FT CONFLICT 686 687 TS->DL (IN REF. 5).
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 739 DMSWL 743

Qy 2 DMSWL 6
 |||||

RESULT 13
 ID IKKA MOUSE STANDARD; PRT; 745 AA.
 AC Q60680; Q9D2X3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.-)
 DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (Ikkappa kinase)
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
 kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1KA).
 GN CHUK OR IKKA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId:10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/c;
 RX MEDLINE=9604444; PubMed=7558004;
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 chromosome 10 and mouse chromosome 19.";
 RT Genomics 27:348-351(1995).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/c;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connolly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RT Cell. Biol. Res. 41:537-549(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamana S.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glast C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai J., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
 RA Blake J., Botfield D., Boujunga N., Carminci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gaitanaris M.,
 RA Guentlich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaserts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaka S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=20198447; PubMed=10735566;
 RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R.,
 RA Gelezianus R., Marcu K.B.;
 RT "Functional isoforms of Ikkappa kinase alpha (IKKalpha) lacking
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
 RT IKKbeta have different activation requirements.";
 RT Mol. Cell. Biol. 20:2635-2649(2000).
 RL [5]
 RP PHOSPHORYLATION BY MAP3K14/NIK.
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of Ikkappa kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RP IKKA-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhaese M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of Ikkappa kinase activity through
 RT IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [7]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [8]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-gamma/MEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1:
 CC IsoId=Q60680-1; Sequence=Displayed;
 CC Name=2; Synonym=Delta LH;
 CC IsoId=Q60680-2; Sequence=VSP_004866; VSP_004867;
 CC Name=3; Synonym=Delta H;
 CC IsoId=Q60680-3; Sequence=VSP_004868; VSP_004869;
 CC TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
 CC 3 are expressed predominantly in brain and T-lymphocytes.
 CC -1- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
 CC E11, E15 and E17 days. In the limb development, its expression
 CC predominates in the limb buds at E12.5 day.
 CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC IKAPPAB KINASE SUBFAMILY.

CC -----

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CC -----

DR EMBL; U12473; AAC52589.1; -

DR EMBL; AK018671; BAB31335.1; -

DR PIR; I49101; I49101.

DR HSSP; O63450; I4A06.

DR MGD; MGI:99484; Chuk.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR Pfam; PF00069; kinase.1.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot_kinase.1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP.1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST.1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM.1.

KM Transferase; Serine/threonine-protein kinase; ATP-binding;

PT Phosphorylation; Alternative splicing.

PT DOMAIN 15 300 PROTEIN_KINASE.

PT DOMAIN 455 476 LEUCINE_ZIPPER (POTENTIAL).

PT NE_BIND 21 29 MEMO-BINDING.

PT BINDING 44 44 ATP (BY SIMILARITY).

PT ACT_SITE 144 144 ATP (BY SIMILARITY).

PT MOD_RES 23 23 PHOSPHORYLATION (BY PKA/AKT1)

PT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14)

PT VARSPPLIC 452 471 MSLRYNANLTQKTKTLIS -> IFRKAVKYSMERNGRKH

PT VARSPPLIC 472 745 SLP (in isoform 2).

PT VARSPPLIC 577 584 Missing (in isoform 2).

PT VARSPPLIC 585 745 Missing (in isoform 3).

PT CONFLICT 236 236 /Frid=VSP_004869.

PT CONFLICT 400 400 K -> E (IN REF. 3).

PT CONFLICT 400 400 S -> Y (IN REF. 3).

PT SEQUENCE 745 AA; 84728 MW; 3FEF582APF92233 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 745;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6

Db 739 DMSWL 743

RESULT 14

IKKB HUMAN STANDARD; PRT; 756 AA.

AC 014920; 075327;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)

DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase

DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).

GN IKKB OR IKKB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RX SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.

RC TISSUE=Cervical carcinoma;

RA MEDLINE=98008813; PubMed=9346484;

RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,

RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;

RT "IKK-1 and IKK-2: cytokine-activated Ikkappa kinases essential for

RT NF-kappa activation.";

RL Science 278:860-866 (1997).

RN [2]

RX SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.

RC MEDLINE=98008814; PubMed=9346485;

RA Moronics J.D., Gao X., Cao Z., Roche M., Goeddel D.V.;

RT "Ikkappa kinase-beta: NF-kappa activation and complex formation with

RT Ikkappa kinase-alpha and NIK.";

RL Science 278:866-869 (1997).

RN [3]

RX SEQUENCE FROM N.A.

RC TISSUE=Heart;

RA MEDLINE=99032998; PubMed=9813230;

RA Hu M.C.-T., Wang Y.-P.;

RT "Ikkappa kinase-alpha and -beta genes are coexpressed in adult and

RT embryonic tissues but localized to different human chromosomes.";

RL Gene 222:31-40 (1998).

RN [4]

RX SEQUENCE FROM N.A., AND GENE MAPPING.

RC MEDLINE=98438415; PubMed=9763654;

RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;

RT "Assignment of Ikkappa kinase beta (IKKB) to human chromosome band

RT 8p12--p11 by in situ hybridization.";

RL Cytogenet. Cell Genet. 82:32-33 (1998).

RN [5]

RX SEQUENCE OF 1-256 FROM N.A.

RC TISSUE=Lung;

RA MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner K.H., Schenker C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,

RA Bosak S.A., Mesman P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,

RA Villalon D.K., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,

RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [6]

RX IKK PHOSPHORYLATION.

RC MEDLINE=99038238; PubMed=9819420;

RA Nemoto S., Didonato J.A., Lin A.;

RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein

RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";

RL Mol. Cell. Biol. 18:7336-7343 (1998).

RN [7]

RX REVIEW.

RC MEDLINE=20178139; PubMed=10712233;

RA Jobin C., Sarcor R.B.;

RT "The I kappa B/NF-kappa B system: a key determinant of mucosal

RT inflammation and protection.";

RL Am. J. Physiol. 278:C451-C462 (2000).

RN [8]

RX IDENTIFICATION IN A COMPLEX WITH CREBBP, NCOA2, NCOA3, IKKA AND IKKB.

RC MEDLINE=21968797; PubMed=11971985;

RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,

RA O'Malley B.W.:
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
 activity by I kappa B kinase.";
 RL Mol. Cell. Biol. 22:3549-3561(2002).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 the dissociation of the inhibitor/NF-kappa-B complex and
 ultimately the degradation of the inhibitor. Also phosphorylates
 NCOA3 (By similarity).
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 also bind to MEK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50
 complex. Phosphorylated IKK-alpha is further released from the
 complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
 and CREBBP.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
 muscle, kidney, pancreas, spleen, thymus, prostate, testis and
 peripheral blood.
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPBAP KINASE SUBFAMILY.

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 or send an email to license@ebi.ac.uk).

 CC EMBL, AF028684; AAC31860.1; -
 DR EMBL, AF080158; AAD08997.1; -
 DR EMBL, AF031416; AAC64675.1; -
 DR EMBL, BC006231; AAH06231.1; -
 DR HSSP, O63450; 1A06.
 DR GeneW: HGNC:5960; IKKB.
 DR MIM: 603258; -
 DR GO, GO:0005737; C:cytoplasm; NAS.
 DR GO, GO:0005524; F:ATP binding activity; NAS.
 DR GO, GO:0004674; F:protein serine/threonine kinase activity; NAS.
 DR GO, GO:0016563; F:transcriptional activator activity; NAS.
 DR GO, GO:0004689; P:protein amino acid phosphorylation; NAS.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR002290; Ser Thr kinase.
 DR Pfam: PF00069; kinase; 1.
 DR Pfam: PF00240; ubiquitin; 1.
 DR ProDom: PD000001; Prot kinase; 1.
 DR PROSITE, PS00107; PROTEIN KINASE_ATP; FALSE_NEG.
 DR PROSITE, PS00108; PROTEIN KINASE_ST; 1.
 DR PROSITE, PS50011; PROTEIN KINASE_DOM; 1.
 KM Transferrase: Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT 458 479 LECTINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION.
 FT MOD_RES 181 181 PHOSPHORYLATION.
 FT MOD_RES 181 181 K->A: LOSS OF KINASE ACTIVITY AND NO
 EFFECT ON BINDING TO NIK.
 FT MUTAGEN 44 44 S->A: DECREASE OF ACTIVITY.
 FT MUTAGEN 177 177 S->E: FULL ACTIVATION.
 FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
 FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
 FT CONFLICT 231 255 HSKRQKSEVIVSEDLNFTVP -> CWRMPETVAHS
 FT CONFLICT 231 255 CNSTLCGRGRT (IN REF. 5).
 FT CONFLICT 425 425 Q -> H (IN REF. 1).
 SQ SEQUENCE 756 AA; 86563 MW; F9CADP671AE9E14E CRC64;

Query Match 90.0%; Score 36; DB 1; Length 756;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DMSWL 6
 DB 738 DMSWL 742
 RESULT 15
 IKKB MOUSE STANDARD; PRT; 757 AA.
 AC 088351; Q9RLG6;
 DT 16-OCT-2001 (Ref. 40, Created)
 DT 16-OCT-2001 (Ref. 40, Last sequence update)
 DT 28-FEB-2003 (Ref. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIX).
 GN IKKB OR IKK2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. AND PHOSPHORYLATION BY MEK1.
 RC STRAIN=C57BL/6; TISSUE=Spleen;
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 Okumura K.;
 RT "Differential regulation of Ikkapab kinase alpha and beta by two
 upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 protein kinase/ERK kinase kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
 RT "Murine IKK kinase-B, a developmentally regulated protein kinase that
 constitutively phosphorylates serine residues of Ikb.";
 RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE=99455228; PubMed=10523628;
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 pathway activates Ikkapab kinases (IKK-alpha/beta) and IKK-beta is a
 developmentally regulated protein kinase.";
 RL Oncogene 18:3514-3524(1999).
 RN [4]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Iin A.;
 RT "Coordinate regulation of Ikkapab kinases by mitogen-activated protein
 kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [5]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 the dissociation of the inhibitor/NF-kappa-B complex and
 ultimately the degradation of the inhibitor. Also phosphorylates
 NCOA3.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 also bind to MEK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50
 complex. Phosphorylated IKK-alpha is further released from the
 complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB

```

CC      and CREBBP (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
CC      -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
CC      the mouse embryo, at E9.5 day its expression begins to be
CC      localized to the brain, neural ganglia, neural tube, and in liver
CC      at E12.5 day. At E15.5 day, the expression is further restricted
CC      to specific tissues of the embryo.
CC      -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
CC      Weakly autophosphorylated.
CC      -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      IKAPPAB KINASE SUBFAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF026524; AAC23557.1; -.
DR      EMBL; AF086910; AAD52095.1; -.
DR      HSSP; 063450; 1A06.
DR      MGD; MGI:1338071; Ikbb.
DR      InterPro; IPR000719; Prot_kinase.
DR      InterPro; IPR002290; Ser_thr_kinase.
DR      InterPro; IPR001245; Tyr_kinase.
DR      Pfam; PF00069; kinase; 1.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW      transferase; Serine/threonine-protein kinase; ATP-binding;
KW      phosphorylation.
FT      DOMAIN 15 300 PROTEIN KINASE.
FT      DOMAIN 458 479 LUCICINE-ZIPPER (POTENTIAL).
FT      DOMAIN 737 742 NEMO-BINDING.
FT      NP_BIND 21 29 ATP (BY SIMILARITY).
FT      BINDING 44 44 ATP (BY SIMILARITY).
FT      ACT_SITE 145 145 BY SIMILARITY.
FT      MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT      MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
FT      MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
FT      CONFLICT 56 56 N -> D (IN REF. 2).
FT      CONFLICT 343 343 N -> E (IN REF. 2).
FT      CONFLICT 356 356 K -> B (IN REF. 2).
FT      CONFLICT 390 390 L -> F (IN REF. 2).
FT      CONFLICT 406 406 P -> Q (IN REF. 2).
FT      CONFLICT 573 573 K -> R (IN REF. 2).
FT      CONFLICT 736 757 TLDMSWLQWDEBERCSLEQACD -> VTA (IN REF.
SQ      SEQUENCE 757 AA; 86690 MW; FED962F095449CSE CRC64;
Query Match 90.0%; Score 36; DB 1; Length 757;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      2 DMSWL 6
DB      738 DMSWL 742

```

Search completed: February 18, 2004, 14:28:03
 Job time : 3.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-4

Perfect score: 40

Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR76:*
2: PIR12:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	132	2	mel-13a protein -
2	37	92.5	1329	2	conserved hypothetical
3	36	90.0	122	2	Ig V-D-J region (M
4	36	90.0	745	1	conserved helix-lo
5	36	90.0	747	2	hypothetical prote
6	36	90.0	803	2	hypothetical prote
7	36	90.0	889	2	Tomb-dependent rec
8	36	90.0	915	2	cellulase (EC 3.2.
9	36	90.0	1039	2	cellulase (EC 3.2.
10	36	90.0	1139	2	AT0379
11	36	90.0	1275	2	TI8556
12	35	87.5	616	2	C69226
13	35	87.5	1202	2	S71424
14	35	87.5	1203	1	A47501
15	35	87.5	1205	1	A38943
16	35	87.5	1409	2	S74916
17	35	87.5	1879	2	S74915
18	34	85.0	214	2	G83692
19	34	85.0	220	2	D64316
20	34	85.0	248	2	T44932
21	34	85.0	276	2	B75337
22	34	85.0	282	1	DGEEMA
23	34	85.0	282	2	B90988
24	34	85.0	282	2	G85833
25	34	85.0	283	2	A86923
26	34	85.0	287	2	C90290
27	34	85.0	289	2	A10770
28	34	85.0	304	1	B70696
29	34	85.0	368	2	AF1434

30	34	85.0	368	2	AA3-600 quinol oxi
31	34	85.0	410	2	lycopene cyclase -
32	34	85.0	529	2	probable GMP synth
33	34	85.0	549	2	hypothetical prote
34	34	85.0	578	2	restriction modifi
35	34	85.0	590	2	GMP synthase (gluc
36	34	85.0	623	2	type I restriction
37	34	85.0	1144	1	A43271
38	34	85.0	1147	1	nitric-oxide synth
39	34	85.0	1147	1	nitric-oxide synth
40	34	85.0	1147	1	nitric-oxide synth
41	34	85.0	1147	1	nitric-oxide synth
42	34	85.0	1147	2	nitric-oxide synth
43	34	85.0	1147	2	nitric-oxide synth
44	34	85.0	1147	2	nitric-oxide synth
45	34	85.0	1147	2	nitric-oxide synth

ALIGNMENTS

RESULT 1
mel-13a protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C/Accession: S65785
R/Retain: O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.
Biochem. Biophys. Acta 1305, 109-112, 1996
A/Title: Cloning and characterization of two transcripts generated from the mel-13 gen
A/Reference number: S65785; MUID:96180310; PMID:8597592
A/Accession: S65785
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-132 <TERT>
A/Cross-references: EMBL:U35309
C/Genetics:
A/Gene: mel-13
C/Superfamily: mouse mel-13a protein
C/Keywords: alternative splicing

Query Match 92.5% Score 37; DB 2; Length 132;
Best Local Similarity 83.3% Pred. No. 28;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;
Q/ 1 ADMSWL 6
: |||||
Db 57 SDMSWL 62

RESULT 2
DB7226
conserved hypothetical protein ML2535 [imported] - Mycobacterium leprae
C/Species: Mycobacterium leprae
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C/Accession: DB7226
R/Retain: S.T.; Sigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; I
R.; Davies, R.M.; Devlin, K.; Dutchy, S.; Fellwell, T.; Fraser, A.; Hamlin, N.; Holroy
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A/Author: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; I
A/Title: Massive gene decay in the leprosy bacillus.
A/Reference number: A86909; MUID:21128732; PMID:11234002
A/Accession: DB7226
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1329 <SNO>
A/Cross-references: GB:AL450380; NID:913093796; PIDN:CAC32066.1; GSPDB:GN00147
C/Genetics:
A/Gene: ML2535
Query Match 92.5% Score 37; DB 2; Length 1329;
Best Local Similarity 83.3% Pred. No. 2.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ADMSWL 6
 : |||||
 Db 260 DMSWL 265

RESULT 3

569909
 Ig V-D-J region (MS) - human
 C/Species: Homo sapiens (man)
 C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C/Accession: S69909
 R/Sakota, S.; Hamblin, T.; Oclet, D.G.; Stevenson, F.K.
 A/Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi-
 A/Reference number: S69909; MUID:9433515; PMID:8057663
 A/Accession: S69909
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-122 <SAH>
 A/Cross-references: EMBL:Z33399; NID:9871348; PIDN:CAA63850.1; PID:9871349
 A/Note: the sequence of residues 112-122 and the corresponding nucleic acid sequence are
 F:15-97/Domain: Immunoglobulin homology <IMM>

Query Match 90.0%; Score 36; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6
 : |||||
 Db 33 DMSWL 37

RESULT 4

149101
 conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: I49101
 R/Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
 A/Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome
 A/Reference number: I49101; MUID:96044444; PMID:7558004
 A/Accession: I49101
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-745 <RES>
 A/Cross-references: EMBL:U12473; NID:91079492; PIDN:AAC52589.1; PID:91079493
 C/Genetics:
 A/Gene: CHUK
 C/Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homolo
 C/Keywords: ATP, phosphotransferase
 F:13-283/Domain: protein kinase homology <KIN>

Query Match 90.0%; Score 36; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 2,3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6
 : |||||
 Db 739 DMSWL 743

RESULT 5

D70802
 hypothetical protein RV3870 - Mycobacterium tuberculosis (strain H37RV)
 C/Species: Mycobacterium tuberculosis
 C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C/Accession: D70802
 R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 ; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squires, S.
 Nature 393, 537-544, 1998
 A/Authors: Squires, R.; Suleston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom
 A/Reference number: A70500; MUID:9825987; PMID:9634230
 A/Accession: D70802
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-747 <COL>
 A/Cross-references: GB:AL022120; GB:AL123456; NID:93261558; PIDN:CAA17962.1; PID:92960
 A/Experimental source: strain H37RV
 C/Genetics:
 A/Gene: RV3870

Query Match 90.0%; Score 36; DB 2; Length 747;
 Best Local Similarity 100.0%; Pred. No. 2,3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6
 : |||||
 Db 267 DMSWL 271

RESULT 6

F90485
 hypothetical protein S803039 [imported] - Sulfolobus solfataricus
 C/Species: Sulfolobus solfataricus
 C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
 C/Accession: F90485
 R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Anayez, M.J.; Cha
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,
 arett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.
 submitted to Genbank, April 2001
 A/Description: Sulfolobus solfataricus complete genome.
 A/Reference number: A99139
 A/Accession: F90485
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-803 <KUR>
 A/Cross-references: GB:AB006641; NID:913816440; PIDN:AAK43141.1; GSPDB:GN00155
 C/Genetics:
 A/Gene: S803039

Query Match 90.0%; Score 36; DB 2; Length 803;
 Best Local Similarity 100.0%; Pred. No. 2,4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6
 : |||||
 Db 540 DMSWL 544

RESULT 7

E87304
 TonB-dependent receptor [imported] - Caulobacter crescentus
 C/Species: Caulobacter crescentus
 C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C/Accession: E87304
 R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kol
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A/Title: Complete Genome Sequence of Caulobacter crescentus.
 A/Reference number: A87249; MUID:21173698; PMID:11259647
 A/Accession: E87304
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-889 <STO>
 A/Cross-references: GB:AB005673; NID:913421615; PIDN:AAK22433.1; GSPDB:GN00148
 C/Genetics:
 A/Gene: CC0446

Query Match 90.0%; Score 36; DB 2; Length 889;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
|||||

Db 618 ADMSW 622

RESULT 8

A:Accession: A43802
C:Cellulase (EC 3.2.1.4) / cellulose 1,4-beta-cellulobiosidase (EC 3.2.1.91) - Caldocellum
N:Alternative names: endo-1,4-beta-glucanase
C:Species: Caldocellum saccharolyticum
C:Date: 30-Jan-1993 #sequence_revision 30-Sep-1993 #text_change 10-Jul-1998
R:Saul, D.J.; Williams, L.C.; Grayling, R.A.; Chamley, L.W.; Love, D.R.; Bergquist, P.L.
Appl. Environ. Microbiol. 56, 3117-3124, 1990
A:Title: celB, a gene coding for a bifunctional cellulase from the extreme thermophile
A:Reference number: A43802; MUID:91136262; PMID:2126700
A:Accession: A43802
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-915 <SAU>
A:Cross-references: EMBL:X13602
C:Function:
A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce
A:Pathway: cellulose degradation
C:Superfamily: Streptomyces endo-1,4-beta-xyylanase A homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:20-320/Domain: Streptomyces endo-1,4-beta-xyylanase A homology <SXY>

Query Match 90.0%; Score 36; DB 2; Length 915;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
|||||

Db 469 DMSWL 473

RESULT 9

A:Accession: S02711
C:Cellulase (EC 3.2.1.4) precursor - Caldocellum saccharolyticum
N:Alternative names: endo-1,4-beta-glucanase
M:Contains: cellulase (EC 3.2.1.4); cellulose 1,4-beta-cellulobiosidase (EC 3.2.1.91)
C:Species: Caldocellum saccharolyticum
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
R:Saul, D.J.; Williams, L.C.; Love, D.R.; Chamley, L.W.; Bergquist, P.L.
Nucleic Acids Res. 17, 439, 1989
A:Title: Nucleotide sequence of a gene from Caldocellum saccharolyticum encoding for exc
A:Reference number: S02711; MUID:8908398; PMID:2789517
A:Accession: S02711
A:Molecule type: DNA
A:Residues: 1-1039 <SAU>
A:Cross-references: EMBL:X13602; NID:g40645; PIDD:CAA1936.1; PIDD:g40646
C:Genetics:
A:Gene: celB
C:Function:
A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce
A:Pathway: cellulose degradation
C:Superfamily: Streptomyces endo-1,4-beta-xyylanase A homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-28/Domain: signal sequence #status predicted <SIG>
F:9-1039/Product: cellulase #status predicted <MAT>
F:12-373/Domain: Streptomyces endo-1,4-beta-xyylanase A homology <SXY>

Query Match 90.0%; Score 36; DB 2; Length 1039;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
|||||

Db 469 DMSWL 473

RESULT 10

A:Accession: A10379
C:Probable potassium efflux system YPO3129 [imported] - Yersinia pestis (strain CO92)
N:Alternative names: Yersinia pestis
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
R:Parthill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.J.
deno-Parraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: A80001; MUID:21470413; PMID:11586360
A:Accession: A10379
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1139 <KIR>
A:Cross-references: GB:AUS90842; PIDD:CA092364.1; PIDD:g15981067; GSPDB:GN00175
C:Genetics:
A:Gene: YPO3129

Query Match 90.0%; Score 36; DB 2; Length 1139;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
|||||

Db 469 DMSWL 473

Db 540 DMSWL 544

RESULT 11

A:Accession: T18556
C:O-antigen biosynthesis protein homolog rfbC - Myxococcus xanthus
N:Alternative names: Myxococcus xanthus
C:Species: Myxococcus xanthus
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R:Guo, D.; Bowden, M.G.; Pershad, R.; Kaplan, H.B.
J. Bacteriol. 178, 1631-1639, 1996
A:Title: The Myxococcus xanthus rfbABC operon encodes an ATP-binding cassette transport
A:Reference number: T18556; MUID:96198166; PMID:8626291
A:Accession: T18556
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1275 <GDO>
A:Cross-references: EMBL:U36795; NID:g1235659; PIDD:g1235662; PIDD:AB05019.1
C:Genetics:
A:Note: rfbC

Query Match 90.0%; Score 36; DB 2; Length 1275;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSW 6
|||||

Db 348 ADMSW 353

RESULT 12

A:Accession: C69226
C:Type I restriction modification enzyme, subunit M - Methanobacterium thermoautotrophic
N:Alternative names: Methanobacterium thermoautotrophicum
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
i; Liu, D.; Spadofora, R.; Vicaire, R.; Wang, Y.; Mierzbowski, J.; Gibson, R.; Jiwani, N.
Kt.S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: C69226
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

F:186/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 87.5%; Score 35; DB 1; Length 1203;

Best Local Similarity 66.7%; Pred. No. 5.2e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6

DB 443 ADMAMI 448

RESULT 15

A38943

nitric-oxide synthase (EC 1.14.13.39), endothelial - bovine

N.Alternate names: ECNOS; nitric-oxide synthase type III

C.Species: Bos primigenius taurus (cattle)

C.Date: 02-Jun-1995 #sequence_revelation 02-Jun-1995 #text_change 03-Mar-2000

C.Accession: A38943; A46033; A45945; A42841; A45946; A38944

R.Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.

Submitted to GenBank, July 1992

A.Reference number: A38943

A.Accession: A38943

A.Molecule type: mRNA

A.Residues: 1-1205 <LAM1>

A.Cross-References: GB:M89952; NID:G162976; PIDs:AAA30494.1; PID:G162977

A.Experimental source: aortic endothelial cells

R.Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.

Proc. Natl. Acad. Sci. U.S.A. 89, 6348-6352, 1992

A>Title: Endothelial nitric oxide synthase: molecular cloning and characterization of a

A.Reference number: A46033; MIMD:92335295; PMID:1378626

A.Accession: A46033

A>Status: nucleic acid sequence not shown

A.Molecule type: mRNA

A.Residues: 1-860, 'T', 862-1205 <LAM2>

A.Cross-References: GB:M89952; NID:G162976

A.Experimental source: endothelial

A>Note: Sequence extracted from NCBI backbone (NCBIP:108720)

R.Nishida, K.; Harrison, D.G.; Navas, J.P.; Fisher, A.A.; Dockery, S.P.; Nerem, R.M.; Al

J. Clin. Invest. 90, 2092-2096, 1992

A>Title: Molecular cloning and characterization of the constitutive bovine aortic Endoth

A.Reference number: A45945; MIMD:9305452; PMID:1385480

A.Accession: A45945

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-1205 <NIS>

A.Cross-References: GB:M99057; NID:G163421; PIDs:AAA30667.1; PID:G163422

R.Seger, W.C.; Harrison, J.K.; Barber, C.M.; Zeng, D.; Durieux, M.B.; D'Angelo, D.D.; Ly

J. Biol. Chem. 267, 15274-15276, 1992

A>Title: Molecular cloning and expression of a cDNA encoding endothelial cell nitric oxi

A.Reference number: A42841; MIMD:92348367; PMID:1379225

A.Accession: A42841

A>Status: nucleic acid sequence not shown

A.Molecule type: mRNA

A.Residues: 1-51, 'N', 53-99, 'R', 101-147, 'M', 149-164, 'I', 166-317, 'GA', 320, 'HTGVVRGP', 329-3

'K', 517-692, 'G', 694-740, 'A', 742-753, 'N', 755-799, 'N', 801-803, 'SA', 806-856, 'V', 858-906, 'LV

A.Experimental source: aortic endothelial cells

A>Note: Sequence extracted from NCBI backbone (NCBIP:109564); contains a number of typog

A.Accession: A45946

A>Status: nucleic acid sequence not shown

A.Molecule type: mRNA

A.Residues: 1-99, 'R', 101-164, 'I', 166-317, 'GA', 320, 'HTGVVRGP', 329-454, 'Y', 456-458, 'P', 460

A.Cross-References: GB:M95674; NID:G163426; PIDs:AAA30669.1; PID:G163427

A.Experimental source: aortic endothelial cells

A>Note: Submitted to GenBank, August 1992

A>Note: GenBank entry BOVNO5, release 103.0, has a typographical error in the reference

C.Function:

A.Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH

C.Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct

C.Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN

F:493-512/Region: calmodulin binding #status predicted

F:522-1161/Domain: NADPH-ferrihemoprotein reductase homology <FEH>

F:524-705/Domain: flavodoxin homology <FLX>

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:3/Modified site: aspartic acid (Asn) #status predicted

F:186/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 87.5%; Score 35; DB 1; Length 1205;

Best Local Similarity 66.7%; Pred. No. 5.2e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6

DB 445 ADMAMI 450

Search completed: February 18, 2004, 14:38:36
Job time : 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-4

Perfect score: 40

Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	10	US-09-847-940B-4
2	40	100.0	6	11	US-09-847-946A-4
3	40	100.0	6	11	US-09-847-946A-39
4	40	100.0	6	11	US-09-847-946A-51
5	40	100.0	7	11	US-09-847-946A-55
6	40	100.0	7	11	US-09-847-946A-48
7	40	100.0	8	11	US-09-847-946A-47
8	40	100.0	9	11	US-09-847-946A-50
9	40	100.0	9	11	US-09-847-946A-53
10	40	100.0	9	11	US-09-847-946A-54
11	40	100.0	10	11	US-09-847-946A-49
12	40	100.0	10	11	US-09-847-946A-52
13	40	100.0	11	11	US-09-847-946A-46
14	40	100.0	11	11	US-10-171-311-234
15	40	100.0	501	15	Sequence 234, App

16	38	95.0	312	12	US-10-306-762-23	Sequence 23, App1
17	38	95.0	605	15	US-10-156-761-9070	Sequence 9070, App
18	36	90.0	6	10	US-09-847-940B-2	Sequence 2, App11
19	36	90.0	6	11	US-09-847-946A-2	Sequence 2, App11
20	36	90.0	6	11	US-09-847-946A-33	Sequence 33, App1
21	36	90.0	6	11	US-09-847-946A-41	Sequence 41, App1
22	36	90.0	6	11	US-09-847-946A-73	Sequence 73, App1
23	36	90.0	7	11	US-09-847-946A-37	Sequence 37, App1
24	36	90.0	7	11	US-09-847-946A-77	Sequence 77, App1
25	36	90.0	8	11	US-09-847-946A-30	Sequence 30, App1
26	36	90.0	8	11	US-09-847-946A-38	Sequence 38, App1
27	36	90.0	8	11	US-09-847-946A-70	Sequence 70, App1
28	36	90.0	8	11	US-09-847-946A-78	Sequence 78, App1
29	36	90.0	9	11	US-09-847-946A-29	Sequence 29, App1
30	36	90.0	9	11	US-09-847-946A-32	Sequence 32, App1
31	36	90.0	9	11	US-09-847-946A-35	Sequence 35, App1
32	36	90.0	9	11	US-09-847-946A-36	Sequence 36, App1
33	36	90.0	9	11	US-09-847-946A-69	Sequence 69, App1
34	36	90.0	9	11	US-09-847-946A-72	Sequence 72, App1
35	36	90.0	9	11	US-09-847-946A-75	Sequence 75, App1
36	36	90.0	9	11	US-09-847-946A-76	Sequence 76, App1
37	36	90.0	10	11	US-09-847-946A-31	Sequence 31, App1
38	36	90.0	10	11	US-09-847-946A-34	Sequence 34, App1
39	36	90.0	10	11	US-09-847-946A-71	Sequence 71, App1
40	36	90.0	10	11	US-09-847-946A-74	Sequence 74, App1
41	36	90.0	11	11	US-09-847-946A-28	Sequence 28, App1
42	36	90.0	11	11	US-09-847-946A-68	Sequence 68, App1
43	36	90.0	11	11	US-09-847-946A-132	Sequence 132, App
44	36	90.0	11	11	US-09-847-946A-140	Sequence 140, App
45	36	90.0	13	11	US-09-847-946A-143	Sequence 143, App

ALIGNMENTS

RESULT 1
US-09-847-940B-4
; Sequence 4, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPT-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR APPLICATION NUMBER: 2001-05-02
; PRIOR FILING DATE: 09/643,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-4

Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
|||||
DB 1 ADMSWL 6

RESULT 2
US-09-847-946A-4
; Sequence 4, Application US/09847946A
; Publication No. US20030054959A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

```

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-4
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Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 ADMSWL 6
        |||||
Db      1 ADMSWL 6
```

```

RESULT 3
US-09-847-946A-39
; Sequence 39, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-39
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```

Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 ADMSWL 6
        |||||
Db      1 ADMSWL 6
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```

RESULT 4
US-09-847-946A-51
; Sequence 51, Application US/09847946A
; Publication No. US20030054999A1
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; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-51
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```

Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 ADMSWL 6
        |||||
Db      1 ADMSWL 6
```

```

RESULT 5
US-09-847-946A-55
; Sequence 55, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-55
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```

Query Match          100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ADMSWL 6
        |||||
Db      1 ADMSWL 6
```

```

RESULT 6
```

US-09-847-946A-48
; Sequence 48, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-48

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6
Db 3 ADMSWL 8

RESULT 7
US-09-847-946A-56
; Sequence 56, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-56

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6
Db 1 ADMSWL 6

RESULT 8
US-09-847-946A-47
; Sequence 47, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-47

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6
Db 1 ADMSWL 6

RESULT 9
US-09-847-946A-50
; Sequence 50, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-50

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 ADMSWL 6

RESULT 10

US-09-847-946A-53
Sequence 53, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 53
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
US-09-847-946A-53

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 3 ADMSWL 8

RESULT 11

US-09-847-946A-54
Sequence 54, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
US-09-847-946A-54

Query Match 100.0%; Score 40; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 ADMSWL 7

RESULT 12

US-09-847-946A-49
Sequence 49, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 49
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
US-09-847-946A-49

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 ADMSWL 7

RESULT 13

US-09-847-946A-52
Sequence 52, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
US-09-847-946A-52

US-09-847-946A-52

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
|||
Db 3 ADMSWL 8

RESULT 14

US-09-847-946A-46
; Sequence 46, Application US/09847946A
; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PFI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 46

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: NEMO binding

; OTHER INFORMATION: sequence

US-09-847-946A-46

Query Match 100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 17;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
|||
Db 3 ADMSWL 8

RESULT 15

US-10-171-311-234

; Sequence 234, Application US/10171311

; Publication No. US20030087270A1

; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert

; APPLICANT: Chen, Yan

; APPLICANT: Zhao, Xumei

; APPLICANT: Monahan, John

; APPLICANT: Kamackar, Shubhangt

; APPLICANT: Glact, Karen

; APPLICANT: Gammavarepu, Manjula

; APPLICANT: Hoerish, Sebastian

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY

; TITLE OF INVENTION: OF CERVICAL CANCER

; FILE REFERENCE: MRI-035

; CURRENT APPLICATION NUMBER: US/10/171,311

; CURRENT FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: US 60/298,159

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/298,155

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/335,936

; PRIOR FILING DATE: 2001-11-14

; NUMBER OF SEQ ID NOS: 238

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 234

; LENGTH: 501

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-171-311-234

Query Match 100.0%; Score 40; DB 15; Length 501;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
|||
Db 387 ADMSWL 392

Search completed: February 18, 2004, 15:41:55
Job time : 16.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:16:19 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-4

Perfect score: 40

Sequence: 1 ADMSWL 6

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	36	90.0	174	4	US-09-325-932A-163
3	36	90.0	225	4	US-09-325-932A-162
4	36	90.0	378	4	US-09-325-932A-158
5	36	90.0	616	4	US-09-136-574A-47
6	36	90.0	745	2	US-08-887-518-3
7	36	90.0	745	2	US-09-023-321-3
8	36	90.0	745	2	US-08-890-853-4
9	36	90.0	745	2	US-09-032-475-3
10	36	90.0	745	2	US-09-099-125A-4
11	36	90.0	745	2	US-09-032-476-4
12	36	90.0	745	3	US-08-890-854-4
13	36	90.0	745	3	US-09-023-324-4
14	36	90.0	745	3	US-09-168-629-2
15	36	90.0	745	3	US-08-910-820-10
16	36	90.0	745	3	US-08-810-131A-2
17	36	90.0	745	4	US-09-109-986-4
18	36	90.0	745	4	US-09-844-908-9
19	36	90.0	745	4	US-09-868-758-4
20	36	90.0	745	4	US-09-868-758-3
21	36	90.0	756	2	US-08-887-518-4
22	36	90.0	756	2	US-09-023-321-4
23	36	90.0	756	2	US-08-890-853-2
24	36	90.0	756	2	US-09-032-475-4
25	36	90.0	756	2	US-09-099-125A-2
26	36	90.0	756	2	US-09-099-124A-2
27	36	90.0	756	3	US-09-032-476-2

28	36	90.0	756	3	US-08-890-854-2	Sequence 2, Appl1
29	36	90.0	756	3	US-09-023-324-2	Sequence 2, Appl1
30	36	90.0	756	3	US-09-168-629-15	Sequence 15, Appl1
31	36	90.0	756	4	US-08-910-820-9	Sequence 9, Appl1
32	36	90.0	756	4	US-09-109-986-2	Sequence 2, Appl1
33	36	90.0	756	4	US-09-844-908-9	Sequence 4, Appl1
34	36	90.0	756	4	US-09-868-758-4	Sequence 4, Appl1
35	36	90.0	997	4	US-09-417-197-123	Sequence 123, App
36	36	90.0	1426	3	US-09-417-197-121	Sequence 121, App
37	36	90.0	1751	3	US-09-136-574A-43	Sequence 43, Appl1
38	36	90.0	1751	3	US-09-136-574A-44	Sequence 44, Appl1
39	35	87.5	1205	1	US-07-908-245-2	Sequence 2, Appl1
40	35	87.5	1205	2	US-08-319-866-10	Sequence 10, Appl1
41	35	87.5	1205	3	US-09-123-708-6	Sequence 6, Appl1
42	35	87.5	1205	3	US-09-123-624-6	Sequence 6, Appl1
43	34	85.0	170	4	US-09-199-637A-339	Sequence 339, App
44	34	85.0	518	4	US-09-065-383-27	Sequence 27, Appl1
45	34	85.0	537	4	US-09-655-270A-11	Sequence 11, Appl1

ALIGNMENTS

RESULT 1
US-09-252-991A-31533
; Sequence 31533, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; SEQ ID NO 31533
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31533

Query Match 90.0%; Score 36; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 94 ADMSW 98

RESULT 2
US-09-325-932A-163
; Sequence 163, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flamm, Barry
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant devel
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-163

Query Match 90.0%; Score 36; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
|||||
Db 109 ADMSW 113

RESULT 3
US-09-325-932A-162

Sequence 162, Application US/09325932A

Patent No. 6451604

GENERAL INFORMATION:

APPLICANT: Flinn, Barry

APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: death and their use in the modification of forestry plant develop

FILE REFERENCE: 1022

CURRENT APPLICATION NUMBER: US/09/325,932A

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 162

LENGTH: 225

TYPE: PRT

ORGANISM: Eucalyptus grandis

US-09-325-932A-162

Query Match 90.0%; Score 36; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
|||||
Db 100 ADMSW 104

RESULT 4
US-09-325-932A-158

Sequence 158, Application US/09325932A

Patent No. 6451604

GENERAL INFORMATION:

APPLICANT: Flinn, Barry

APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: death and their use in the modification of forestry plant develop

FILE REFERENCE: 1022

CURRENT APPLICATION NUMBER: US/09/325,932A

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 158

LENGTH: 378

TYPE: PRT

ORGANISM: Eucalyptus grandis

US-09-325-932A-158

Query Match 90.0%; Score 36; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
|||||
Db 128 ADMSW 132

RESULT 5
US-09-136-574A-47

Sequence 47, Application US/09136574A

Patent No. 6294366

GENERAL INFORMATION:

APPLICANT: Farrington, Graham K.

Anderson, Paige

Gibbs, Moreland

Bergquist, Peter

Daniels, Roy

Morgan, Hugh W.

Williams, Diane P.

TITLE OF INVENTION: Compositions and Methods for

Treating Cellulose Containing Fabrics Using Truncated

Cellulase Enzyme Compositions

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Center, P.O. Box 457

CITY: Spring House

STATE: PA

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/136,574A

FILING DATE: 19-Aug-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/932,571

FILING DATE: September 19, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: 1997US001/CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

TELEFAX: 215-540-5818

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 616 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Query Match 90.0%; Score 36; DB 3; Length 616;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
|||||
Db 123 DMSWL 127

RESULT 6
US-08-887-518-3

Sequence 3, Application US/08887518

Patent No. 5843721

GENERAL INFORMATION:

APPLICANT: Roche, Mlke

APPLICANT: Ml, lln

TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6
Db 739 DMSWL 743

RESULT 7
US-09-023-321-3
Sequence 3, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6
Db 739 DMSWL 743

RESULT 8
US-08-890-853-4
Sequence 4, Application US/08890853
Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goedel, David V.
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6
Db 739 DMSWL 743

RESULT 9
US-09-032-475-3
Sequence 3, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032.475
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
Db 739 DMSWL 743

RESULT 10
US-09-099-125A-4
Sequence 4, Application US/09099125A
Patent No. 5916760
GENERAL INFORMATION:
APPLICANT: Goedel, David V.
ATTORNEY/AGENT INFORMATION:
NAME: Moronitz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099.125A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890.853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-124A-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
Db 739 DMSWL 743

RESULT 11
US-09-099-124A-4
Sequence 4, Application US/09099124A
Patent No. 5939302
GENERAL INFORMATION:
APPLICANT: Goedel, David V.
ATTORNEY/AGENT INFORMATION:
NAME: Moronitz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099.124A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890.853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-124A-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
Db 739 DMSWL 743

DB 739 DMSWL 743

RESULT 12
US-09-032-476-4
Sequence 4, Application US/09032476
Patent No. 6235492
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaoan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-476-4

Query Match 90.0%; Score 36; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
DB 739 DMSWL 743

RESULT 13
US-08-890-854-4
Sequence 4, Application US/08890854
Patent No. 6235512
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaoan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA

ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-854-4

Query Match 90.0%; Score 36; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
DB 739 DMSWL 743

RESULT 14
US-09-023-324-4
Sequence 4, Application US/09023324
Patent No. 6235513
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaoan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 90.0%; Score 36; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWL 6
|||||
DB 739 DMSWL 743

RESULT 15
US-09-168-629-2
Sequence 2, Application US/09168629
Patent No. 6242253
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: Didonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ibrahim
TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 745
TYPE: PRT
ORGANISM: Homo sapiens
US-09-168-629-2

Query Match 90.0%; Score 36; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWL 6
|||||
DB 739 DMSWL 743

Search completed: February 18, 2004, 14:41:46
Job time : 8.06579 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 / Search time 3.55263 seconds
(without alignments)
79,423 Million cell updates/sec

Title: US-09-643-260-3

Perfect score: 26

Sequence: 1 LDASAL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	214	1 RADC_RHOCA	P72255 rhodocact
2	26	100.0	259	1 ECX2_ARCFU	O29756 archaeoglob
3	26	100.0	550	1 SYR_MYCTU	Q10609 mycobacteri
4	26	100.0	638	1 SCAD_HUMAN	P51172 homo sapien
5	26	100.0	638	1 SCAD_PANTH	O65474 pan troglod
6	26	100.0	745	1 METE_CORGL	O82833 corynebact
7	26	100.0	855	1 GARP_SCHPO	Q10280 schizosacch
8	26	100.0	858	1 SYL_VIRCH	O98768 vibrio chol
9	26	100.0	1006	1 MT10_SCHPO	O09878 schizosacch
10	26	100.0	1313	1 ACE_RAT	P47820 rattus norv
11	24	92.3	197	1 YET4_METUA	O58869 methanococ
12	24	92.3	298	1 CDK2_HUMAN	P24941 homo sapien
13	24	92.3	298	1 CDK2_HUMAN	O63698 rattus norv
14	24	92.3	346	1 CDK2_MOUSE	P27377 mus musculi
15	24	92.3	358	1 ALF_ECOLI	P11604 esche richia
16	24	92.3	386	1 ALR_ANASP	O84936 anabaena sp
17	24	92.3	393	1 DCM_HORCH	O42829 hordeum chl
18	24	92.3	404	1 ODO2_ECOLI	P07016 esche richia
19	24	92.3	446	1 DTA2_BALSO	O82836 raltionia b
20	24	92.3	505	1 HUTN_SALTU	O82836 raltionia b
21	24	92.3	506	1 HUTN_SALTU	O82836 raltionia b
22	24	92.3	518	1 FLAA_AQUAB	O67803 aquifex aeo
23	24	92.3	933	1 SLAP_CAMPF	P25847 campylobact
24	24	92.3	964	1 MSH2_YEAST	P25847 campylobact
25	24	92.3	970	1 SBGA_YEAST	O92765 schizosacch
26	24	92.3	3255	1 POLG_LMYVO	P31999 1 genome po
27	24	92.3	3255	1 POLG_LMYVO	P31999 1 genome po
28	23	88.5	145	1 MA29_DRRFA	P39674 dermatophag
29	23	88.5	161	1 PHAB_STNPF	P06113 synecchococ
30	23	88.5	193	1 ACD1_XANAC	P58902 xanthomonas
31	23	88.5	201	1 CTPL_HUMAN	Q16619 homo sapien
32	23	88.5	242	1 PPGI_PBBPU	O9679 pseudomonas
33	23	88.5	247	1 PPGI_MYCTU	O06814 mycobacteri

34	23	88.5	249	1 CYSX_SYNY3	P72794 synecchocyc
35	23	88.5	249	1 STXA_HUMAN	O60499 homo sapien
36	23	88.5	295	1 XPR3_METMA	O82833 methanocarc
37	23	88.5	351	1 PTA_FICFR	O92639 rickettsia
38	23	88.5	355	1 LEU3_SPIPL	O00412 spilitula p
39	23	88.5	366	1 REQ2_XENLA	O9636 xenopus lae
40	23	88.5	372	1 MTQX_SALTI	P58524 salmoneilla
41	23	88.5	372	1 MTQX_SALTI	P58524 salmoneilla
42	23	88.5	380	1 SCHL_STRHA	O05361 streptomyc
43	23	88.5	388	1 REOL_XENLA	O9638 xenopus lae
44	23	88.5	400	1 DCM_MAIZE	O24575 zea mays (m
45	23	88.5	411	1 BHB2_MOUSE	O35185 mus musculi

ALIGNMENTS

RESULT 1

RADC_RHOCA STANDARD; PRT; 214 AA.

AC P72255; 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE DNA repair protein radc homolog.

GN RADC.

OS Rhodococcus capsulatus (Rhodospseudomonas capsulata).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhododacterales;

OC Rhododacterales; Rhododacterales.

OX NCBI_TaxId=1061;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33303 / B10;

RX MEDLINE=20118379; PubMed=10652786;

RA Katsiou E., Michel C.M., Garcia A.F., Tadros M.H.;

RT "Molecular analysis and identification of the radc gene from the

RT phototrophic bacterium Rhodococcus capsulatus B10."

RL Microbiol. Res. 154:233-239 (1999).

CC - FUNCTION: INVOLVED IN DNA REPAIR (BY SIMILARITY).

CC - INDUCTION: Induced about five-fold after UV-irradiation.

CC - SIMILARITY: Belongs to the radc family.

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CC -----

DR EMBL: U74017; AAB18255.1; -

DR HAMAP: MF_00018; -; 1.

DR InterPro: IPR001405; RADC.

DR Pfam: PF04002; RADC; 1.

DR ProDom: PD007415; RADC; 1.

DR TIGRFAMs: TIGR00608; radc; 1.

DR PROSITE: PS01302; RADC; 1.

KW DNA repair.

SO SEQUENCE 214 AA; 23792 MW; D008997B20C6743D CRC64;

Query Match Best Local Similarity 100.0%; Score 26; DB 1; Length 214;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6

DB 154 LDASAL 159

RESULT 2

ECX2_ARCFU STANDARD; PRT; 259 AA.

ID ECX2_ARCFU STANDARD; PRT; 259 AA.

AC O29756;

DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Probable exosome complex exonuclease 2 (EC 3.1.13.-).
 GN AF0494.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 ON NCBI_TaxID=2234;
 RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Kleck H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodok A., Zhou L.,
 RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 CC -1- FUNCTION: Probably involved in the 3'-5' degradation of a variety
 CC of RNA species (Potential).
 CC -1- SUBUNIT: Component of the archaeal exosome multienzyme
 CC ribonuclease complex (Potential).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- SIMILARITY: BELONGS TO THE RNASE PH FAMILY.
 CC -----
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 CC -----
 CC EMBL; AE001070; AAB90743.1; -.
 DR DR PIR; P69311; F69311.
 DR TIGR; AF0494; -.
 DR HAMAP; MF_00623; -; 1.
 DR InterPro; IPR001247; 3_ExoRNase.
 DR Pfam; PF01138; RNase_PH; 1.
 DR Pfam; PF03725; RNase_PH_C; 1.
 KW Exosome; Hydrolase; Nuclease; Exonuclease; Complete proteome.
 SO SEQUENCE 259 AA; 26646 MW; E8289D46PDDCCB3 CRC64;
 QY Query Match 100.0%; Score 26; DB 1; Length 259;
 Db Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASAL 6
 Db 149 LDASAL 154

OK NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Broeck R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gao S., Barry C.B. III, Tekle A.,
 RA Badcock K., Bauman D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Krogan A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellern S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Pletschmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J.F., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Uitterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
 CC di-phosphate + L-arginyl-tRNA(Arg).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
 CC -----
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 CC -----
 CC EMBL; Z73419; CA9757.1; -.
 DR DR EMBL; AE007007; AAK45593.1; -.
 DR DR PIR; H70772; H70772.
 DR TIGR; MT1331; -.
 DR TubercuList; Rv1292; -.
 DR HAMAP; MF_00123; -; 1.
 DR InterPro; IPR001276; Arg_tRNA-lynt_1c.
 DR InterPro; IPR005148; N.
 DR InterPro; IPR001412; tRNA-lynt_1.
 DR Pfam; PF03485; N-Arg; 1.
 DR Pfam; PF00750; tRNA-lynt_1d; 1.
 DR PRINTS; PRO1038; TRNASYNTHARG.
 DR TIGRFAMs; TIGR00456; argS; 1.
 DR PROSITE; PS00178; AA_tRNA_LIGASE_1; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 SO SEQUENCE 550 AA; 59709 MW; 4F11239A6238124D CRC64;
 QY Query Match 100.0%; Score 26; DB 1; Length 550;
 Db Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASAL 6
 Db 23 LDASAL 28

RESULT 4
 SCAD HUMAN STANDARD; PRT; 638 AA.
 ID SCAD HUMAN
 AC P51172;

```

01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DE Amloride-sensitive sodium channel delta-subunit (Epithelial Na+
channel) delta subunit (Delta ENaC) (Nonvoltage-gated sodium channel
1 delta subunit) (SCNED) (Delta NaCh).
GN SCNNID OR DNACH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteleia; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96070858; PubMed=7499195;
RA Waldmann R., Champigny G., Bassilana F., Volley N., Lazdunski M.;
RT "Molecular cloning and functional expression of a novel aniloride-
sensitive Na+ channel."
RL J. Biol. Chem. 270:27411-27414(1995).
CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL.
INHIBITED BY THE DIURETIC AMILORIDE. MEDIATES THE ELECTRODIFFUSION
OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC -1- SUBUNIT: HETEROTRIMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL
FAMILY.
-----
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-----
DR EMBL: U38254; AAC50283.1; -
DR PIR: I39196; I39196.
DR Genew; HGNC:10601; SCNNID.
DR MIM: 601328; -
DR GO; GO:0015280; P:amiloride-sensitive sodium channel activity; TAS.
DR GO; GO:0006814; P:sodium ion transport; TAS.
DR InterPro; IPR004724; Enac.
DR InterPro; IPR01873; Na-channel_Asc.
DR Pfam; PF00858; Asc; 1.
DR TIGRfam; TIGR00859; Enac; 1.
DR PROSITE; PS01206; Asc; 1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT DOMAIN 1 86
FT TRANSMEM 87 107
FT DOMAIN 108 530
FT TRANSMEM 531 551
FT DOMAIN 552 638
FT CARBOHYD 166 166
FT CARBOHYD 211 211
FT CARBOHYD 384 384
SQ SEQUENCE 638 AA; 70274 MW; 7CD5181F8497F5CF CRC64;

Query Match 100.0%; Score 26; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DE Amloride-sensitive sodium channel delta-subunit (Epithelial Na+
channel) delta subunit (Delta ENaC) (Nonvoltage-gated sodium channel
1 delta subunit) (SCNED) (Delta NaCh).
GN SCNNID OR DNACH.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteleia; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue-Testis;
RA Al-Khalili O.K., Eaton D.C.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL.
INHIBITED BY THE DIURETIC AMILORIDE. MEDIATES THE ELECTRODIFFUSION
OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION (By similarity).
CC -1- SUBUNIT: HETEROTRIMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT (By
similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL
FAMILY.
-----
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-----
DR EMBL: AF038165; AAB92659.1; -
DR InterPro; IPR004724; Enac.
DR InterPro; IPR001873; Na-channel_Asc.
DR Pfam; PF00858; Asc; 1.
DR PRINTS; PRO1078; AMINACHANNEL.
DR TIGRfam; TIGR00859; Enac; 1.
DR PROSITE; PS01206; Asc; 1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT TRANSMEM 87 107
FT DOMAIN 108 530
FT TRANSMEM 531 551
FT DOMAIN 552 638
FT CARBOHYD 166 166
FT CARBOHYD 211 211
FT CARBOHYD 384 384
SQ SEQUENCE 638 AA; 70187 MW; 321B9597D6A78D38 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 LDASAL 6
DB 551 LDASAL 556
RESULT 5
SCAD PANTR STANDARD; PRT; 638 AA.
AC 046547;

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OY 1 LDASAL 6
DB 551 LDASAL 556
RESULT 6
MTE CORGL
ID MTE CORGL STANDARD; PRT; 745 AA.
AC 08NRB3;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 5-methyltetrahydropteroyltryptophan--homocysteine methyltransferase
(EC 2.1.1.14) (methionine synthase, vitamin-B12 independent isozyme)

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DE (Cobalamin-independent methionine synthase).
 GN METE OR CG1139.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteri; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Completed genomic sequence of Corynebacterium glutamicum ATCC 13032."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Catalyzes the transfer of a methyl group from 5-methyltetrahydrofolate to homocysteine resulting in methionine formation (By similarity).
 CC -1- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyl-L-glutamate + L-homocysteine = tetrahydropteroyl-L-glutamate + L-methionine.
 CC -1- COFACTOR: Zinc; binds one ion per subunit (By similarity).
 CC -1- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
 CC -1- SIMILARITY: Belongs to the vitamin-B12 independent methionine synthase family.
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 CC -----
 DR EMBL; A005277; BAB9632.1; -.
 DR HAMAP; MF_00172; -1.
 DR InterPro; IPR002629; Methionine_synth.
 DR InterPro; IPR006276; Met_synth_B12ind.
 DR Pfam; PF01717; Methionine_synth; 1.
 DR ProDom; PD004692; Methionine_synth; 2.
 DR TIGRfam; TIGR01371; met_synth_B12ind; 1.
 DR Transferrase; Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
 KW Complete proteome.
 KM METAL 628 ZINC (BY SIMILARITY).
 FT METAL 630 ZINC (BY SIMILARITY).
 FT METAL 713 ZINC (BY SIMILARITY).
 SO SEQUENCE 745 AA; 81312 MW; 856E05DE7398BDF CRC64;
 CC -----
 Query Match 100.0%; Score 26; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LDASAL 6
 Db 140 LDASAL 145
 RESULT 7
 ID GAF1_SCHPO STANDARD; PRT; 855 AA.
 AC Q10280; O94482; Q9USK9;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transcription factor gaf1 (Gaf-1).
 GN GAF1 OR SPEC1902.01 OR SPEC417.01C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsle K., James K., Jones L., Jones M., Leather S., McDonald S., Mclean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Ocell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittowitch B., RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K., RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Woodward J., Volkert E., Aert R., Robben J., Grymmez B., RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Meller-Auer S., RA Gabel C., Fuchs M., Fritze C., Holzer E., Moser D., Hilbert H., RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M., RA Beyer P., Zimmermann W., Wedler H., Wambut R., Purcell B., RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S., RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forebury S.L., RA Cerruttl L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., RA Sipakovskii G.V., Uesery D., Barrrell B.G., Nurse P.;
 RA "The genome sequence of Schizosaccharomyces pombe."
 RA Nature 415:871-880(2002).
 RL [2]
 RN SEQUENCE OF 566-855 FROM N.A.
 RP MEDLINE=98382525; PubMed=9714831;
 RX Hoe K.-L., Won M.S., Chung K.-S., Park S.-K., Kim D.-U., Jang Y.-J., RA Yoo O.-J., Yoo H.-S.;
 RT "Molecular cloning of gaf1, a Schizosaccharomyces pombe GATA factor, which can function as a transcriptional activator."
 RL Gene 215:319-328(1998).
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: Contains 1 GATA-type zinc finger.
 CC -----
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 CC -----
 DR EMBL; AL035076; GA22647.1; -.
 DR EMBL; AL049521; CAB40003.1; -.
 DR EMBL; L31601; AAC35593.1; -.
 DR PIR; T41336; T41336.
 DR HSP; P17429; 4GAT.
 DR TRANSFAC; T02831; -.
 DR Genedb_Spomb; SPEC1902.01; -.
 DR InterPro; IPR000679; Znf_GATA.
 DR Pfam; PF00320; GATA; 1.
 DR PRINTS; PR00619; GATAZNFINGER.
 DR SMART; SM00401; ZNF_GATA; 1.
 DR PROSITE; PS00344; GATA_ZNF_FINGER_1; 1.
 DR PROSITE; PS50114; GATA_ZNF_FINGER_2; 1.
 KW Transcription regulation; Activator; DNA-binding; Zinc-finger; Nuclear protein.
 FT ZN FING 635 GATA-TYPR.
 SO SEQUENCE 855 AA; 91776 MW; 3D932F83D2DE6774 CRC64;
 CC -----
 Query Match 100.0%; Score 26; DB 1; Length 855;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LDASAL 6
 Db 211 LDASAL 216
 RESULT 8
 SYL_VIBCH

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ID  SVL_VIBCH  STANDARD;  PRT;  858 AA.
AC  Q9KTB6;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  LeuGyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA Ligase) (LeuRS).
GN  LEUS OR VCO956.
OS  Vibrio cholerae.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
CC  Vibrionaceae; Vibrrio.
OX  NCBI_TaxID=666;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=El Tor N16961 / Serotype O1;
RX  MEDLINE=20406833; PubMed=10953301;
RA  Hagedberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA  Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unyam L.A.,
RA  Gill S.R., Nelson K.E., Read T.D., Tettein H., Richardson D.,
RA  Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA  McDonald L., Uterback T., Fleischmann R.D., Niernan W.C., White O.,
RA  Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA  Fraser C.M.;
RT  "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT  cholerae.";
RL  Nature 406:477-483(2000).
CC  -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
CC  diphosphate + L-leucyl-tRNA(Leu).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  EMBL; AE004177; AAP94118.1; ALT_INIT.
CC  TIGR; VCO956; -.
DR  HAMAP; MF_00049; -, 1.
DR  InterPro; IPR002302; Leu-tRNA synthetase.
DR  InterPro; IPR002300; tRNA-synt 1a.
DR  InterPro; IPR001412; tRNA-synt 1.
DR  Pfam; PF00133; tRNA-synt 1; 1.
DR  PRINTS; PR00985; TRANSVYTHLEU.
DR  TIGRFAIR; TIGR00396; LeuS_Dact; 1.
DR  PROSITE; PS00178; AA_tRNA_Ligase_1; 1.
KW  Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW  Complete proteome.
FT  SITE 42 52 "HIGH" REGION.
FT  SITE 618 622 "KMSKS" REGION.
FT  BINDING 621 621 ATP (BY SIMILARITY).
SQ  SEQUENCE 858 AA; 96621 MW; AAD59A2E1C9F192 CRC64;
Query Match 100.0%; Score 26; DB 1; Length 858;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GN  SPEC584.01C.
OS  Schizosaccharomyces pombe (Fission yeast).
OC  Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC  Schizosaccharomycetales; Schizosaccharomycetaceae;
CC  Schizosaccharomycetes.
OX  NCBI_TaxID=4896;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=972;
RX  MEDLINE=21948401; PubMed=11859360;
RA  Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA  Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA  Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA  Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA  Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA  Holtroyd S., Hornby T., Howarth S., Huckle S.J., Hunt S., Jagsels K.,
RA  James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA  Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA  Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA  Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA  Skelton J., Simmonds M., Squares R., Stevens K.,
RA  Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA  Woodward J., Wolckaert G., Aert R., Robben J., Grynolprez B.,
RA  Welter J., Vanstelele E., Rieger M., Schaefer M., Mueller-Auer S.,
RA  Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA  Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA  Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA  Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motter S.,
RA  Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA  Lucas M., Rocher M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA  Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA  Dominguez A., Revuelta J.L., Moreno S., Ametrano J., Fotsburg S.L.,
RA  Carrutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
RA  Shipavskii G.V., Useery D., Barrell B.G., Nurse P.;
RT  "The genome sequence of Schizosaccharomyces pombe.";
RL  Nature 415:871-880(2002).
CC  -1- FUNCTION: THIS ENZYME CATALYZES THE 6-ELECTRON REDUCTION OF
CC  SULFITE TO SULFIDE. THIS IS ONE OF SEVERAL ACTIVITIES REQUIRED
CC  FOR THE BIOSYNTHESIS OF L-CYSTEINE FROM SULFATE (BY SIMILARITY).
CC  -1- CATALYTIC ACTIVITY: H(2)S + 3 NADP(+) + 3 H(2)O = sulfite + 3
CC  NADPH.
CC  -1- COFACTOR: THIS SUBUNIT IS A FLAVOPROTEIN THAT BINDS ONE FMN AND
CC  ONE FAD PER CHAIN (BY SIMILARITY).
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  EMBL; AL032824; CAA21818.2; -.
CC  PIR; T41439; T41439.
DR  HSP; P00388; IAMD.
DR  GeneDB; Spombe; SPEC584.01C; -.
DR  InterPro; IPR003097; FAD binding.
DR  InterPro; IPR001709; FMN_cyt_redctase.
DR  InterPro; IPR001433; Oxid. FAD/NAD(P).
DR  Pfam; PF00667; FAD binding_1; 1.
DR  Pfam; PF00175; NAD binding_1; 1.
DR  PRINTS; PR00371; FMNR.
KW  Oxidoreductase; Flavoprotein; NADP; FAD; FMN; Electron transport;
KW  Cysteine biosynthesis.
FT  NP_BIND 658 669 FAD (ADP PART) (BY SIMILARITY).
FT  NP_BIND 788 798 FAD (FLAVIN PART) (BY SIMILARITY).
SQ  SEQUENCE 1006 AA; 111352 MW; 2EA2086D5951D33 CRC64;
Query Match 100.0%; Score 26; DB 1; Length 1006;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 554 LDASAL 559

RESULT 10

ACE_RAT STANDARD; PRT; 1313 AA.

AC P47820; 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)

DE (ACE) (dipeptidyl carboxypeptidase I) (kininase II).

GN ACE OR DCP1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX MEDLINE=94121658; PubMed=8292044;

RA Koike G., Krieger J.E., Jacob H.J., Mukoyama M., Pratt R.E., Dzuu V.J., Angiotensin converting enzyme and genetic hypertension: cloning of rat cDNAs and characterization of the enzyme."

RT Biochem. Biophys. Res. Commun. 198:380-386 (1994).

RL [2]

RN SEQUENCE FROM N.A.

RC STRAIN=Lewis/N; TISSUE=Lung;

RA Jafarian-Tehrani M., Liswak S., Barrientos R.M., Michaud A., Corvol P., Sternberg E.M.; Characterization of a missense mutation in the angiotensin I-converting enzyme cDNA in exudate inflammation resistant F344/N rats."

RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RL -1- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF THE TERMINAL HIS-LEU. THIS RESULTS IN AN INCREASE OF THE VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.

CC -1- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide-I-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither Asp nor Glu. Converts angiotensin I to angiotensin II.

CC -1- COFACTOR: Binds 2 zinc ions (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Somatic;

CC IsoId=P47820-1; Sequence=Displayed;

CC Name=Testis-specific;

CC IsoId=P47820-2; Sequence=Not described;

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.

CC -----

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CC -----

DR EMBL, U03708; AAA82110.1; -

DR EMBL, U03734; AAA82111.1; -

DR EMBL, AF201332; AAG35597.1; -

DR PIR, JC2038; JC2038.

DR MEROPS, M02.001; -

DR MEROPS, M02.004; -

DR InterPro, IPR001548; Peptidase_M2.

DR InterPro, IPR006025; Zn_Mpeptidase.

DR Pfam, PF01401; Peptidase_M2; 2.

DR PRINTS, PR00791; PEPDIPRTSEA.

DR ProDom, PD004184; Peptidase_M2; 2.

DR PROSITE, PS00142; ZINC_PROTEASE; 2.

KW Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;

KW Glycoprotein; Transmembrane; Repeat; Signal; Alternative splicing.

FT SIGNAL 1 35

FT CHAIN 36 1313

FT DOMAIN 36 1265

FT TRANSMEM 1266 1282

FT DOMAIN 1283 1313

FT REPEAT 233 589

FT REPEAT 831 1187

FT METAL 396 396

FT ACT SITE 397 397

FT METAL 400 400

FT METAL 994 994

FT ACT SITE 995 995

FT METAL 998 998

FT CARBOHYD 44 44

FT CARBOHYD 60 60

FT CARBOHYD 80 80

FT CARBOHYD 117 117

FT CARBOHYD 152 152

FT CARBOHYD 166 166

FT CARBOHYD 324 324

FT CARBOHYD 515 515

FT CARBOHYD 683 683

FT CARBOHYD 701 701

FT CARBOHYD 720 720

FT CARBOHYD 766 766

FT CARBOHYD 948 948

FT CARBOHYD 1197 1197

FT VARIANT 207 207

SO SEQUENCE 1313 AA; 150907 MW; 8CB5D0015F129591 CRC64;

Query Match Best Local Similarity 100.0%; Score 26; DB 1; Length 1313; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6

DB 600 LDASAL 605

RESULT 11

YER4_METUA STANDARD; PRT; 197 AA.

ID YER4_METUA

AC Q58869; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypothetical protein MJ1474.

GN MJ1474.

OS Methanococcus jannaschii.

OC Archaea; Euryarchaeota; Methanococci; Methanococcales;

OC Methanocaldococcaceae; Methanocaldococcus.

OX NCBI_TaxID=2190;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VAL-1 / DSM 2661 / ATCC 43067;

RX MEDLINE=96337999; PubMed=8688087;

RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake O., Olsen G.J., Fletzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-P., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D., Utecherback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Huret M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii."

RT Science 273:1058-1073 (1996).

CC -1- SIMILARITY: BELONGS TO THE UPF0129 FAMILY.

CC -----

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CC -----
 CC EMBL: U67588; AAB99480.1; -
 CC PIR: A64484; A64484.
 CC TIGR: M1474; -
 CC HAMAP: MF_00265; - 1
 CC InterPro: IPR002851; DUF133.
 CC InterPro: IPR002716; PIN.
 CC InterPro: IPR006596; PIN.
 CC Pfam: PF01850; PIN: 1
 CC ProDom: PD013236; DUF133; 1.
 CC SMART: SM00670; PIN: 1.
 CC KEGG: Hypothetical protein; Complete proteome.
 CC KW DOMAIN 181 197 LYS-RICH.
 CC FT SEQUENCE 197 AA; 22781 MW; 70075B862934F58 CRC64;
 CC

Query Match 92.3%; Score 24; DB 1; Length 197;
 Best Local Similarity 83.3%; Pred. No. 51;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
 Db 36 LDASAI 41

RESULT 12
 CDK2_HUMAN
 ID CDK2_HUMAN STANDARD; PRT; 298 AA.
 AC P24911;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cell division protein kinase 2 (EC 2.7.1.1) (p33 protein kinase).
 GN CDK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 OX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91330891; PubMed=1714386;
 RA Elledge S.U., Spottswood M.R.;
 RT "A new human p34 protein kinase, CDK2, identified by complementation
 RT of a cdc28 mutation in *Saccharomyces cerevisiae*, is a homolog of
 RT Xenopus Egl.;"
 RT EMBO J. 10:2653-2659(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91367262; PubMed=1653904;
 RA Teal L.H., Harlow E., Meyerson M.;
 RT "Isolation of the human cdk2 gene that encodes the cyclin A- and
 RT adenovirus E1A-associated p33 kinase.;"
 RT Nature 353:174-177(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92020980; PubMed=1717994;
 RA Nishitani-Tsuji J., Nomoto S., Yasuda H., Reed S.I., Matsumoto K.;
 RT "Cloning of a human cDNA encoding a CDK2-related kinase by
 RT complementation of a budding yeast cdc28 mutation.;"
 RT Proc. Natl. Acad. Sci. U.S.A. 88:9006-9010(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
 RA Riedinger K.B., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schmitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta; RL

RX MEDLINE=22388257; PubMed=12477932;
 RA Strasserberg R.L., Feringola E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bucof C.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.U., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallegange D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marrs M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.;"
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP PHOSPHORYLATION SITES.
 RX MEDLINE=93010995; PubMed=1396589;
 RA Gu Y., Rosenblatt J., O'Morgan D.O.;
 RT "Cell cycle regulation of CDK2 activity by phosphorylation of Thr160
 RT and Tyr15.;"
 RT EMBO J. 11:3995-4005(1992).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=93288132; PubMed=8510751;
 RA de Bondt H.L., Rosenblatt J., Jancarik J., Jones H.D.,
 RA Morgan D.O., Kim S.-H.;
 RT "Crystal structure of cyclin-dependent kinase 2.;"
 RT Nature 363:595-602(1993).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH CYCLIN A.
 RX MEDLINE=95356811; PubMed=7630387;
 RA Jeffrey P.D., Russo A.A., Polyak K., Gibbs E., Hurwitz J.,
 RA Massague J., Pavletich N.P.;
 RT "Mechanism of CDK activation revealed by the structure of a
 RT cyclinA-CDK2 complex.;"
 RT Nature 376:313-320(1995).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.33 ANGSTROMS) OF COMPLEX WITH L868276.
 RX MEDLINE=96181476; PubMed=8610110;
 RA de Azavedo W.F., Jr., Muleer-Dieckmann H.-J., Schulze-Gahmen U.,
 RA Worland P.J., Sauvillie E., Kim S.-H.;
 RT "Structural basis for specificity and potency of a flavonoid
 RT inhibitor of human CDK2, a cell cycle kinase.;"
 RT Proc. Natl. Acad. Sci. U.S.A. 93:2735-2740(1996).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH CG2A AND KIP1.
 RX MEDLINE=96300318; PubMed=8684460;
 RA Russo A.A., Jeffrey P.D., Patena A.K., Massague J., Pavletich N.P.;
 RT "Crystal structure of the p27kip1 cyclin-dependent-kinase inhibitor
 RT bound to the cyclin A-Cdk2 complex.;"
 RT Nature 382:325-331(1996).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH CG2A.
 RX MEDLINE=96311326; PubMed=8756328;
 RA Russo A.A., Jeffrey P.D., Pavletich N.P.;
 RT "Structural basis of cyclin-dependent kinase activation by
 RT phosphorylation.;"
 RT Nat. Struct. Biol. 3:696-700(1996).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=97075215; PubMed=8917641;
 RA Schulze-Gahmen U., de Bondt H.L., Kim S.-H.;
 RT "High-resolution crystal structures of human cyclin-dependent kinase
 RT 2 with and without ATP: bound waters and natural ligand as guides for
 RT inhibitor design.;"
 RT J. Med. Chem. 39:4540-4546(1996).

RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=97475219; PubMed=9334743;
 RA Lawrie A.M., Noble M.E.M., Tunnah P., Brown N.R., Johnson L.N.,
 RA Endicott J.A.;
 RT "Protein kinase inhibition by staurosporine revealed in details of
 RT the molecular interaction with CDK2.";
 RL Nat. Struct. Biol. 4:796-801(1997).
 RP [14]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH GSK1.
 RX MEDLINE=96182647; PubMed=8601310;
 RA Bourne Y., Watson M.H., Hickey M.J., Holmes W., Rocque W., Reed S.I.,
 RA Tanner J.A.;
 RT "Crystal structure and mutational analysis of the human CDK2 kinase
 RT complex with cell cycle-regulatory protein CksHsl.";
 RL Cell 84:663-674(1996).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
 RX MEDLINE=96342369; PubMed=9677190;
 RA Gray N.S., Modicka L., Thunnissen A.-M.W.H., Norman T.C., Kwon S.,
 RA Espinoza F.H., Morgan D.O., Barnes G., Leclerc S., Meijer L.,
 RA Kim S.H., Lockhart D.J., Schultz P.G.;
 RT "Exploiting chemical libraries, structure, and genomics in the search
 RT for kinase inhibitors.";
 RL Science 281:533-538(1998).
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.
 CC INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL
 CC DURING S PHASE AND G2.
 CC -1- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
 CC THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC2/CDKX SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL, X61622; CAA43807.1; -;
 DR EMBL, X62071; CAA43985.1; -;
 DR EMBL, M68520; AAA3567.1; -;
 DR EMBL, AF512553; AAM34794.1; -;
 DR EMBL, BC003065; AA03065.1; -;
 DR PIR, A41227; A41227.
 DR PIR, JFIN; 27-JAN-97.
 DR PDB, 1HCK; 07-DEC-96.
 DR PDB, 1HCL; 07-DEC-96.
 DR PDB, 1A01; 12-NOV-97.
 DR PDB, 1JST; 11-JAN-97.
 DR PDB, 1JSU; 29-JUL-97.
 DR PDB, 1BDH; 09-SEP-98.
 DR PDB, 1B38; 23-DEC-98.
 DR PDB, 1B39; 23-DEC-98.
 DR PDB, 1CKP; 13-JAN-99.
 DR PDB, 1D18; 28-JAN-03.
 DR PDB, 1DM2; 31-MAY-00.
 DR PDB, 1E1V; 10-MAY-01.
 DR PDB, 1E1X; 10-MAY-01.
 DR PDB, 1F5Q; 27-DEC-00.
 DR PDB, 1FQ1; 09-MAY-01.
 DR PDB, 1FVJ; 17-JAN-01.
 DR PDB, 1FVJ; 17-JAN-01.
 DR PDB, 1G5S; 14-NOV-01.
 DR PDB, 1G1H; 06-FEB-02.
 DR PDB, 1G1J; 06-FEB-02.
 DR PDB, 1G1J; 06-FEB-02.
 DR PDB, 1G1J; 06-FEB-02.
 DR PDB, 1G1J; 06-FEB-02.
 DR PDB, 1H1P; 19-SEP-02.
 DR PDB, 1H1Q; 19-SEP-02.
 DR PDB, 1H1R; 19-SEP-02.

DR PDB, 1H1S; 19-SEP-02.
 DR PDB, 1H24; 01-FEB-03.
 DR PDB, 1H25; 01-FEB-03.
 DR PDB, 1H26; 01-FEB-03.
 DR PDB, 1H28; 01-FEB-03.
 DR PDB, 1J5V; 29-AUG-01.
 DR PDB, 1JVP; 21-DEC-01.
 DR PDB, 1KE5; 14-MAY-02.
 DR PDB, 1KE6; 14-MAY-02.
 DR PDB, 1KE7; 14-MAY-02.
 DR PDB, 1KE8; 14-MAY-02.
 DR PDB, 1KE9; 14-MAY-02.
 DR PDB, 1KE9; 14-MAY-02.
 Query Match 92.3%; Score 24; DB 1; Length 298;
 Best Local Similarity 83.3%; Pred. No. 80;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASAL 6
 DB 91 MDASAL 96
 RESULT 13
 CDK2_RAT
 ID CDK2_RAT STANDARD; PRT; 298 AA.
 AC Q63699; O09136;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cell division protein kinase 2 (EC 2.7.1.-).
 GN CDK2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=thymoid;
 RX MEDLINE=9516553; PubMed=7862443;
 RA Kozaki S., Endo T., Kitagawa M., Higashi H., Onaya T.;
 RT "A variant form of cyclin-dependent kinase 2 (Cdk2) in a malignantly
 RT transformed rat thymoid (FRTL-Tc) cell line.";
 RL Oncogene 10:663-669(1995).
 RN [2]
 RP SEQUENCE OF 19-124 FROM N.A.
 RX MEDLINE=96113578; PubMed=8673024;
 RA Hosokawa Y., Yang M., Kaneko S., Tanaka M., Nakashima K.;
 RT "Synergistic gene expressions of cyclin B, cdk2, cdk5 and B2F-1
 RT during the prolactin-induced G1/S transition in rat Nb2 pre-T
 RT lymphoma cells.";
 RL Biochem. Mol. Biol. Int. 37:393-399(1995).
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.
 CC INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL
 CC DURING S PHASE AND G2.
 CC -1- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
 CC THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT (BY
 CC SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=alternative splicing; Named isoforms=2;
 CC Name=CDK2- α ;
 CC IsoId=O63699-1; Sequence=Displayed;
 CC Name=CDK2- β ;
 CC IsoId=O63699-2; Sequence=Not described;
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC2/CDKX SUBFAMILY.
 CC -----
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 CC -----

CC EMBL: D28753; BAA05947.1; -
 DR EMBL: D6162; BAA09638.1; -
 DR HSSP: P24941; 1A01.
 DR InterPro: IPR007719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_ATP; 1.
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
 KW Cell division; Mitosis; Phosphorylation; Alternative splicing.
 FT DOMAIN 4 286
 FT NP_BIND 10 18 ATP (BY SIMILARITY).
 FT BINDING 33 33 ATP (BY SIMILARITY).
 FT ACT_SITE 127 127 BY SIMILARITY.
 FT MOD_RES 14 14 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 160 160 PHOSPHORYLATION (BY CAK) (BY SIMILARITY).
 FT CONFLICT 79 79 V -> C (IN REF. 2).
 FT CONFLICT 99 99 L -> I (IN REF. 2).
 FT CONFLICT 124 124 L -> C (IN REF. 2).
 SO SEQUENCE 298 AA; 33887 MW; C8CB3ACB3B97F88 CRC64;

Query Match 92.3%; Score 24; DB 1; Length 298;
 Best Local Similarity 83.3%; Pred. No. 80;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6
 Db 91 MDASAL 96

RESULT 14
 CDK2_MOUSE STANDARD; PRT; 346 AA.
 ID P97377; O55105; Created)
 AC 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cell division protein kinase 2 (EC 2.7.1.1).
 GN CDK2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM CDK2-ALPHA).
 RC STRAIN=CS7BL/6;
 RA Jun D., Lee Y.H., Park H.K., Kim Y.H.;
 RT "Exon-intron organization of the murine cyclin-dependent kinase-2
 gene Cdk2-alpha and Cdk2-beta.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RA Ellenrieder C., Bartosch B., Lee G.Y., Murphy M., Sweeney C.,
 RA Hegerberg M., Hunt T., Carrington M., Jauch R.;
 RT "The 39 kDa form of CDK2 arises through alternative splicing, is
 expressed in many but not all mammals, and is an active kinase.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.
 CC INTERACTS WITH CYCLIN A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL
 CC DURING S PHASE AND G2.
 CC -1- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
 CC THE ENZYME. WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT (BY
 CC SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=CDK2-beta;
 CC IsoId=P97377-1; Sequence=Displayed;
 CC Name=CDK2-alpha;

CC IsoId=P97377-2; Sequence=VSP 004800;
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC2/CDK2 SUBFAMILY.

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CC EMBL: U63377; AAB37128.1; -
 DR EMBL: AJ223732; CA11533.1; -
 DR EMBL: AJ223733; CA11534.1; -
 DR EMBL: AJ223733; CA11535.1; -
 DR HSSP: P24941; 1A01.
 DR MGD: MG1:104772; Cdk2.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
 KW Cell division; Mitosis; Phosphorylation; Alternative splicing.
 FT DOMAIN 4 334
 FT NP_BIND 10 18 ATP (BY SIMILARITY).
 FT BINDING 33 33 ATP (BY SIMILARITY).
 FT ACT_SITE 127 127 BY SIMILARITY.
 FT MOD_RES 14 14 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 15 15 PHOSPHORYLATION (BY CAK) (BY SIMILARITY).
 FT MOD_RES 160 160 PHOSPHORYLATION (BY CAK) (BY SIMILARITY).
 FT VARSPLIC 197 244 Missing (in isoform CDK2-alpha).
 SO SEQUENCE 346 AA; 38978 MW; D806BC2F150AEDFC CRC64;

Query Match 92.3%; Score 24; DB 1; Length 346;
 Best Local Similarity 83.3%; Pred. No. 94;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6
 Db 91 MDASAL 96

RESULT 15
 ALF_ECOLI STANDARD; PRT; 358 AA.
 ID P11604; Created)
 AC 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fructose-bisphosphate aldolase class II (EC 4.1.2.13) (FBP aldolase).
 GN FBA OR FBA OR FDA OR B2925 OR Z4263 OR ECS3796 OR SF2910.
 GN Escherichia coli O157:H7, and
 OS Escherichia coli.
 OS Shigella flexneri.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxId=562, 83334, 623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / CS520;
 RX MEDLINE=8913302; PubMed=2546007;
 RA Alefounder P.R., Baldwin S.A., Pernam S.A., Short N.J.;
 RT "Identification, molecular cloning and sequence analysis of a gene
 RT cluster encoding the class II fructose 1,6-bisphosphate aldolase, 3-
 RT phosphate dehydrogenase kinase and a putative second glyceraldehyde 3-
 RT Mol. Microbiol. 3:723-732(1989).

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-26.
RC SPECIES=E.coli; PubMed=2649077.
RX MEDLINE=89193446; PubMed=9742661; PubMed=9278503;
RA Alfounder P.R., Baldwin S.A., Perham R.N., Short N.J.;
RT "Cloning, sequence analysis and over-expression of the gene for the
RL class II fructose 1,6-bisphosphate aldolase of Escherichia coli";
RN Biochem. J. 257:529-534 (1989).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=9742661; PubMed=9278503;
RA Blattner F.R., Plunkett G. II, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474 (1997).
RL [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. II, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lam A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533 (2001).
RL [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakiwa C., Ogasawara N., Yasunaga T.,
RA Kihara S., Shibata T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22 (2001).
RL [6]
RP SEQUENCE OF 1-12.
RC SPECIES=E.coli; STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298446;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RL in the genome of Escherichia coli K-12";
RN Electrophoresis 18:1259-1313 (1997).
RN [7]
RP SEQUENCE OF 1-4.
RC SPECIES=E.coli; STRAIN=K12 / W3110;
RX MEDLINE=96263247; PubMed=9600841;
RA Williams R.R., Gaesteliger E., Tonella L., Ou K., Tyler M.,
RA Sanchez J.-C., Gooley A.A., Welsh J.B., Batroch A., Appel R.D.,
RA Williams K.L., Hochreiter D.F.;
RT "Protein identification with N and C-terminal sequence tags in
RT proteome projects";
RL J. Mol. Biol. 278:599-608 (1998).
RL [8]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157";
RL Nucleic Acids Res. 30:4432-4441 (2002).
RL [9]
RP ZINC-LIGANDS, AND MUTAGENESIS.

```

RC SPECIES-E.coli;
RX MEDLINE=93170474; PubMed=8435219;
RA Berry A., Marshall K.R.;
RT "Identification of zinc-binding ligands in the class II fructose-1,6-
RT bisphosphate aldolase of Escherichia coli.";
RT FEBS Lett. 318:11-16(1993).
RN [10]
RN X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS).
RC SPECIES-E.coli;
RX MEDLINE=96433074; PubMed=8835102;
RA Blom N.S., Tetreault S., Coulombe R., Sygusch J.;
RT "Novel active site in Escherichia coli fructose 1,6-bisphosphate
RT aldolase.";
RL Nat. Struct. Biol. 3:856-862(1996).
RN [11]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RC SPECIES-E.coli;
RX MEDLINE=97094986; PubMed=8939754;
RA Cooper S.J., Leonard G.A., McSweeney S.M., Thompson A.W.,
RA Natsumi J.H., Gamar S., Plater A., Berry A., Hunter W.N.;
RT "The crystal structure of a class II fructose-1,6-bisphosphate
RT aldolase shows a novel binuclear metal-binding active site embedded
RT in a familiar fold.";
RL Structure 4:1303-1315(1996).
RN [12]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC SPECIES-E.coli;
RX MEDLINE=99187425; PubMed=10080900;
RA Hall D.R., Leonard G.A., Reed C.D., Watt C.I., Berry A., Hunter W.N.;
RT "The crystal structure of Escherichia coli class II fructose-1,
RT 6-bisphosphate aldolase in complex with phosphoglycolohydroxamate
RT reveals details of mechanism and specificity.";
RL J. Mol. Biol. 287:383-394(1999).
CC -1 CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glyceralone
CC phosphate + D-glyceraldehyde 3-phosphate.
CC -1 COPACTOR: ZINC
CC -1 PATHWAY: Glycolysis; sixth step.
CC -1 SUBUNIT: Homodimer.
CC -1 SIMILARITY: Belongs to class II fructose-bisphosphate aldolase
CC family.
CC -----
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CC -----
DR EMBL, U14436; CAAG3605.1; -
DR EMBL, U28377; AAA69092.1; -
DR EMBL, AE000376; AAC75962.1; -
DR EMBL, AE000522; AAG58051.1; ALT_INIT.
DR EMBL, AP002563; BAB37219.1; -
DR EMBL, AE015305; AAN44392.1; ALT_INIT.
DR PIR, D91103; D91103.
DR PIR, S02177; ADSC2A.
DR PDB, 1DO5; 07-JUL-97.
DR PDB, 1ZEN; 07-JUL-97.
DR PDB, 1B57; 07-JAN-00.
DR SWISS-2DPAGE, P11604; COLI.
DR EcoGene, EG10282; Ebaa.
DR InterPro, IPR006411; Fruct biap bact.
DR InterPro, IPR000771; K bp aldolase.
DR Pfam, PF0116; F_bp_aldolase; 1.
DR ProDom, PD002376; K_bp_aldolase; 1.
DR TIGRFAMs, TIGR00167; Cdba; 1.
DR TIGRFAMs, TIGR01520; FruBaldII_A; 1.
DR PROSITE, PS00602; ALDOLASE CLASS II 1; 1.
DR PROSITE, PS00806; ALDOLASE CLASS II 2; 1.
DR Lyase, Glycolysis, zinc; 3D-structure; Complete proteome.
FT INIT_MET 0
FT METAL 107 107 ZINC.

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PT	MUTAGEN	110	110	H->A: LOSS OF ACTIVITY.
PT	MUTAGEN	111	111	C->A: PARTIAL LOSS OF ACTIVITY.
PT	HELIX	3	5	
PT	TURN	6	6	
PT	STRAND	10	11	
PT	TURN	14	14	
PT	HELIX	15	26	
PT	TURN	27	28	
PT	STRAND	31	35	
PT	HELIX	39	52	
PT	TURN	53	53	
PT	STRAND	56	60	
PT	HELIX	62	69	
PT	TURN	71	72	
PT	TURN	78	79	
PT	HELIX	80	100	
PT	TURN	101	101	
PT	STRAND	103	108	
PT	HELIX	113	115	
PT	HELIX	116	133	
PT	STRAND	140	143	
PT	TURN	146	147	
PT	HELIX	150	166	
PT	TURN	167	168	
PT	STRAND	170	174	
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Query Match 92.3%; Score 24; DB 1; Length 358;
Best Local Similarity 83.3%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASL 6
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Db 190 MDASL 195

Search completed: February 18, 2004, 14:28:03
Job time : 5.55263 secs

GenCore version 5.1.6
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OW protein - protein search, using SW model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-3

Perfect score: 1 LDASAL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:
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2: /cgn2_6/ptodata/1/pubppa/PCP_NEM_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEM_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_FUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_FUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubppa/PCPUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US08_NEM_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	26	100.0	11	11	US-09-847-946A-3
3	26	100.0	28	10	US-09-847-940B-19
4	26	100.0	28	11	US-09-847-946A-19
5	26	100.0	191	15	US-10-156-761-8434
6	26	100.0	191	15	US-10-156-761-13332
7	26	100.0	191	15	US-10-156-761-13333
8	26	100.0	191	15	US-10-156-761-14915
9	26	100.0	240	10	US-09-738-626-4338
10	26	100.0	374	12	US-10-104-047-3578
11	26	100.0	600	11	US-09-746-660A-106
12	26	100.0	638	10	US-09-893-204-18
13	26	100.0	638	14	US-10-133-157-8
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16	26	100.0	745	10	US-09-919-835-2	Sequence 2, Appl1
17	26	100.0	745	10	US-09-738-626-4761	Sequence 4761, Ap
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19	26	100.0	1006	12	US-10-369-493-22729	Sequence 22729, A
20	26	92.3	14	14	US-10-038-612-107	Sequence 107, Ap
21	26	92.3	20	14	US-10-038-612-35	Sequence 35, Appl
22	26	92.3	21	14	US-10-038-612-106	Sequence 106, Ap
23	26	92.3	40	15	US-10-044-967-18	Sequence 18, Appl
24	26	92.3	157	16	US-10-080-170-565	Sequence 565, App
25	26	92.3	191	15	US-10-156-761-1181	Sequence 1181, A
26	26	92.3	259	12	US-10-369-493-9612	Sequence 9612, Ap
27	26	92.3	294	12	US-10-334-143-181	Sequence 181, App
28	26	92.3	298	10	US-09-771-161A-187	Sequence 187, App
29	26	92.3	298	12	US-10-174-794-13	Sequence 27, Appl
30	26	92.3	298	12	US-10-295-681-27	Sequence 29, Appl
31	26	92.3	298	12	US-10-295-681-29	Sequence 31, Appl
32	26	92.3	298	12	US-10-295-681-31	Sequence 43, Appl
33	26	92.3	298	12	US-10-295-681-43	Sequence 31, Appl
34	26	92.3	298	12	US-10-394-322A-7	Sequence 7, Appl1
35	26	92.3	304	10	US-09-976-059-3	Sequence 3, Appl1
36	26	92.3	346	12	US-10-295-681-33	Sequence 45, Appl
37	26	92.3	346	12	US-10-295-681-45	Sequence 2, Appl1
38	26	92.3	359	10	US-09-823-109-2	Sequence 23545, A
39	26	92.3	359	12	US-10-369-493-23545	Sequence 2, Appl1
40	26	92.3	359	15	US-10-164-204-2	Sequence 10096, A
41	26	92.3	405	9	US-09-815-242-10096	Sequence 6, Appl1
42	26	92.3	405	12	US-10-077-745-6	Sequence 759, App
43	26	92.3	405	12	US-10-338-915-6	Sequence 6, Appl1
44	26	92.3	405	12	US-10-369-493-759	Sequence 6, Appl1
45	26	92.3	405	14	US-10-078-107-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-847-940B-3
Sequence 3, Application US/09847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
FILE REFERENCE: Ghosh, Sanak
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/847, 940B
CURRENT FILING DATE: 2001-05-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ. ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-3

Query Match 100.0%; Score 26; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDASAL 6
Db 1 LDASAL 6
RESULT 2
US-09-847-946A-3
Sequence 3, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J

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; APPLICANT: Ghosh, Sankar
; APPLICANT: Firdels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hamnig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-3
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Query Match          100.0%; Score 26; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDASAL 6
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Db       1 LDASAL 6
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RESULT 3
US-09-847-940B-19
; Sequence 19, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-19
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Query Match          100.0%; Score 26; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDASAL 6
        |||||
Db       20 LDASAL 25
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RESULT 4
US-09-847-946A-19
; Sequence 19, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Firdels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hamnig, Gerhard
```

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; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19
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Query Match          100.0%; Score 26; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDASAL 6
        |||||
Db       20 LDASAL 25
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RESULT 5
US-10-156-761-8434
; Sequence 8434, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8434
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8434
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Query Match          100.0%; Score 26; DB 15; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDASAL 6
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Db       41 LDASAL 46
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RESULT 6
US-10-156-761-13332
; Sequence 13332, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
```

APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13332
LENGTH: 191
TYPE: PR1
ORGANISM: Streptomyces avermitilis
US-10-156-761-13332

Query Match 100.0%; Score 26; DB 15; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
Db 41 LDASAL 46

RESULT 7
US-10-156-761-13333
Sequence 13333, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13333
LENGTH: 191
TYPE: PR1
ORGANISM: Streptomyces avermitilis
US-10-156-761-13333

Query Match 100.0%; Score 26; DB 15; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
Db 41 LDASAL 46

RESULT 8
US-10-156-761-14915
Sequence 14915, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14915
LENGTH: 191
TYPE: PR1
ORGANISM: Streptomyces avermitilis
US-10-156-761-14915

Query Match 100.0%; Score 26; DB 15; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
Db 41 LDASAL 46

RESULT 9
US-09-738-626-4338
Sequence 4338, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIJO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 4338
LENGTH: 240
TYPE: PR1
ORGANISM: Corynebacterium glutamicum
US-09-738-626-4338

Query Match 100.0%; Score 26; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
Db 70 LDASAL 75

RESULT 10
US-10-104-047-3578
Sequence 3578, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE

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; TITLE OF INVENTION: NO. US2003026392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3578
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3578

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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 287 LDASAL 292

RESULT 11
US-09-746-660A-106
; Sequence 106, Application US/09746660A
; Publication No. US20030049804A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; APPLICANT: Kim, Jun-Won
; APPLICANT: Lee, Heung-Schick
; APPLICANT: Hwang, Byung-Joon
; TITLE OF INVENTION: CORINNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CP2
; CURRENT APPLICATION NUMBER: US/09/746,660A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/606740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 09/603124
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-746-660A-106

Query Match          100.0%; Score 26; DB 11; Length 600;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 140 LDASAL 145

RESULT 12
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US-09-983-204-18
; Sequence 18, Application US/09983204
; Patent No. US20020173000A1
; GENERAL INFORMATION:
; APPLICANT: RENARD, STEPHANE
; APPLICANT: BESNARD, FRANCOIS
; APPLICANT: GRAHAM, DAVID
; TITLE OF INVENTION: SODIUM CHANNEL RECEPTOR
; FILE REFERENCE: 07586.0010
; CURRENT APPLICATION NUMBER: US/09/983,204
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/424,666
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/EP98/02884
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 97401196.7
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: HNACHD
US-09-983-204-18

Query Match          100.0%; Score 26; DB 10; Length 638;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 551 LDASAL 556

RESULT 13
US-10-133-157-8
; Sequence 8, Application US/10133157
; Publication No. US20020184054A1
; GENERAL INFORMATION:
; APPLICANT: CALAMARAS, NICHOLAS
; APPLICANT: CHANG, HONG
; TITLE OF INVENTION: HIGH THROUGHPUT CELL-BASED ASSAY FOR MONITORING SODIUM
; TITLE OF INVENTION: CHANNEL ACTIVITY AND DISCOVERY OF SALTY TASTE
; FILE REFERENCE: 078003-0280790
; CURRENT APPLICATION NUMBER: US/10/133,157
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: 60/287,413
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-133-157-8

Query Match          100.0%; Score 26; DB 14; Length 638;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 551 LDASAL 556

RESULT 14
US-09-738-626-6815
; Sequence 6815, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
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APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6815
LENGTH: 659
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-6815

Query Match 100.0%; Score 26; DB 10; Length 659;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
Db 132 LDASAL 137

RESULT 15
US-10-104-047-3501
Sequence 3501, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
FILE REFERENCE: HI-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3501
LENGTH: 704
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3501

Query Match 100.0%; Score 26; DB 12; Length 704;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
Db 617 LDASAL 622

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Job time : 17.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-3

Perfect score: 26

Sequence: 1 LDASAL 6

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Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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6	24	92.3	83	1	US-08-370-225-16
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15	24	92.3	298	2	US-08-869-106-2
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17	24	92.3	298	4	US-09-457-040B-29
18	24	92.3	298	4	US-09-411-628-13
19	24	92.3	298	4	US-09-338-125-2
20	24	92.3	298	4	US-09-266-225D-14
21	24	92.3	359	4	US-09-098-219B-2
22	24	92.3	405	1	US-08-370-193A-9
23	24	92.3	544	4	US-09-417-197-113
24	24	92.3	544	4	US-09-417-197-115
25	24	92.3	723	4	US-09-434-408-2
26	24	92.3	970	4	US-09-198-452A-906
27	24	92.3	1042	4	US-09-512-250C-32

28	24	92.3	2618	3	US-09-413-814-28	Sequence 28, Appl
29	23	88.5	44	3	US-08-905-223-345	Sequence 345, App
30	23	88.5	65	1	US-08-227-536-6	Sequence 6, Appl1
31	23	88.5	65	5	PCT-US95-04682-6	Sequence 6, Appl1
32	23	88.5	159	4	US-09-252-991A-24779	Sequence 24779, A
33	23	88.5	201	1	US-08-444-083-8	Sequence 8, Appl1
34	23	88.5	201	1	US-08-286-304-8	Sequence 8, Appl1
35	23	88.5	201	1	US-08-442-745-8	Sequence 8, Appl1
36	23	88.5	201	1	US-08-443-129-8	Sequence 8, Appl1
37	23	88.5	201	1	US-08-443-952-8	Sequence 8, Appl1
38	23	88.5	201	1	US-08-443-130-8	Sequence 8, Appl1
39	23	88.5	201	1	US-08-792-019B-11	Sequence 11, Appl1
40	23	88.5	201	3	US-09-106-182-4	Sequence 4, Appl1
41	23	88.5	201	3	US-08-988-819-11	Sequence 11, Appl1
42	23	88.5	201	3	US-08-898-911-8	Sequence 8, Appl1
43	23	88.5	201	4	US-09-016-534-11	Sequence 11, Appl1
44	23	88.5	201	4	US-09-648-183-3	Sequence 3, Appl1
45	23	88.5	201	5	PCT-US95-04467-8	Sequence 8, Appl1

ALIGNMENTS

```

RESULT 1
US-09-252-991A-17296
; Sequence 17296, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17296
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17296

Query Match          100.0%; Score 26; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 LDASAL 6
Db      91 LDASAL 96

RESULT 2
US-08-989-299-9
; Sequence 9, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Action, Susan L.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FOLEY, HONG & BLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,299
FILING DATE: 11-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold E., Beth
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-025.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-989-299-9

Query Match 100.0%; Score 26; DB 3; Length 1313;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
:|||||
DB 600 MDASAL 605

RESULT 3
US-09-140-149-9
Sequence 9, Application US/09140149
Patent No. 6117680
GENERAL INFORMATION:
APPLICANT: Natesan, Sridaran
APPLICANT: Gilman, Michael Z
TITLE OF INVENTION: No. 6117680el Compositions and Methods for Regulation of
FILE REFERENCE: 363C
CURRENT APPLICATION NUMBER: US/09/140,149
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 08/918,401
EARLIER FILING DATE: 1997-08-26
EARLIER APPLICATION NUMBER: 08/920,610
EARLIER FILING DATE: 1997-08-27
EARLIER APPLICATION NUMBER: 09/126,009
EARLIER FILING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: PCT/US97/15219
EARLIER FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 9
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-09-140-149-9

Query Match 92.3%; Score 24; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
:|||||
DB 11 MDASAL 16

RESULT 4

US-09-615-917-9
Sequence 9, Application US/09615917
Patent No. 6479653
GENERAL INFORMATION:
APPLICANT: Natesan, Sridaran
APPLICANT: Gilman, Michael Z
TITLE OF INVENTION: No. 6479653el Compositions and Methods for Regulation of
FILE REFERENCE: 363C continuation
CURRENT APPLICATION NUMBER: US/09/615,917
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 08/918,401
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 08/920,610
PRIOR FILING DATE: 1997-08-27
PRIOR APPLICATION NUMBER: 09/126,009
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 09/140,149
PRIOR FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 9
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-09-615-917-9

Query Match 92.3%; Score 24; DB 4; Length 20;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
:|||||
DB 11 MDASAL 16

RESULT 5
US-09-480-993-18
Sequence 18, Application US/09480993
Patent No. 6383790
GENERAL INFORMATION:
APPLICANT: Shokat, Kevan M.
TITLE OF INVENTION: High Affinity Kinase Inhibitors for Target Validation
FILE REFERENCE: 51538-5001-US
CURRENT APPLICATION NUMBER: US/09/480,993
CURRENT FILING DATE: 2000-01-11
EARLIER APPLICATION NUMBER: US 60/115,340
EARLIER FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 18
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Cdk2, cyclin-dependent kinase
US-09-480-993-18

Query Match 92.3%; Score 24; DB 4; Length 40;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
:|||||
DB 33 MDASAL 38

RESULT 6
US-08-370-225-16

Sequence 16, Application US/08370225
Patent No. 5580736
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: Gyuris, Jeno
APPLICANT: Golemis, Erica
TITLE OF INVENTION: Interaction Trap System for Isolating
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,225
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,038
FILING DATE: 10/30/92
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/143001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 83
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-370-225-16

Query Match 92.3%; Score 24; DB 1; Length 83;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 18 MDASAL 23

RESULT 7
US-08-461-859-16
Sequence 16, Application US/08461859
Patent No. 5786169
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: Gyuris, Jeno
APPLICANT: Golemis, Erica
TITLE OF INVENTION: Interaction Trap System for Isolating
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
FILING DATE: June 5, 1995
APPLICATION NUMBER: US/08/461,859
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/370,225
FILING DATE: January 9, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,038
FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen P.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/143002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 83
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-461-859-16

Query Match 92.3%; Score 24; DB 1; Length 83;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 18 MDASAL 23

RESULT 8
PCT-US93-10069-16
Sequence 16, Application PC/TUS9310069
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: Gyuris, Jeno
APPLICANT: Golemis, Erica
TITLE OF INVENTION: Interaction Trap System for Isolating
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10069
FILING DATE: 20-OCT-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,038
FILING DATE: 10/30/92
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/143001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 83
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-10069-16

Query Match 92.3%; Score 24; DB 5; Length 83;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 18 MDASAL 23

RESULT 9
US-09-252-991A-23877
Sequence 23877, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23877
LENGTH: 165
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23877

Query Match 92.3%; Score 24; DB 4; Length 165;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 150 IDASAL 155

RESULT 10
US-09-328-352-4324
Sequence 4324, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4324
LENGTH: 257
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4324

Query Match 92.3%; Score 24; DB 4; Length 257;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6

DB :|||||
5 IDASAL 10

RESULT 11
US-08-318-947A-20
Sequence 20, Application US/08318947A
Patent No. 5798245
GENERAL INFORMATION:
APPLICANT: Anderson, Paul J.
TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrie, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, NW Suite 800
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,947A
FILING DATE: 06-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/133,530
FILING DATE: 07-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
REFERENCE/DOCKET NUMBER: A6462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-2820
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-947A-20

Query Match 92.3%; Score 24; DB 1; Length 274;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 91 MDASAL 96

RESULT 12
US-08-795-303-20
Sequence 20, Application US/08795303
Patent No. 5948656
GENERAL INFORMATION:
APPLICANT: Anderson, Paul J.
TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrie, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, NW Suite 800
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,303
FILING DATE: 04-FEB-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/318,947
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: 08/133,530
FILING DATE: 07-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
REFERENCE/DOCKET NUMBER: A6462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-2920
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-303-20

Query Match 92.3%; Score 24; DB 2; Length 274;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 91 MDASAL 96

RESULT 13
US-09-107-532A-4402
Sequence 4402, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneka
REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4402:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...289
SEQUENCE DESCRIPTION: SEQ ID NO: 4402:
US-09-107-532A-4402

Query Match 92.3%; Score 24; DB 4; Length 289;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 96 IDASAL 101

RESULT 14
US-08-874-347-25
Sequence 25, Application US/08874347
Patent No. 5863741
GENERAL INFORMATION:
APPLICANT: Limger, Andrew H.
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-874-347-25

Query Match 92.3%; Score 24; DB 2; Length 298;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6
:|||||
Db 91 MDASAL 96

RESULT 15

US-08-969-106-2
; Sequence 2, Application US/08969106
; Patent No. 5986055

; GENERAL INFORMATION:

; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.

; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS

; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRES:

; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas

; CITY: New York
; STATE: New York

; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: Mastrock, S. Leslie
; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741

; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids

; TYPE: amino acid
; STRANDEDNESS:

; TOPOLOGY: unknown
; MOLECULE TYPE: protein

; US-08-969-106-2

Query Match 92.3%; Score 24; DB 2; Length 298;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6
:|||||
Db 91 MDASAL 96

Search completed: February 18, 2004, 14:41:45
Job time: 7.06579 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-2

Perfect score: 40

Sequence: 1 LDMSWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodara/1/pubpaa/PCT_NEW_PUB.pep.*
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18: /cgn2_6/ptodara/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	40	100.0	6	11	US-09-847-946A-2
3	40	100.0	6	11	US-09-847-946A-3
4	40	100.0	7	11	US-09-847-946A-37
5	40	100.0	8	11	US-09-847-946A-30
6	40	100.0	8	11	US-09-847-946A-38
7	40	100.0	9	11	US-09-847-946A-29
8	40	100.0	9	11	US-09-847-946A-32
9	40	100.0	9	11	US-09-847-946A-35
10	40	100.0	9	11	US-09-847-946A-36
11	40	100.0	10	11	US-09-847-946A-31
12	40	100.0	10	11	US-09-847-946A-34
13	40	100.0	11	11	US-09-847-946A-28
14	40	100.0	11	11	US-09-847-946A-132
15	40	100.0	11	11	US-09-847-946A-140

16	40	100.0	13	11	US-09-847-946A-143	Sequence 143, App
17	40	100.0	13	11	US-09-847-946A-144	Sequence 144, App
18	40	100.0	13	11	US-09-847-946A-145	Sequence 145, App
19	40	100.0	13	11	US-09-847-946A-148	Sequence 148, App
20	40	100.0	17	11	US-09-847-946A-141	Sequence 141, App
21	40	100.0	17	11	US-09-847-946A-142	Sequence 142, App
22	40	100.0	17	11	US-09-847-946A-146	Sequence 146, App
23	40	100.0	17	11	US-09-847-946A-147	Sequence 147, App
24	40	100.0	18	11	US-09-847-946A-135	Sequence 135, App
25	40	100.0	18	11	US-09-847-946A-136	Sequence 136, App
26	40	100.0	22	11	US-09-847-946A-133	Sequence 133, App
27	40	100.0	22	11	US-09-847-946A-134	Sequence 134, App
28	40	100.0	22	11	US-09-847-946A-137	Sequence 137, App
29	40	100.0	22	11	US-09-847-946A-138	Sequence 138, App
30	40	100.0	22	11	US-09-847-946A-139	Sequence 139, App
31	40	100.0	28	11	US-09-847-940B-18	Sequence 18, App
32	40	100.0	28	11	US-09-847-940B-18	Sequence 18, App
33	40	100.0	28	11	US-09-847-946A-18	Sequence 18, App
34	40	100.0	222	10	US-09-771-161A-141	Sequence 141, App
35	40	100.0	745	9	US-09-796-872-2	Sequence 2, App1
36	40	100.0	745	10	US-09-844-908-10	Sequence 10, App1
37	40	100.0	745	10	US-09-844-988-10	Sequence 10, App1
38	40	100.0	745	12	US-10-408-636-3	Sequence 3, App1
39	40	100.0	745	12	US-10-394-322A-32	Sequence 32, App1
40	40	100.0	745	15	US-10-243-408-4	Sequence 4, App1
41	40	100.0	745	15	US-10-059-585-35	Sequence 35, App1
42	40	100.0	745	15	US-10-338-462-10	Sequence 10, App1
43	40	100.0	756	9	US-09-796-872-15	Sequence 15, App1
44	40	100.0	756	10	US-09-771-161A-232	Sequence 232, App
45	40	100.0	756	10	US-09-844-908-9	Sequence 9, App1

ALIGNMENTS

RESULT 1
US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPT-117CE
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-2

Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSWL 6
DB 1 LDMSWL 6
RESULT 2
US-09-847-946A-2
; Sequence 2, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

```
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-2
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Query Match      100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDMSWL 6
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Db      1 LDMSWL 6
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RESULT 3
US-09-847-946A-33
Sequence 33, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-33
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Query Match      100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDMSWL 6
        |||||
Db      1 LDMSWL 6
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RESULT 4
US-09-847-946A-37
Sequence 37, Application US/09847946A
Publication No. US20030054999A1
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GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-37
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Query Match      100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDMSWL 6
        |||||
Db      1 LDMSWL 6
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RESULT 5
US-09-847-946A-30
Sequence 30, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-30
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Query Match      100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDMSWL 6
        |||||
Db      3 LDMSWL 8
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RESULT 6
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US-09-847-946A-38
Sequence 38, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 38
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
US-09-847-946A-38

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6
DB 1 LDMSWL 6

RESULT 7
US-09-847-946A-29
Sequence 29, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
US-09-847-946A-29

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6
DB 1 LDMSWL 6

RESULT 8
US-09-847-946A-32
Sequence 32, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
US-09-847-946A-32

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6
DB 1 LDMSWL 6

RESULT 9
US-09-847-946A-35
Sequence 35, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
US-09-847-946A-35

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
|||
Db 3 LDMSWL 8

RESULT 10

US-09-847-946A-36
; Sequence 36, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-36

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
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Db 2 LDMSWL 7

RESULT 11

US-09-847-946A-31
; Sequence 31, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-31

Query Match 100.0%; Score 40; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
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Db 2 LDMSWL 7

RESULT 12

US-09-847-946A-34
; Sequence 34, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-34

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
|||
Db 3 LDMSWL 8

RESULT 13

US-09-847-946A-28
; Sequence 28, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-28

US-09-847-946A-28

Query Match 100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
DB 3 LDMSWL 8

RESULT 14

US-09-847-946A-132
; Sequence 132, Application US/09847946A
; Publication No. US2003054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Fandels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hamnig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-132

Query Match 100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
DB 3 LDMSWL 8

RESULT 15

US-09-847-946A-140
; Sequence 140, Application US/09847946A
; Publication No. US2003054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Fandels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hamnig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 140
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-140

Query Match 100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
DB 3 LDMSWL 8

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Job time : 16.7529 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
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Title: US-09-643-260-2
Perfect score: 40
Sequence: 1 LDMSWL 6

Scoring table: BLOSUM62
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	745	2 US-08-887-518-3	Sequence 3, Appl1
2	40	100.0	745	2 US-09-023-321-3	Sequence 3, Appl1
3	40	100.0	745	2 US-08-890-853-4	Sequence 4, Appl1
4	40	100.0	745	2 US-09-032-475-3	Sequence 3, Appl1
5	40	100.0	745	2 US-09-099-124A-4	Sequence 4, Appl1
6	40	100.0	745	2 US-09-099-124A-4	Sequence 4, Appl1
7	40	100.0	745	3 US-09-032-476-4	Sequence 4, Appl1
8	40	100.0	745	3 US-08-890-854-4	Sequence 4, Appl1
9	40	100.0	745	3 US-09-023-324-4	Sequence 4, Appl1
10	40	100.0	745	3 US-09-168-629-2	Sequence 2, Appl1
11	40	100.0	745	3 US-08-910-820-10	Sequence 10, Appl1
12	40	100.0	745	3 US-08-810-131A-2	Sequence 2, Appl1
13	40	100.0	745	4 US-09-109-986-4	Sequence 4, Appl1
14	40	100.0	745	4 US-09-844-908-10	Sequence 10, Appl1
15	40	100.0	745	4 US-09-868-758-3	Sequence 3, Appl1
16	40	100.0	745	2 US-08-887-518-4	Sequence 4, Appl1
17	40	100.0	745	2 US-09-023-321-4	Sequence 2, Appl1
18	40	100.0	745	2 US-08-890-853-2	Sequence 2, Appl1
19	40	100.0	745	2 US-09-032-475-4	Sequence 4, Appl1
20	40	100.0	745	2 US-09-099-125A-2	Sequence 2, Appl1
21	40	100.0	745	2 US-09-099-124A-2	Sequence 2, Appl1
22	40	100.0	745	3 US-09-032-476-2	Sequence 2, Appl1
23	40	100.0	745	3 US-08-890-854-2	Sequence 2, Appl1
24	40	100.0	745	3 US-09-023-324-2	Sequence 2, Appl1
25	40	100.0	745	3 US-09-168-629-15	Sequence 15, Appl1
26	40	100.0	745	3 US-08-910-820-9	Sequence 9, Appl1
27	40	100.0	745	4 US-09-109-986-2	Sequence 2, Appl1

28	40	100.0	756	4 US-09-844-908-9	Sequence 9, Appl1
29	40	100.0	756	4 US-09-868-758-4	Sequence 4, Appl1
30	40	100.0	996	4 US-09-417-197-123	Sequence 123, App
31	40	100.0	997	4 US-09-417-197-121	Sequence 28, App
32	36	90.0	100	1 US-08-241-853-28	Sequence 29, Appl
33	36	90.0	100	1 US-08-241-853-28	Sequence 28, Appl
34	36	90.0	100	2 US-08-850-917-28	Sequence 28, Appl
35	36	90.0	100	2 US-08-850-917-28	Sequence 28, Appl
36	36	90.0	242	4 US-09-345-236B-3	Sequence 3, Appl1
37	36	90.0	334	4 US-09-252-991A-22395	Sequence 22395, A
38	36	90.0	454	4 US-09-252-991A-28780	Sequence 47, Appl
39	36	90.0	616	3 US-09-136-574A-47	Sequence 4, Appl1
40	36	90.0	982	2 US-08-673-789-4	Sequence 16, Appl
41	36	90.0	983	1 US-08-162-809-16	Sequence 10, Appl
42	36	90.0	983	1 US-08-167-919A-10	Sequence 21, Appl
43	36	90.0	983	2 US-08-449-645A-21	Sequence 21, Appl
44	36	90.0	983	2 US-08-702-367A-21	Sequence 10, Appl
45	36	90.0	983	3 US-08-715-106-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-887-518-3
Sequence 3, Application US/08887518
Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887, 518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 100.0% Score 40; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
DB 738 LDMSWL 743

Query Match 100.0%; Score 40; DB 2; Length 745;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6
 |||||
 Db 738 LDMSWL 743

RESULT 5
 US-09-099-125A-4
 ; Sequence 4, Application US/09099125A
 ; Patent No. 5916760

GENERAL INFORMATION:
 APPLICANT: Goeddel, David V.
 TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/099,125A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/890,853

ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-006-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 745 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-099-125A-4

Query Match 100.0%; Score 40; DB 2; Length 745;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6
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 Db 738 LDMSWL 743

RESULT 6
 US-09-099-124A-4
 ; Sequence 4, Application US/09099124A
 ; Patent No. 5939502

GENERAL INFORMATION:
 APPLICANT: Goeddel, David V.
 TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESSES:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/099,124A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/890,853

ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-006-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 745 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-099-124A-4

Query Match 100.0%; Score 40; DB 2; Length 745;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6
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 Db 738 LDMSWL 743

RESULT 7
 US-09-032-476-4
 ; Sequence 4, Application US/09032476
 ; Patent No. 6235492

GENERAL INFORMATION:
 APPLICANT: Roche, Mike
 APPLICANT: Cao, Zhaoan
 TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/032,476
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/890,854
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-476-4

Query Match          100.0%; Score 40; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSWL 6
DB      738 LDMSWL 743

RESULT 8
US-08-890-854-4
Sequence 4, Application US/08890854
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
APPLICANT: R gnter, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-854-4

Query Match          100.0%; Score 40; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSWL 6
DB      738 LDMSWL 743
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RESULT 9
US-09-023-324-4
Sequence 4, Application US/09023324
Patent No. 6235513
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
APPLICANT: R gnter, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match          100.0%; Score 40; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSWL 6
DB      738 LDMSWL 743

RESULT 10
US-09-168-629-2
Sequence 2, Application US/09168629
Patent No. 6242253
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: Didonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: IKK Kinase, Subunits Thereof, and Methods of Using Same
FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 745
TYPE: PRT
ORGANISM: Homo sapiens
US-09-168-629-2

Query Match
Best Local Similarity 100.0%; Score 40; DB 3; Length 745;
Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6
Db 738 LDMSWL 743

RESULT 11
US-08-910-820-10
Sequence 10, Application US/08910820
Patent No. 6258579

GENERAL INFORMATION:
APPLICANT: Mercurio, Frank
APPLICANT: Zhu, Henry
APPLICANT: Barbosa, Miguel
APPLICANT: Li, Gian
APPLICANT: Murray, Brian W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910, 820
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-910-820-10

Query Match
Best Local Similarity 100.0%; Score 40; DB 3; Length 745;
Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6
Db 738 LDMSWL 743

RESULT 12
US-08-810-131A-2
Sequence 2, Application US/08810131A
Patent No. 6268194

GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: Didonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using
TITLE OF INVENTION: Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Plores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810, 131A
FILING DATE: 25-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-131A-2

Query Match
Best Local Similarity 100.0%; Score 40; DB 3; Length 745;
Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6
Db 738 LDMSWL 743

RESULT 13
US-09-109-986-4
Sequence 4, Application US/09109986
Patent No. 6479266
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaodan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109, 986

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
TELEPHONE/DOCKET NUMBER: 797-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-109-986-4

Query Match
Best Local Similarity 100.0%; Score 40; DB 4; Length 745;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
Db 738 LDMSWL 743

RESULT 14
US-09-844-908-10
Sequence 10, Application US/09844908
Patent No. 6576437
GENERAL INFORMATION:
APPLICANT: Mercurio, Frank
Zhu, Hengyi
Barbosa, Miguel
Li, Gian
Murray, Brian W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
COMPLEX AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/844,908
FILING DATE: 27-Apr-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
TELEPHONE/DOCKET NUMBER: 860098.413C1
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid

STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-844-908-10

Query Match
Best Local Similarity 100.0%; Score 40; DB 4; Length 745;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
Db 738 LDMSWL 743

RESULT 15
US-09-868-758-3
Sequence 3, Application US/09868758
Patent No. 6576439
GENERAL INFORMATION:
APPLICANT: Glaxo Wellcome KK
APPLICANT: Takemoto, Yoshihiro
APPLICANT: Sakai, Yutaka
APPLICANT: Hashimoto, Yasuhiro
TITLE OF INVENTION: IKK3
FILE REFERENCE: 9950986P
CURRENT APPLICATION NUMBER: US/09/868,758
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: GB 9826704.8
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 745
TYPE: PRT
ORGANISM: Homo sapiens
US-09-868-758-3

Query Match
Best Local Similarity 100.0%; Score 40; DB 4; Length 745;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
Db 738 LDMSWL 743

Search completed: February 18, 2004, 14:41:45
Job time : 8.06579 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-2
Perfect score: 40
Sequence: 1 LDMSWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96166682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	38	95.0	1139	2	A10379 probable potassium
3	37	92.5	122	2	A13395 NMDH dehydrogenase
4	36	90.0	132	2	S69909 Ig V-D-J region (M
5	36	90.0	132	2	S65785 mel-13a protein -
6	36	90.0	277	1	JC5900 bo-type ubiquinol
7	36	90.0	296	2	A84985 cytochrome o ubiqn
8	36	90.0	307	1	A36885 bo-type ubiquinol
9	36	90.0	318	2	AD0384 cytochrome o ubiqn
10	36	90.0	321	2	D83480 cytochrome o ubiqn
11	36	90.0	344	2	AG3489 cytochrome o ubiqn
12	36	90.0	353	2	A87469 ubiquinol oxidase
13	36	90.0	362	2	S23471 uroporphyrinogen d
14	36	90.0	386	2	C96006 probable cytochrom
15	36	90.0	409	2	T47298 probable replicati
16	36	90.0	747	2	D70802 hypochlorite prote
17	36	90.0	803	2	P90485 hypochlorite prote
18	36	90.0	915	2	A43802 cellulase (EC 3.2.
19	36	90.0	983	2	B45583 receptor tyrosine
20	36	90.0	983	2	A38224 receptor tyrosine k
21	36	90.0	983	2	A45583 receptor tyrosine
22	36	90.0	1039	2	S02711 cellulase (EC 3.2.
23	36	90.0	1329	2	D87226 conserved hypochl
24	35	87.5	162	2	C70829 hypochlorite prote
25	35	87.5	162	2	AE2733 NMDH dehydrogenase
26	35	87.5	348	2	G97514 probable sugar tra
27	35	87.5	443	2	AE0309 hypochlorite prote
28	34	85.0	82	2	C69013 conserved hypochl
29	34	85.0	116	2	T03472

30	34	85.0	214	2	G83692 hypochlorite prote
31	34	85.0	282	1	D83692 DNA-3-methyladenin
32	34	85.0	282	2	E90988 3-methyl-adenine D
33	34	85.0	282	2	G85833 DNA-3-methyladenin
34	34	85.0	289	2	A10770 hypochlorite prote
35	34	85.0	299	2	B83243 cytochrome o ubiqn
36	34	85.0	332	2	AH2593 cytochrome ba(3) (
37	34	85.0	377	2	B97376 cytochrome ba(3) (
38	34	85.0	394	2	C85064 tetrahydrofolylipo
39	34	85.0	411	2	E84949 hypochlorite prote
40	34	85.0	414	2	B82408 hypochlorite prote
41	34	85.0	418	2	D85064 cytochrome ba(3) c
42	34	85.0	420	2	A54759 probable glucan 1,
43	34	85.0	501	2	S45914 formate dehydrogen
44	34	85.0	764	2	AD3144 cbbC protein (U60
45	34	85.0	764	2	H98143

ALIGNMENTS

RESULT 1
149101
conserved helix-loop-helix ubiquitons kinase (EC 2.7.1.-) CHUK - mouse
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: I49101
R/Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Genomics 27, 348-351, 1995
A/Title: CHUK, a conserved helix-loop-helix ubiquitons kinase, maps to human chromosome
A/Reference number: I49101; MIM:19604444; PMID:7558004
A/Accession: I49101
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-745 <RES>
A/Cross-references: EMBL:U12473; NID:G1079492; PIRN:AC52589.1; PID:G1079493
C/Genetics:
A/Gene: CHUK
C/Superfamily: mouse conserved helix-loop-helix ubiquitons kinase; protein kinase homo
C/Keywords: ATP; phosphotransferase
F/13-283/Domain: protein kinase homology <KIN>

Query Match 100.0% Score 40; DB 1; Length 745;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
DB 738 LDMSWL 743

RESULT 2
A10379
Probable potassium efflux system YPO3129 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C/Accession: A10379
R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibbail, R.W.; Holden, M.T.G.; Prentice, M.
demo-Tarrag, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MIM:21470413; PMID:11586360
A/Accession: A10379
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1139 <KUR>
A/Cross-references: GB:AL590842; PIRN:CA92364.1; PID:G15981067; GSPDB:GN00175
C/Genetics:
A/Gene: YPO3129

Query Match 95.0% Score 38; DB 2; Length 1139;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSWL 6
 |||||
 Db 480 MDMSWL 485

RESULT 3

A13395
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) [imported] - Brucella melitensis (strain 1
 C/Species: Brucella melitensis
 C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
 C/Accession: A13395
 R:DelVecchio, V.G.; Kaparatzi, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
 .; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A/Reference number: AD3252; PMID:1175688
 A/Accession: A13395
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-322 <KIR>
 A/Cross-references: GB:AE008917; PIDN:AAU52332.1; PID:G17983126; GSPDB:GN00190
 A/Experimental source: strain 16M
 C/Genetics:
 A/Gene: BME1151
 A/Map position: 1
 C/Superfamily: NADH dehydrogenase (ubiquinone) chain 1
 C/Keywords: oxidoreductase

Query Match 92.5%; Score 37; DB 2; Length 322;
 Best Local Similarity 83.3%; Pred. No. 67;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
 |||||
 Db 174 LDMSWL 179

RESULT 4

669909
 Ig V-D-J region (MS) - human
 C/Species: Homo sapiens (man)
 C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C/Accession: S69909
 R:Shore, S.; Hamblin, T.; Oester, D.G.; Stevenson, F.K.
 Leukemia 8, 1285-1289, 1994
 A/Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi
 A/Reference number: S69909; MUID:94335315; PMID:8057663
 A/Accession: S69909
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-122 <SAH>
 A/Cross-references: EMBL:Z33399; NID:9871348; PIDN:CAA83850.1; PID:9871349
 A/Note: the sequence of residues 112-122 and the corresponding nucleic acid sequence are
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/15-97/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 36; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
 |||||
 Db 33 DMSWL 37

RESULT 5

565785
 mel-13a protein - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
 C/Accession: S65785

R:Tetsu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.
 Biochim. Biophys. Acta 1305, 109-112, 1996
 A/Title: Cloning and characterization of two transcripts generated from the mel-13 gen
 A/Reference number: S65785; MUID:96180310; PMID:8597592

A/Accession: S65785
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-132 <TET>
 A/Cross-references: EMBL:U35309
 C/Genetics:
 A/Gene: mel-13
 C/Superfamily: mouse mel-13a protein
 C/Keywords: alternative splicing

Query Match 90.0%; Score 36; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
 |||||
 Db 58 DMSWL 62

RESULT 6

JCS900
 bo-type ubiquinol oxidase (EC 1.10.3.-) chain II - Bradyrhizobium japonicum
 C/Species: Bradyrhizobium japonicum
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: JCS900
 R:Surpin, M.A.; Lueden, M.; Maier, R.J.
 Gene 183, 201-206, 1996
 A/Title: The Bradyrhizobium japonicum coxwxyz gene cluster encodes a bb3-type ubiquinol
 A/Reference number: JCS900; MUID:97149299; PMID:8996107
 A/Accession: JCS900
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-277 <SUR>
 C/Genetics:
 A/Gene: coxw
 C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
 C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; re

Query Match 90.0%; Score 36; DB 1; Length 277;
 Best Local Similarity 83.3%; Pred. No. 83;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWL 6
 |||||
 Db 108 LDMSWL 113

Query Match 90.0%; Score 36; DB 1; Length 277;
 Best Local Similarity 83.3%; Pred. No. 83;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWL 6
 |||||
 Db 108 LDMSWL 113

RESULT 7

A84985
 cytochrome o ubiquinol oxidase subunit II [imported] - Buchnera sp. (strain APS)
 C/Species: Buchnera sp.
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2001
 C/Accession: A84985
 R:Shigenobu, S.; Matanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
 Nature 407, 81-86, 2000
 A/Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
 A/Reference number: A84930; MUID:20445173; PMID:10993077
 A/Accession: A84985
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-296 <STO>
 A/Cross-references: GB:AP000398; GSPDB:GN00144
 A/Experimental source: strain APS
 C/Genetics:

A/Gene: cyoA; B0472
 C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
 C/Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.0%; Score 36; DB 2; Length 296;

Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWL 6
|||
|||
Db 125 LDWKWL 130

RESULT 8

A36885
bo-type ubiquinol oxidase (EC 1.10.3.-) chain II precursor - Acetobacter aceti

N/Alternate names: cytochrome a1 chain II

C/Species: Acetobacter aceti

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C/Accession: A36885

R/Pukaya, M.; Tayam, K.; Tamaki, T.; Ebisuya, H.; Okumura, H.; Kawamura, Y.; Horiuchi,

J. Bacteriol. 175, 4307-4314, 1993

A/Title: Characterization of a cytochrome a-1 that functions as a ubiquinol oxidase in A

A/Reference number: A36885; PMID:93322308; PMID:8392509

A/Accession: A36885

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-307 <PUC>

A/Cross-references: GB:D13185; NID:9409064; PIDN:BAA02480.1; PID:9433186

A/Experimental source: isolate 1023

C/Genetics:

A/Gene: cybB

C/Complex: heterotetramer; chains I, II, III and IV

C/Function:

A/Description: terminal oxidase for ethanol oxidation

C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain

C/Keywords: copper; electron transfer; heterotetramer; membrane-associated complex; oxid

F/1-23/Domain: signal sequence #status predicted <Sig>

F/24-307/Product: bo-type ubiquinol oxidase chain II #status predicted <TM1>

F/48-64/Domain: transmembrane #status predicted <TM1>

F/89-105/Domain: transmembrane #status predicted <TM2>

QY 1 LDMSWL 6
|||
|||
Db 135 LDWKWL 140

RESULT 9

AD0384
cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Yersinia pestis (stra

C/Species: Yersinia pestis

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

C/Accession: AD0384

R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tildall, R.W.; Holden, M.T.G.; Prentice, M.B.

demo-Tarrega, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;

11. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A/Reference number: AB0001; NCID:21470413; PMID:11586360

A/Accession: AD0384

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-318 <KUR>

A/Cross-references: GB:AL590842; PIDN:CAC92399.1; PID:915981102; GSPDB:GN00175

C/Genetics:

A/Gene: cyoA

C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain

C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; resp

Db 135 LDWKWL 140
|||
|||

RESULT 10

D83480
cytochrome o ubiquinol oxidase subunit II PA1317 [imported] - Pseudomonas aeruginosa (

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C/Accession: D83480

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.T.;

adman, S.; Yan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lin

., Loy, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat

A/Reference number: A82950; NCID:20437337; PMID:10984043

A/Accession: D83480

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-331 <STO>

A/Cross-references: GB:AE004561; GB:AE004091; NID:99947253; PIDN:AA04706.1; GSPDB:GN0

A/Experimental source: strain PA01

C/Genetics:

A/Gene: cyoA; PA1317

C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain

C/Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

QY 1 LDMSWL 6
|||
|||
Db 133 LDWKWL 138

RESULT 11

AG3489
cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Brucella melitensis

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 22-Mar-2002

C/Accession: AG3489

R/DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Muir, C.; Lo, T.; Ivanova,

., Mazur, M.; Goldstein, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lete

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen Brucella melite

A/Reference number: AD3252; PMID:11756688

A/Accession: AG3489

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-344 <KUR>

A/Cross-references: GB:AE008917; PIDN:AA53082.1; PID:917983945; GSPDB:GN00190

A/Experimental source: strain 16M

C/Genetics:

A/Gene: BME11901

A/Map position: I

C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain

C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; res

QY 1 LDMSWL 6
|||
|||
Db 141 LDWKWL 146

RESULT 12

A87469
ubiquinol oxidase subunit II [imported] - Caulobacter crescentus

C/Species: Caulobacter crescentus

C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-May-2001

C/Accession: A87469
 R/Nerman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Lubb, M.T.; DeBey, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A/Title: Complete Genome Sequence of *Caibacter crescentus*.
 A/Reference number: A87469; MUID:21173696; PMID:11259647
 A/Accession: A87469
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-353 <STO>
 A/Cross-references: GB:AE005673; NID:913423199; PIDN:AAK3749.1; GSPDB:GN00148
 C/Genetics:
 A/Genes: CCL773
 C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
 C/Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.0%; Score 36; DB 2; Length 353;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSW 5
 Db 146 LDMSW 151

RESULT 13
 S23471
 uroporphyrinogen decarboxylase (EC 4.1.1.37) - Yeast (*Saccharomyces cerevisiae*)
 N/Alternate names: protein YD9609.03; protein YDR047W
 C/Species: *Saccharomyces cerevisiae*
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
 C/Accession: S23471; S33965; S54033; S20390; S27348; S31312
 R/Garey, J.R.; Labbe-Bois, R.; Chelstowska, A.; Rycka, J.; Harrison, L.; Kushner, J.; La
 eur, J. Biochem. 205, 1011-1016, 1992
 A/Title: Uroporphyrinogen decarboxylase in *Saccharomyces cerevisiae*. HEM12 gene sequence
 A/Reference number: S23471; MUID:92249304; PMID:1156986
 A/Accession: S23471
 A/Molecule type: DNA
 A/Residues: 1-362 <GAR>
 A/Cross-references: EMBL:X63721; NID:93766; PIDN:CAA45253.1; PID:93767
 R/Hunt, S.; Bowman, S.; Harris, D.
 Submitted to the EMBL Data Library, May 1995
 A/Reference number: S54031
 A/Accession: S54031
 A/Molecule type: DNA
 A/Residues: 1-362 <DTF>
 A/Cross-references: EMBL:Z19089; NID:94775; PIDN:CAA79514.1; PID:94776
 R/Hunt, S.; Bowman, S.; Harris, D.
 Submitted to the EMBL Data Library, May 1995
 A/Reference number: S54031
 A/Accession: S54031
 A/Molecule type: DNA
 A/Residues: 1-362 <HIN>
 A/Cross-references: EMBL:Z49209; NID:9798897; PIDN:CAA89078.1; PID:9798900; MIPS:YDR047W
 C/Genetics:
 A/Genes: HEM12, HEM6, POB3
 A/Cross-references: MIPS:YDR047W; SGD:S0002454
 A/Map position: 4R
 C/Superfamily: uroporphyrinogen decarboxylase
 C/Keywords: carbon-carbon lyase; carboxy-lyase; porphyrin biosynthesis

Query Match 90.0%; Score 36; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSW 5
 Db 279 LDMSW 283

RESULT 14

C96006
 Probable cytochrome c ubiquinol oxidase chain II protein (EC 1.10.3.-) [Imported] - St
 C/Species: *Sinorhizobium meliloti*
 C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C/Accession: C96006
 R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hern
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A/Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing en
 A/Reference number: A95842; MUID:21396508; PMID:11481431
 A/Accession: C96006
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-386 <KUR>
 A/Cross-references: GB:AL591985; PIDN:CA49715.1; PID:915141202; GSPDB:GN00167
 A/Experimental source: strain 1021, megaplasmid pSymB
 R/Galber, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Huble
 pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpohl, N.A.; Fisher, R.F.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Leleur
 hebaud, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
 A/Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A/Reference number: A96039; MUID:21368234; PMID:11474104
 A/Contents: annotation
 C/Genetics:
 A/Genes: cyoA, SMD21487
 A/Genome: plasmid
 C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
 C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; re

Query Match 90.0%; Score 36; DB 2; Length 386;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSW 6
 Db 141 LDMSW 146

RESULT 15
 T47298
 probable replication protein - *Arabidopsis thaliana*
 N/Alternate names: protein T14K23.110
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C/Accession: T47298
 R/Wakutara, G.; Fartmann, B.; Danner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.
 Mayer, K.F.X.
 Submitted to the Protein Sequence Database, April 2000
 A/Reference number: Z24458
 A/Accession: T47298
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-409 <NTA>
 A/Cross-references: EMBL:AL132909
 A/Experimental source: cultivar Columbia; BAC clone T14K23
 C/Genetics:
 A/Map position: 3
 A/Intons: 47/3; 95/3; 131/2; 175/3; 240/2; 281/3; 304/1; 336/3
 A/Note: T14K23.110

Query Match 90.0%; Score 36; DB 2; Length 409;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSW 5
 Db 190 LDMSW 194

Search completed: February 18, 2004, 14:38:33
 Job time: 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-2
Perfect score: 40
Sequence: 1 LDMSWL 6

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	40	100.0	745	1 IKKA_HUMAN	O15111 h inhibitor
2	40	100.0	745	1 IKKA_MOUSE	O60680 m inhibitor
3	40	100.0	756	1 IKKB_HUMAN	O14920 homo sapien
4	40	100.0	757	1 IKKB_MOUSE	O88351 mus musculu
5	40	100.0	757	1 IKKB_RAT	O9QV78 ratius norv
6	36	90.0	296	1 CYOA_BUCAL	P57544 buchnera ap
7	36	90.0	307	1 COX2_ACEAC	P50653 acetobacter
8	36	90.0	314	1 CYOA_PSEPU	Q9WWT1 pseudomonas
9	36	90.0	362	1 DCUP_YEAST	P32347 saccharomyc
10	36	90.0	983	1 EPB3_CHICK	P29338 gallus gall
11	36	90.0	983	1 EPB3_HUMAN	P29330 homo sapien
12	36	90.0	983	1 EPB3_MOUSE	P29319 mus musculu
13	36	90.0	984	1 EPB3_RAT	O08680 ratius norv
14	36	90.0	1039	1 GUNB_CALSA	P10474 c endogluc
15	36	87.5	290	1 CYOA_BUCAP	Q8K993 buchnera ap
16	34	85.0	282	1 3MG2_ECOLI	P24355 escherichia
17	34	85.0	411	1 FOLC_ECOLI	P38081 buchnera ap
18	34	85.0	501	1 YB06_YEAST	P25533 caldocellum
19	34	85.0	1331	1 YANB_CALSA	P22553 caldocellum
20	34	85.0	1742	1 GUNA_CALSA	O34453 bacillus su
21	33	82.5	336	1 NOSO_BACSU	O31215 chromatinu
22	33	82.5	411	1 CYB_CHRVI	P03470 influenza a
23	33	82.5	453	1 NRAM_IAMIL	P03468 influenza a
24	33	82.5	454	1 NRAM_IAPUE	O05047 catharantlu
25	33	82.5	524	1 CP72_CATRO	O9ZWM7 rhidiccephal
26	33	82.5	552	1 NUSW_RHISA	Q48458 klebsiella
27	33	82.5	579	1 YC12_KLEPN	P43112 salmonella
28	33	82.5	656	1 VEXE_SALTI	P32553 saccharomyc
29	33	82.5	840	1 VPB1_YEAST	Q20406 caenorhabdi
30	32	80.0	191	1 GDIR_CABEL	P36590 schizosacch
31	32	80.0	210	1 KTHY_SCHPO	P33135 rhodospiril
32	32	80.0	272	1 CYL_RHORI	P75227 mycoplasma
33	32	80.0	281	1 Y373_MYCPN	

34	32	80.0	360	1 WNT2_CABEL	P34889 caenorhabdi
35	32	80.0	376	1 PGR_PENGR	O93883 penicillium
36	32	80.0	387	1 INTD_ECOLI	P24218 escherichia
37	32	80.0	400	1 HOCF_ECOLI	P36646 escherichia
38	32	80.0	470	1 NOS2_ONCMY	O92091 oncorhynch
39	32	80.0	470	1 NRAM_IADBU	O07570 influenza a
40	32	80.0	470	1 NRAM_IADCH	O07571 influenza a
41	32	80.0	470	1 NRAM_IADH2	O07572 influenza a
42	32	80.0	470	1 NRAM_IADH3	O07573 influenza a
43	32	80.0	470	1 NRAM_IADJ3	O07599 influenza a
44	32	80.0	470	1 NRAM_IAGFN	O07574 influenza a
45	32	80.0	470	1 NRAM_IAGBD	O07577 influenza a

ALIGNMENTS

RESULT 1
ID IKKA_HUMAN STANDARD; PRT; 745 AA.
AC O15111; 014666; 013132; 092467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (BC 2.7.1.-)
DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (Ikappab kinase)
DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKB1KA).
GN CHUK OR IKKA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RC TISSUE=T-cell;
RX MEDLINE=97386461; PubMed=92443310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
RT "Identification and characterization of an Ikappab kinase.";
RL Cell 90:373-383(1997).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97394468; PubMed=9252186;
RA Didonato J.A., Hayakawa M., Rouchart D.M., Zandi E., Karin M.;
RT "A cytokine-responsive Ikappab kinase that activates the transcription
RT factor NF-kappaB.";
RL Nature 388:548-554(1997).
RN [3]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
RP SER-176.
RX TISSUE=Cervical carcinoma;
RC MEDLINE=98008813; PubMed=9346484;
RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated Ikappab kinases essential for
RT NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "Ikappab kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40(1998).
RN [5]
RP SEQUENCE OF 32-745 FROM N.A.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=96258427; PubMed=8777433;
RA Connolly M.A., Marcu K.B.;
RT "CHUK, a new member of the helix-loop-helix and leucine zipper
RT families of interacting proteins, contains a serine-threonine kinase
RT catalytic domain.";

RL Cell. Mol. Biol. Res. 41:537-549(1995).

RP [6] PHOSPHORYLATION BY MAPK14/NIK, AND MUTAGENESIS OF SBR-176; THR-179

RP AND SER-180.

RA MEDLINE=98188283; PubMed=9520446;

RX Ling L., Cao Z., Goeddel D.V.;

RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of Ser-176.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).

RP [7] PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.

RP MEDLINE=99413720; PubMed=10485710;

RA Ozes O.N., Mayo L.D., Guetin J.A., Pfeiffer S.R., Pfeiffer L.M.,

RA Donner D.B.;

RT "NF-kappaB activation by tumour necrosis factor requires the Akt

RT serine-threonine kinase.";

RL Nature 401:82-85(1999).

RP [8] IKKA-IKKB BINDING.

RP MEDLINE=99212141; PubMed=10195894;

RA Delhase M., Hayakawa M., Chen Y., Karin M.;

RT "Positive and negative regulation of IkappaB kinase activity through

RT IKKbeta subunit phosphorylation.";

RL Science 284:309-313(1999).

RP [9] IKK PHOSPHORYLATION.

RP MEDLINE=99038238; PubMed=9819420;

RA Nemoto S., DiDonato J.A., Lin A.;

RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein

RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";

RL Mol. Cell. Biol. 18:7336-7343(1998).

RP [10] REVIEW.

RP MEDLINE=20178139; PubMed=10712233;

RA Jobin C., Sartor R.B.;

RT "The I kappa B/NF-kappa B system: a key determinant of mucosal

RT inflammation and protection.";

RL Am. J. Physiol. 278:C451-C462(2000).

RP [11] SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKKB AND IKKGA.

RP MEDLINE=21968797; PubMed=11971985;

RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,

RA O'Malley B.W.;

RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator

RT activity by I kappa B kinase.";

RL Mol. Cell. Biol. 22:3549-3561(2002).

RP [12] FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to

RP the dissociation of the inhibitor/NF-kappa-B complex and

RP ultimately the degradation of the inhibitor. Also phosphorylates

RP NCOA3.

CC [13] ENZYME REGULATION: Activated when phosphorylated and inactivated

CC when dephosphorylated.

CC [14] SUBUNIT: Preferentially found as a heterodimer with IKK-beta but

CC also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.

CC Heterodimers form the active complex. The tripartite complex can

CC also bind to MAPK14/NIK, MEKK1, IKAP and IKK-alpha-P65-P50

CC complex. A weak interaction with TRAF2 cannot be excluded. Part of

CC a complex composed of NCOA2, NCOA3, IKKB, IKKGA and CREBBP.

CC [15] SUBCELLULAR LOCATION: Cytoplasmic.

CC [16] TISSUE SPECIFICITY: Widely expressed.

CC [17] PTM: Phosphorylated by MAPK14/NIK, AKT and to a lesser extent by

CC MEKK1, and dephosphorylated by PP2A. Autophosphorylated.

CC [18] SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC IKAPAB KINASE SUBFAMILY.

CC [19] This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).

DR EMBL; AF012890; AAC5162.1; -

DR EMBL; AF009225; AAC5167.1; -

DR EMBL; AF080157; AAD08996.1; -

DR EMBL; U22512; AAC50713.1; -

DR HSPF; 063450; 1A06.

DR Genem; H8NC; 1974; CHUK.

DR MIM; 600664; -

DR GO; GO:0005737; C:cytoplasm; TAS.

DR GO; GO:0008384; F:IkappaB kinase activity; TAS.

DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.

DR GO; GO:0007252; P:I-kappaB phosphorylation; TAS.

DR GO; GO:0006955; P:immune response; TAS.

DR InterPro; IPR000719; Prot_Kinase.

DR InterPro; IPR002290; Ser_Thr_Kinase.

DR InterPro; IPR001245; Tyr_Kinase.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR Transfaser; Serine/threonine-protein kinase; ATP-binding; phosphorylation.

KW TRANSFERASE; Serine/threonine-protein kinase; ATP-binding; phosphorylation.

FT DOMAIN 15 302

FT DOMAIN 455 476

FT DOMAIN 738 743

FT NP_BIND 21 29

FT BINDING 44 44

FT ACT_SITE 144 144

FT MOD_RES 23 23

FT MOD_RES 176 176

FT MUTAGEN 23 23

FT MUTAGEN 44 44

FT MUTAGEN 44 44

FT MUTAGEN 176 176

FT MUTAGEN 176 176

FT MUTAGEN 179 179

FT MUTAGEN 180 180

FT CONFLICT 543 543

FT CONFLICT 604 604

FT CONFLICT 679 680

FT CONFLICT 684 684

FT CONFLICT 686 687

FT CONFLICT 687 687

FT SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 745;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6

Db 738 LDMSWL 743

RESULT 2

ID IKKA_MOUSE STANDARD; PRT; 745 AA.

AC 060680; Q9D2X3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (RC 2.7.1.1-)

DE (1-kappa-B kinase alpha) (IKKalpha) (IKK-A) (IkappaB kinase

DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).

GN CHUK OR IKKA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

FT VARSPLIC 452 471 MSLRYNANLTKMTLIS -> IFRKAVSMERNKKGH
 FT SLP (in isoform 2).
 FT VARSPLIC 472 745 /FridaVSP.004866.
 FT Missing (in isoform 2).
 FT VARSPLIC 577 584 /FridaVSP.004867.
 FT DMLSDST -> GKTQSQY (in isoform 3).
 FT VARSPLIC 585 745 Missing (in isoform 3).
 FT /FridaVSP.004869.
 FT CONFLICT 236 236 K -> E (IN REF. 3).
 FT CONFLICT 400 400 S -> Y (IN REF. 3).
 SQ SEQUENCE 745 AA; 84728 MW; 3FEF5582AF92233 CRC64;
 Query Match 100.0%; Score 40; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LDMSWL 6
 Db 738 LDMSWL 743
 RESULT 3
 IKKB HUMAN STANDARD; PRT; 756 AA.
 AC 014920; 075327;
 DT 16-OCT-2001 (Ref. 40, Created)
 DT 16-OCT-2001 (Ref. 40, Last sequence update)
 DT 15-SEP-2003 (Ref. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase subunit (IC 2.7.1.-)
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB)
 GN IKKB OR IKKB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
 RC TISSUE=Cervical carcinoma;
 RA MEDLINE=98008813; PubMed=9346484;
 RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RA "IKK-1 and IKK-2: cytokine-activated Ikkappa kinases essential for
 RA NF-kappaB activation.";
 RL Science 278:860-866(1997).
 RN [2]
 RC SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RC MEDLINE=98008814; PubMed=9346485;
 RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
 RA "IkappaB kinase-beta: NF-kappaB activation and complex formation with
 RA IkappaB kinase-alpha and NIK.";
 RL Science 278:866-869(1997).
 RN [3]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA MEDLINE=99032998; PubMed=981230;
 RA Hu M.C.-T., Wang Y.-P.;
 RA "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 RA embryonic tissues but localized to different human chromosomes.";
 RL Gene 222:31-40(1998).
 RN [4]
 RC SEQUENCE FROM N.A., AND GENE MAPPING.
 RA MEDLINE=98438415; PubMed=9763654;
 RA Shindo M., Nakano H., Sakon S., Yasgita H., Mihara M., Okumura K.;
 RA "Assignment of IkappaB kinase beta (IKKB) to human chromosome band
 RA 8p12--p11 by in situ hybridization.";
 RL Cytogenet. Cell Genet. 82:32-33(1998).
 RN [5]
 RC SEQUENCE OF 1-256 FROM N.A.
 RC TISSUE=Lung;
 RA MEDLINE=22388257; PubMed=1247793;
 RA Straubenberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.B.,
 RA Brownstein M.J., Ueda T.B., Tohyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abraham R.D., Millaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnartrine P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalske U., Smalls D.E.,
 RA Schenker A., Schein J.E., Jones S.J.W., Marz M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RA human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP IKK PHOSPHORYLATION.
 RP MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RA "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RA kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [7]
 RP REVIEW.
 RP MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RA "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RA inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 RN [8]
 RP IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKB.
 RP MEDLINE=21968797; PubMed=11971985;
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 RA O'Malley B.W.;
 RA "Regulation of SRC-3 (pCTP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
 RA activity by I kappa B kinase.";
 RL Mol. Cell. Biol. 22:3549-3561(2002).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3 (By similarity).
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEK1, MAPK14/NIK, IKAP and IKB-alpha-P65-P50
 CC complex. Phosphorylated IKB-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
 CC and CREBBP.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
 CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and
 CC peripheral blood.
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAPK14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; AF029684; AAC51860.1; -
 CC EMBL; AF080158; AAD08997.1; -
 CC EMBL; AF031416; AAC64675.1; -
 CC EMBL; BC006231; AA006231.1; -

DR HSSE; Q63450; 1A06.
 DR Genew; HGNC:5960; IKKB.
 DR MIM; 603258; -.
 DR CO; GO:0005737; C:cytoplasm; NAS.
 DR CO; GO:0005524; F:ATP binding activity; NAS.
 DR CO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
 DR CO; GO:0016563; F:transcriptional activator activity; NAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00240; Ubiquitin; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding; phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT NP_BIND 737 742 NEMO-BINDING.
 FT BINDING 21 29 ATP (BY SIMILARITY).
 FT ACT_SITE 44 44 ATP (BY SIMILARITY).
 FT MOD_RES 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION.
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO EFFECT ON BINDING TO NIK.
 FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
 FT MUTAGEN 177 177 S->E: FULL ACTIVATION.
 FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
 FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
 FT CONFLICT 231 255 WHSKVQKSEVDIVSDNLQTVWF -> CWRMPEGVVHNS
 FT CONFLICT 231 255 CNSTLTGGRWVI (IN REF. 5).
 FT CONFLICT 425 425 Q -> H (IN REF. 1).
 SO SEQUENCE 756 AA; 86563 MW; P9CADP671AE914E CRC64;

Query Match 100.0%; Score 40; DB 1; Length 756;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSML 6
 |||||
 Db 737 LDMSML 742

RESULT 4
 ID IKKB MOUSE STANDARD; PRT; 757 AA.
 AC 088351; Q9RLJ6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-EBR-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1X).
 GN IKKB OR IKKB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKK1.
 RC STRAIN=C57BL/6; TISSUE=SPLEEN;
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of Ikappab kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/SRK kinase kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
 RT constitutively phosphorylates serine residues of Ikb.";
 RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE=99455228; PubMed=10523828;
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates Ikappab kinases (IKK-alpha/beta) and IKK-beta is a
 RL developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of Ikappab kinases by mitogen-activated protein
 RT kinase kinase regulation of Ikappab-1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [5]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -I- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P5-P50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
 CC and CREBBP (by similarity).
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
 CC -I- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
 CC the mouse embryo, at E9.5 day its expression begins to be
 CC localized to the brain, neural ganglia, neural tube, and in liver
 CC at E12.5 day. At E15.5 day, the expression is further restricted
 CC to specific tissues of the embryo.
 CC -I- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AF026524; AAC23557.1; -;
 CC EMBL; AF088910; AAD52095.1; -;
 CC HSSE; Q63450; 1A06.
 CC MGD; MGI:1338071; Ikbb.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR002290; Ser_Thr_kinase.
 CC InterPro; IPR001245; Tyr_kinase.
 CC Pfam; PF00069; Kinase; 1.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
 CC PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC phosphorylation.

FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 MEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> E (IN REF. 2).
 FT CONFLICT 356 356 L -> F (IN REF. 2).
 FT CONFLICT 390 390 P -> Q (IN REF. 2).
 FT CONFLICT 406 406 K -> R (IN REF. 2).
 FT CONFLICT 573 573 TLDMSWLOWEEDERCSLEQACD -> VTA (IN REF. 2).
 FT CONFLICT 736 757
 SQ SEQUENCE 757 AA; 86690 MW; FED962P095449CSE CRC64;
 Query Match 100.0%; Score 40; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSWL 6
 DB 737 LDMSWL 742
 RESULT 5
 ID IKKB_RAT STANDARD; PRT; 757 AA.
 AC Q90Y78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1-)
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IKK beta in megakaryocyte differentiation."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RA MEDLINE=9903838; PubMed=9819420;
 RA Nemoto S., D'Onato J.A., Lin A.;
 RT "Coordinate regulation of I-kappaB kinases by mitogen-activated protein
 kinase kinase kinase 1 and NF-kappaB-inducing kinase."
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW.
 RA MEDLINE=20178139; PubMed=10712233;
 RA Jodin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 inflammation and protection."
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 the dissociation of the inhibitor/NF-kappa-B complex and
 ultimately the degradation of the inhibitor. Also phosphorylates
 NCOA3.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50
 complex. Phosphorylated IKK-alpha is further released from the
 complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
 and CREBBP (by similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC -----
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 or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; AF115282; AAF21978.1; --
 CC HSSP; Q63450; 1A06.
 DR InterPro; IPR000719; Prot Kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP_PALSE_NEG.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 MEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 757 AA; 86866 MW; 3AFB6A7D931PFC CRC64;
 Query Match 100.0%; Score 40; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSWL 6
 DB 737 LDMSWL 742
 RESULT 6
 ID CVOA_BUCAL STANDARD; PRT; 296 AA.
 AC P57544;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
 subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
 subunit 2).
 GN CVOA OR BU472.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Tokyo 1998;
 RA MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 Buchnera sp. Aps."
 RL Nature 407:81-86(2000).
 CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
 OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE


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CC GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(1/2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
CC -----
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CC or send an email to license@1sb-sib.ch).
CC -----
CC EMBL: AP001119; BAB13169.1; -.
CC HSSP: P18400; 1CYW.
CC InterPro: IPR001505; Copper_CuA.
CC InterPro: IPR006333; CytoA_II.
CC InterPro: IPR002429; Cyt_cox_2.
CC InterPro: IPR000437; Prok_LipoProt.
CC Pfam: PF00116; COX2; 1.
CC ProDom: PD000131; Copper_CuA; 1.
CC TIGRfam: TIGR01433; CytoA; 1.
CC PROSITE: PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.
CC Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
CC Signal; Lipoprotein; Complete proteome.
CC FT SIGNAL 1 15 POTENTIAL.
CC FT CHAIN 16 296 UBIQUINOL OXIDASE POLYPEPTIDE II.
CC FT LIPID 16 16 N-ACYL DIGLYCERIDE (POTENTIAL).
CC FT DOMAIN 34 33 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 34 34 POTENTIAL.
CC FT TRANSMEM 55 78 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 79 99 POTENTIAL.
CC FT DOMAIN 100 296 EXTRACELLULAR (POTENTIAL).
CC SQ SEQUENCE 296 AA; 34180 MW; 1AB2BAF0408FBA64;
CC -----
Query Match 90.0%; Score 36; DB 1; Length 296;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC -----
ID Q0X2 ACEAC STANDARD; PRT; 307 AA.
ID Q0X2 ACEAC P0653;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome
DE A1 subunit 2) (Oxidase BA(3) subunit 2).
GN CYAB.
OS Acetobacter acetii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Acetobacter.
OX NCBI_TaxId=435;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=1023;
RX MEDLINE=93322308; PubMed=8392509;
RA Fukaya M., Tayama K., Tamaki T., Edisawa H., Okumura H.,
RA Kawamura Y., Horinouchi S., Bepko T.;
RT "Characterization of a cytochrome a1 that functions as a ubiquinol
RT oxidase in Acetobacter acetii."
RL J. Bacteriol. 175:4307-4314(1993).
CC -1- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.

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CC or send an email to license@1sb-sib.ch).
CC -----
CC EMBL: D13185; BAA02480.1; -.
CC PIR: A36885; A36885.
CC HSSP: P18400; 1CYW.
CC InterPro: IPR001505; Copper_CuA.
CC InterPro: IPR006333; CytoA_II.
CC InterPro: IPR002429; Cyt_cox_2.
CC Pfam: PF00116; COX2; 1.
CC PRINTS: PR01166; CYCOXINDASEII.
CC ProDom: PD000131; Copper_CuA; 1.
CC TIGRfam: TIGR01433; CytoA; 1.
CC PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
CC Oxidoreductase; Transmembrane; Respiratory chain; Signal;
CC Lipoprotein.
CC FT SIGNAL 1 23 POTENTIAL.
CC FT CHAIN 24 307 UBIQUINOL OXIDASE POLYPEPTIDE II.
CC FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
CC FT TRANSMEM 46 66 POTENTIAL.
CC FT TRANSMEM 87 107 POTENTIAL.
CC SQ SEQUENCE 307 AA; 33921 MW; E66734B8441096D CRC64;
CC -----
Query Match 90.0%; Score 36; DB 1; Length 307;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC -----
ID Q9WRL1 STANDARD; PRT; 314 AA.
ID Q9WRL1 Q9WRL1;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
DE subunit 2).
GN CYOA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxId=303;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=IH-2000;
RX MEDLINE=99085656; PubMed=9868765;
RA Hirayama H., Takami H., Inoue A., Horikoshi K.;
RT "Isolation and characterization of toluene-sensitive mutants from
RT Pseudomonas putida IH-2000."
RL FEMS Microbiol. Lett. 169:219-225(1998).
CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
CC GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(1/2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
CC -----
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 CC -----
 DR EMBL; AB016787; BAA76356.1; -
 DR HSSP; P18400; 1CM.
 DR InterPro; IPR001505; Copper Cua.
 DR InterPro; IPR006333; CytoA_II.
 DR InterPro; IPR002429; Cyt_Cox_2.
 DR Pfam; PF00116; COX2; 1.
 DR ProDom; PD000131; Copper Cua; 1.
 DR TIGRfam; TIGR01433; CytoA; 1.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KM Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
 KM Inner membrane; Signal; Lipoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 1 23 UBIQUINOL OXIDASE POLYPEPTIDE II.
 FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT DOMAIN 24 24 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 43 63 POTENTIAL.
 FT DOMAIN 64 86 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 87 107 POTENTIAL.
 FT DOMAIN 108 314 PERIPLASMIC (POTENTIAL).
 SQ SEQUENCE 314 AA; 34702 MW; 96EB04FC3AA77F07 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 314;
 Best Local Similarity 83.3%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 LDMSWL 6
 Db 133 LDMSWL 138
 RESULT 9
 DCPUP_YEAST STANDARD; PRT; 362 AA.
 AC P32347;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).
 GN HEM12 OR HEME OR POP3 OR YD9609.03.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92249304; PubMed=1576986;
 RA Garey J.R., Labbe-Bois R., Chelstowska A., Rycka J., Harrison L.,
 RA Kushner J., Labbe P.;
 RT "Uroporphyrinogen decarboxylase in Saccharomyces cerevisiae. HEM12
 RT gene sequence and evidence for two conserved glycines essential for
 RT enzymatic activity";
 RL Eur. J. Biochem. 205:1011-1016(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93348774; PubMed=8346678;
 RA Dilemurti C., Laroque R., Keng T.;
 RT "Molecular analysis of HEME (HEM12) in Saccharomyces cerevisiae, the
 RT gene for uroporphyrinogen decarboxylase";
 RL Yeast 9:613-623(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=8288C / AB972;
 RA Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP MUTANTS.
 RX MEDLINE=93111946; PubMed=1471989;
 RA Chelstowska A., Zosdek T., Garey J.R., Kushner J., Rycka J.,
 RA Labbe-Bois R.;

RT "Identification of amino acid changes affecting yeast
 RT uroporphyrinogen decarboxylase activity by sequence analysis of hem12
 RT mutant alleles";
 RL Biochem. J. 288:753-757(1992).
 CC -1- CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4
 CC CO(2).
 CC -1- PATHWAY: Porphyrin and heme biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X63721; CAA45253.1; -
 DR EMBL; Z19089; CAA79514.1; -
 DR EMBL; Z49209; CAA89078.1; -
 DR PIR; S23471; S23471.
 DR HSSP; P06132; URO.
 DR SGD; S0002454; HEM12.
 DR GO; GO:0004853; F:uroporphyrinogen decarboxylase activity; IMP.
 DR GO; GO:006783; F:heme biosynthesis; IMP.
 DR InterPro; IPR006361; Heme.
 DR InterPro; IPR00257; Uro_decarboxyls.
 DR Pfam; PF01208; URO-D; 1.
 DR ProDom; PD003225; Uro_decarboxyls; 1.
 DR TIGRfam; TIGR01464; heme; 1.
 DR PROSITE; PS00906; UROD_1; 1.
 DR PROSITE; PS00907; UROD_2; 1.
 KM Lyase; Decarboxylase; Porphyrin biosynthesis; Heme biosynthesis.
 FT VARIANT 59 59 S -> F (IN HEM12-6 AND HEM12-12).
 FT VARIANT 62 62 T -> I (IN HEM12-14).
 FT VARIANT 107 107 L -> S (IN HEM12-3 AND HEM12-13).
 FT VARIANT 215 215 S -> N (IN HEM12-2 AND HEM12-11).
 FT MOTAGEN 33 33 G->D: INACTIVATION.
 FT MOTAGEN 300 300 G->D: INACTIVATION.
 SQ SEQUENCE 362 AA; 41349 MW; B9CB3A48E62BC277 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LDMSW 5
 Db 279 LDMSW 283
 RESULT 10
 EPPA3_CHICK STANDARD; PRT; 983 AA.
 AC P29318;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Eppin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor ETK1) (CEK4).
 GN EPPA3 OR ETK1 OR CEK4.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phaethonidae; Phaethoninae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92031278; PubMed=1657122;
 RA Sajjadi F.G., Pasquale R.B., Subramani S.;
 RT "Identification of a new eph-related receptor tyrosine kinase gene
 RT from mouse and chicken that is developmentally regulated and encodes
 RT at least two forms of the receptor.";

RL New Biol. 3:769-778 (1991).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING BRAIN AND
 CC EMBRYONIC TISSUES. IN ADULT, THE GREATEST LEVELS OF EXPRESSION
 CC OCCURS IN THE BRAIN. IT IS EXPRESSED IN A GRADDED MANNER ACROSS THE
 CC RETINA WITH THE HIGHEST EXPRESSION AT ITS TEMPORAL POLE.
 CC DETECTABLE IN ALL OTHER ADULT TISSUES EXAMINED, EXCEPT THE LIVER.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; M68514; AAA48666.1; -
 CC PIR; B45583; B45583.
 CC HSSP; P00523; 2PTK.
 CC InterPro: IPR006209; EGF like.
 CC InterPro: IPR001090; Ephrin_receptor.
 CC InterPro: IPR003961; FN11T.
 CC InterPro: IPR003962; FN11T_subd.
 CC InterPro: IPR000719; Proc_Kinase.
 CC InterPro: IPR001650; SAM.
 CC InterPro: IPR001425; Tyr_kinase.
 CC InterPro: IPR001426; YKase_receptorV.
 CC Pfam; PF01404; EPH_Lbd; 1.
 CC Pfam; PF00041; Fn3; 2.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00536; SAM; 1.
 CC PRINTS; PR00014; FMYPEB11.
 CC PRINTS; PR00109; TYRKINASE.
 CC PRODOM; PD001495; Ephrin_receptor; 1.
 CC PRODOM; PD000001; Proc_Kinase; 1.
 CC SMART; SM00615; EPH_Lbd; 1.
 CC SMART; SM00060; FN3; 2.
 CC SMART; SM00454; SAM; 1.
 CC SMART; SM00219; TYRK; 1.
 CC PROSITE; PS01186; EGF_2; UNKNOWN_1.
 CC PROSITE; PS01107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS50011; PROTEIN_KINASE_TYR; 1.
 CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 CC PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 CC PROSITE; PS50105; SAM_DOMAIN; 1.
 CC Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 CC SIGNAL; 19
 CC CHAIN; 20
 CC DOMAIN; 20
 CC TRANSMEM; 541
 CC DOMAIN; 565
 CC DOMAIN; 188
 CC DOMAIN; 322
 CC DOMAIN; 432
 CC DOMAIN; 621
 CC DOMAIN; 911
 CC SITE; 981
 CC NP_BIND; 627
 CC BINDING; 653
 CC ACT_SITE; 746
 CC MOD_RES; 596
 CC MOD_RES; 602
 CC MOD_RES; 779

FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 983 AA; 109910 MW; B8895F08DF77651E CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSM 5
 DB 342 LDMSM 346
 RESULT 11
 ID EPI3 HUMAN STANDARD; PRT; 983 AA.
 AC P29320; OGH2V3; OGH2V4;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor ETK) (HEK) (HEK4).
 GN EPHA3 OR ETK1 OR ETK OR HEK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=92179233; PubMed=1311845;
 RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;
 RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine
 RT kinase expressed by human lymphoid tumor cell lines."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
 RL [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Melanoma;
 RA Chari R., Hamei G., Stroobant V., Maille B., Textier C., Mach B.,
 RA Boon T., Coule P.G.;
 RT "Identification of a tumor specific shared antigen derived from an
 RT Eph-receptor and presented to CD4 T cells on HLA class II
 RT molecules."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
 RX MEDLINE=92147681; PubMed=1737782;
 RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wicks A.,
 RA Welch K., Loudovaris M., Rockman S., Buemante I.;
 RT "Isolation and characterization of a novel receptor-type protein
 RT tyrosine kinase (tek) from a human pre-B cell line."
 RL J. Biol. Chem. 267:3262-3267(1992).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID
 CC FUNCTION.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1);
 CC SECRETED (ISOFORM 2).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC Name=2;
 CC IsoId=P29320-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P29320-2; Sequence=VSP 002995, VSP 002996;
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVEL IN PLACENTA.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----

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 CC or send an email to license@isb-sib.ch).

DR EMBL: M6813; AA53521.1; -
 DR EMBL: AF21459; AA643576.1; -
 DR EMBL: AF21460; AA643577.1; -
 DR EMBL: A28003; CAA01906.1; -
 DR PIR: A38224; A38224.
 DR HSSP: P00523; 2PTK.
 DR GeneW: HGNC:3387; EPHA3.
 DR MIM: 178611; -
 DR GO: GO:000587; C: integral to plasma membrane; TAS.
 DR GO: GO:0007165; P: signal transduction; TAS.
 DR InterPro: IPR006209; EGF_1like.
 DR InterPro: IPR001090; Ephrin_receptor.
 DR InterPro: IPR003961; FN_III-
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR001600; SAM.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR001426; YKase_receptor.
 DR Pfam: PF01404; EPH_1bd; 1.
 DR Pfam: PF00041; FN3_2.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00536; SAM; 1.
 DR PRINTS: PR00014; FNTPEIIT.
 DR PRINTS: PR00109; TYRKINSE.
 DR ProDom: PD001495; Ephrin_receptor; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00615; EPH_1bd; 1.
 DR SMART: SM00060; FN3_2.
 DR SMART: SM00454; SAM; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS01186; EGF_21_UNKNOWN; 1.
 DR PROSITE: PS01107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V2; 1.
 DR PROSITE: PS50105; SAM_DOMAIN; 1.
 DR Transfaser: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 DR Alternative splicing.

FT CHAIN 1 983 EPHRIN TYPE-A RECEPTOR 3.
 FT DOMAIN 21 541 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 542 565 POTENTIAL.
 FT DOMAIN 566 983 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 189 322 CYS-RICH.
 FT DOMAIN 323 432 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 433 530 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 621 882 PROTEIN KINASE.
 FT DOMAIN 911 975 SAM.
 FT SITE 981 983 PDZ-BINDING MOTIF (POTENTIAL).
 FT NE_BIND 627 635 ATP (BY SIMILARITY).
 FT BINDING 653 653 ATP (BY SIMILARITY).
 FT ACT_SITE 746 746 BY SIMILARITY.
 FT MOD_RES 596 596 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 602 602 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 337 337 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 391 391 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 493 493 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPPLIC 532 539 SEGISGS -> CMYFNAY (in isoform 2).
 FT VARSPPLIC 540 983 /FTid=VSP_002995 (in isoform 2).
 FT VARSPPLIC 540 983 Missing (in isoform 2).

FT CONFLICT 507 507 /FTid=VSP_002996.
 FT CONFLICT 724 724 F -> L (IN REF. 1; CAA01906).
 FT CONFLICT 911 911 V -> L (IN REF. 1; CAA01906).
 FT CONFLICT 924 924 R -> T (IN REF. 2).
 FT CONFLICT 924 924 R -> W (IN REF. 2).
 SQ SEQUENCE 983 AA; 110086 MW; B8D900FA80FF5121 CRC64;

Query Match
 Best Local Similarity 90.0%; Score 36; DB 1; Length 983;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LDMSW 5
 Db 343 LDMSW 347

RESULT 12
 ID EPH3_MOUSE STANDARD; PRT; 983 AA.
 AC EPH3_MOUSE
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
 GN kinase receptor ETK1) (MEK4).
 GN EPHA3 OR ETK1 OR MEK4 OR TYR04.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RP STRAIN=ICR X Swiss Webster; TISSUE=Embryo;
 RX MEDLINE=92031278; PubMed=1657122;
 RA Sajjadi F.G., Pasquale E.B., Subramani S.;
 RT "Identification of a new eph-related receptor tyrosine kinase gene
 RT from mouse and chicken that is developmentally regulated and encodes
 RT at least two forms of the receptor";
 RL New Biol. 3:769-778 (1991).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SHORT ISOFORM
 CC IS SECRETED.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=P29319-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=P29319-2; Sequence=VSP_002997;
 CC -1- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE
 CC BRAIN. ALSO DETECTED IN TESTIS.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.

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 CC or send an email to license@isb-sib.ch).

DR EMBL: M6813; AA39521.1; -
 DR EMBL: M6815; AA39522.1; ALT_SEQ.
 DR PIR: A45583; A45583.
 DR HSSP: P00523; 2PTK.
 DR MGD: MGI:99612; Epha3.
 DR InterPro: IPR006209; EGF_1like.
 DR InterPro: IPR001090; Ephrin_receptor.

DR InterPro: IPR003961; FN III.
 DR InterPro: IPR003962; FNIII subd.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR001660; SAM.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR001426; YKase_receptorV.
 DR Pfam: PF01404; EPH_lbd; 1.
 DR Pfam: PF000041; fn3_2.
 DR Pfam: PF00069; kinase; 1.
 DR Pfam: PF00536; SAM; 1.
 DR PRINTS: PRO0014; ENTPEBII.
 DR PRINTS: PRO0109; TYRKINASE.
 DR ProDom: PD000495; Ephrin_receptor; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00615; EPH_lbd; 1.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00454; SAM; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS50105; SAM_DOMAIN; 1.
 KM Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KM Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 983
 FT DOMAIN 21 540
 FT TRANSMEM 541 564
 FT DOMAIN 565 983
 FT DOMAIN 188 321
 FT DOMAIN 322 431
 FT DOMAIN 432 529
 FT DOMAIN 621 882
 FT DOMAIN 911 975
 FT SITE 981 983
 FT NP_BIND 627 635
 FT BINDING 653 653
 FT ACT_SITE 746 746
 FT MOD_RES 596 596
 FT MOD_RES 602 602
 FT MOD_RES 779 779
 FT CARBOHYD 231 231
 FT CARBOHYD 336 336
 FT CARBOHYD 390 390
 FT CARBOHYD 403 403
 FT CARBOHYD 492 492
 FT VARSPLIC 530 983
 FT SEQUENCE 983 AA; 109955 MW; BE4A655D8107A2 CRC64;
 SQ
 Query Match 90.0%; Score 36; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 1.7e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=98120505; PubMed=9458884;
 RA Li Y.Y., Mettenen C.F., Feldman A.M.,
 RT "IL-1 beta alters the expression of the receptor tyrosine kinase gene
 RL t-EphA3 in neonatal rat cardiomyocytes".
 RL Am. J. Physiol. 274:H331-H341(1998).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN THE HEART, BRAIN, AND LUNG.
 CC -1- INDUCTION: DOWN-REGULATED BY IL1-BETA IN NEONATAL CARDIAC
 CC MYOCYTES.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U69278; AAC06273.1; -.
 DR HSSP: P00523; 2PTK.
 DR InterPro: IPR006209; EGF_1like.
 DR InterPro: IPR001090; Ephrin_receptor.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003962; FNIII subd.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR001660; SAM.
 DR InterPro: IPR001426; YKase_receptorV.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF01404; EPH_lbd; 1.
 DR Pfam: PF00041; fn3_2.
 DR Pfam: PF00069; kinase; 1.
 DR Pfam: PF00536; SAM; 1.
 DR PRINTS: PRO0014; ENTPEBII.
 DR PRINTS: PRO0109; TYRKINASE.
 DR ProDom: PD001495; Ephrin_receptor; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00615; EPH_lbd; 1.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00454; SAM; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS50105; SAM_DOMAIN; 1.
 KM Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KM Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 984
 FT DOMAIN 21 541
 FT TRANSMEM 542 565
 FT DOMAIN 566 984
 FT DOMAIN 189 322
 FT DOMAIN 328 431
 FT DOMAIN 436 529
 FT DOMAIN 622 983
 FT SEQUENCE 984 AA; 109956 MW; BE4A655D8107A2 CRC64;
 SQ
 Query Match 90.0%; Score 36; DB 1; Length 984;
 Best Local Similarity 100.0%; Pred. No. 1.7e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FT DOMAIN 912 976 SAM.
 FT SITE 982 984 PDI-BINDING MOTIF (POTENTIAL).
 FT NP BIND 628 636 ATP (BY SIMILARITY).
 FT BINDING 654 654 ATP (BY SIMILARITY).
 FT ACT SITE 747 747 BY SIMILARITY.
 FT MOD RES 597 597 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD RES 603 603 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD RES 780 780 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLUCNAC. . .) (POTENTIAL).
 FT CARBOHYD 337 337 N-LINKED (GLUCNAC. . .) (POTENTIAL).
 FT CARBOHYD 391 391 N-LINKED (GLUCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLUCNAC. . .) (POTENTIAL).
 FT CARBOHYD 493 493 N-LINKED (GLUCNAC. . .) (POTENTIAL).
 SO SEQUENCE 984 AA; 110227 MW; F170C49312F7A0AB CRC64;

Query Match 90.0%; Score 36; DB 1; Length 984;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 343 LDMSM 347
 RESULT 14
 GUNB_CALSA STANDARD; PRT; 1039 AA.

AC P10474;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endoglucanase/exoglucanase B precursor [includes: Endoglucanase
 DE (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (cellulase)
 DE (Cellulohydrolase); Exoglucanase (EC 3.2.1.91) (Exocellulohydrolase)
 DE (1,4-beta-cellulohydrolase)].

GN CELB.
 OS Caldicellum saccharolyticum (Caldicellulosiraptor saccharolyticus).
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
 OC Caldicellulosiraptor.
 NCBI TaxID=44001;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8909398; PubMed=2789517;
 RA Saul D.J., Williams L.C., Love D.R., Chanley I.W., Bergquist P.I.;
 RT "Nucleotide sequence of a gene from Caldicellum saccharolyticum
 RT encoding for exoglucanase and endocellulase activity.";
 RL Nucleic Acids Res. 17:439-439(1989).

CC -1- FUNCTION: THIS PROTEIN IS MADE UP OF TWO DOMAINS: THE N-TERMINAL
 CC DOMAIN HAS EXOGLUCANASE ACTIVITY WHILE THE C-TERMINAL DOMAIN IS
 CC AN ENDOGLUCANASE.

CC -1- CATALYTIC ACTIVITY: Endohydrolase of 1,4-beta-D-glucosidic
 CC linkages in cellulose, lichenin and cereal beta-D-glucans;
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
 CC in cellulose and cellobiose, releasing cellobiose from the non-
 CC reducing ends of the chains.

CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO CELLULASE FAMILY
 CC F (FAMILY 10 OF GLYCOSYL HYDROLASES).
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CELLULASE FAMILY
 CC A (FAMILY 5 OF GLYCOSYL HYDROLASES).

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 CC or send an email to license@isb-sib.ch).

DR EMBL: X13602; CAA31936.1; -
 DR PIR: S02711; S02711.
 DR HSRF: Q06851; INBC.
 DR InterPro: IPR001956; CBD_3.
 DR InterPro: IPR001000; Glyco_hydro_10.

DR InterPro: IPR001547; Glyco_hydro_5.
 DR Pfam: PF00942; CBM_3; 1.
 DR Pfam: PF00150; cellulase; 1.
 DR Pfam: PF00331; Glyco_hydro_10; 1.
 DR PRINTS: PR00134; GLHYDRLASE10.
 DR ProDom: PD001947; CBD_3; 1.
 DR SMART: SM00633; Glyco_10; 1.
 DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
 DR PROSITE: PS00659; GLYCOSYL_HYDROL_F5; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Repeat;
 KW Multifunctional enzyme; Signal.
 FT CHAIN 1 28
 FT DOMAIN 29 1039 ENDOGLUCANASE/EXOGLUCANASE B.
 FT DOMAIN 376 416 THR/PRO-RICH, TANDM REPEATS OF T-P.
 FT DOMAIN 417 570 CELLULOSE-BINDING (BY SIMILARITY).
 FT ACT SITE 571 618 THR/PRO-RICH, TANDM REPEATS OF T-P.
 FT ACT SITE 177 177 PROTON DONOR (POTENTIAL).
 FT ACT SITE 285 285 NUCLEOPHILE (BY SIMILARITY).
 FT ACT SITE 792 792 BY SIMILARITY.
 SO SEQUENCE 1039 AA; 117641 MW; 080378171594DAB CRC64;

Query Match 90.0%; Score 36; DB 1; Length 1039;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6
 Db 540 DMSWL 544
 RESULT 15
 CYOA_BUCAP STANDARD; PRT; 290 AA.

AC 08X93;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
 DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
 DE subunit 2).

GN CYOA OR BUSG456.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 NCBI TaxID=98794;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22084549; PubMed=12089438;
 RA Tamas I., Klaesson L., Canhaeck B., Naeelund A.K., Eriksson A.-S.,
 RA Martegren J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;
 RT "50 million years of genomic stasis in endosymbiotic bacteria.";
 RL Science 296:2376-2379(2002).

CC -1- FUNCTION: Cytochrome O terminal oxidase complex is the component
 CC of the aerobic respiratory chain that predominates when cells are
 CC grown at high aeration (by similarity).
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).

DR EMBL: AE014121; AAM67999.1; -
 DR InterPro: IPR001505; Copper_Gua.
 DR InterPro: IPR006333; CYOA_II.
 DR InterPro: IPR002429; Cyf_cox_2.
 DR InterPro: IPR000437; Prok_1lipoprot.

DR Pfam: PF00116; COX2; 1.
 DR PRINTS: PR01166; CYCOXIDASE1.
 DR ProDom: PD000131; Copper_Gua; 1.
 DR TIGRFAMs: TIGR01433; Cyto; 1.
 DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.
 KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
 KW Signal; Lipoprotein; Complete proteome.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 290 UBIQUINOL OXIDASE POLYPEPTIDE II.
 FT LIPID 25 25 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT DOMAIN 25 42 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 43 63 POTENTIAL.
 FT DOMAIN 64 87 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 88 108 POTENTIAL.
 FT DOMAIN 109 290 EXTRACELLULAR (POTENTIAL).
 SQ SEQUENCE 290 AA; 33730 MW; 3D80A02A84732963 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 290;
 Best Local Similarity 83.3%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LDMSWL 6
 ||||
 Db 134 LDMSWL 139

Search completed: February 18, 2004, 14:28:01
 Job time : 5.55263 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 / Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-2

Perfect score: 40

Sequence: 1 LDMSWL 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Listing first 45 summaries

SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_prokaryote:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	40	100.0	740 6 Q95KVL	Q95KVL bos taurus
2	40	100.0	745 11 Q8CMT3	Q8CMT3 mus musculus
3	40	100.0	756 6 Q95KVL0	Q95KVL0 bos taurus
4	38	95.0	1139 16 Q8C91	Q8C91 yersinia pe
5	37	92.5	173 16 Q8E5U2	Q8E5U2 streptococ
6	37	92.5	173 16 Q8E5U2	Q8E5U2 streptococ
7	37	92.5	310 2 Q9XBS7	Q9XBS7 zymomonas m
8	37	92.5	322 16 Q8YK7	Q8YK7 brucella me
9	37	92.5	347 16 Q8G1B0	Q8G1B0 brucella su
10	37	92.5	361 16 Q8P955	Q8P955 xanthomonas
11	37	92.5	645 2 Q9X6C6	Q9X6C6 thermus bro
12	36	90.0	85 16 Q8PBL8	Q8PBL8 escherichia
13	36	90.0	205 16 Q9ACRS	Q9ACRS streptomyce
14	36	90.0	227 4 Q8IXK8	Q8IXK8 homo sapien
15	36	90.0	242 12 Q919K8	Q919K8 culex nigri

17	36	90.0	261 2 Q9ACG7	Q9ACG7 caldicellul
18	36	90.0	282 16 Q8D354	Q8D354 wigglewort
19	36	90.0	288 2 Q8V7T4	Q8V7T4 pseudomonas
20	36	90.0	308 2 Q8K252	Q8K252 acetobacter
21	36	90.0	313 2 Q8YU06	Q8YU06 pseudomonas
22	36	90.0	318 16 Q8ZC58	Q8ZC58 yersinia pe
23	36	90.0	329 16 Q8XVB4	Q8XVB4 raietonia s
24	36	90.0	331 16 Q914Z7	Q914Z7 pseudomonas
25	36	90.0	341 16 Q8C3A8	Q8C3A8 brucella su
26	36	90.0	344 16 Q8YEH7	Q8YEH7 brucella me
27	36	90.0	353 16 Q9A7F0	Q9A7F0 callobacter
28	36	90.0	355 11 Q8B1T9	Q8B1T9 mus musculu
29	36	90.0	366 16 Q92U27	Q92U27 rhizobium l
30	36	90.0	393 16 Q8B7Z1	Q8B7Z1 rhizobium l
31	36	90.0	409 10 Q9M3F6	Q9M3F6 arabidopsis
32	36	90.0	452 4 Q96AB7	Q96AB7 homo sapien
33	36	90.0	477 11 Q8CYU6	Q8CYU6 mus musculu
34	36	90.0	484 4 Q9BTV6	Q9BTV6 homo sapien
35	36	90.0	538 11 Q8C9K6	Q8C9K6 mus musculu
36	36	90.0	703 10 Q9P1S0	Q9P1S0 arabidopsis
37	36	90.0	743 10 Q8YXG3	Q8YXG3 arabidopsis
38	36	90.0	747 16 Q69735	Q69735 mycobacteri
39	36	90.0	803 17 Q97UH8	Q97UH8 sulfobolus
40	36	90.0	984 11 Q8C3U1	Q8C3U1 mus musculu
41	36	90.0	984 11 Q8B8B1	Q8B8B1 mus musculu
42	36	90.0	986 2 Q9ACD0	Q9ACD0 caldicellul
43	36	90.0	1329 16 Q9CD30	Q9CD30 mycobacteri
44	36	90.0	1426 2 Q9X3P6	Q9X3P6 caldicellul
45	36	90.0	1751 2 Q9A0G4	Q9A0G4 caldicellul

ALIGNMENTS

RESULT 1
ID Q95KVL PRELIMINARY; PRT; 740 AA.
AC Q95KVL;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE IKB kinase-alpha.
GN BIKKALPHA.
OS Bos taurus (bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Rottenberg S., Dobbelaere D.A.B., Heussler V.T.;
RT "Identification and characterisation of the bovine IKB kinases (IKKs)
RT alpha, beta and gamma.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ414555; CAC93686.1; -
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 740 AA; 84343 MW; 01903BE11F4AD176 CRC64;

Query Match 100.0%; Score 40; DB 6; Length 740;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; LDMSWL 6

Db 733 LDMSWL 738

RESULT 2

ID 08CBT3 PRELIMINARY; PRT; 745 AA.

AC 08CBT3; 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE Conserved helix-loop-helix ubiquitous kinase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=22354683; PubMed=1246851;
 RA The FANTOM Consortium,
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK035326; BAC29034.1; -
 SQ SEQUENCE 745 AA; 84770 MW; 48C9B01C17A61184 CRC64;

Query Match 100.0%; Score 40; DB 11; Length 745;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
Db 738 LDMSWL 743

ID 09SKV0 PRELIMINARY; PRT; 756 AA.

AC 09SKV0; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE 1KB kinase-beta.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 [1]
 RP SEQUENCE FROM N.A.
 RC Rottenberg S., Dobbelaere D.A.B., Heuseler V.T.;
 RT "Identification and characterisation of the bovine 1KB kinases (IKKs)
 alpha, beta and gamma.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AJ144556; CAC93687.1; -
 DR InterPro; IPR000719; Ser_kinase.
 DR InterPro; IPR002290; Ser_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; KINASE; Serine/threonine-protein kinase; Transferase.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 756 AA; 86647 MW; A072D15614A17655 CRC64;

Query Match 100.0%; Score 40; DB 6; Length 756;

Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
Db 737 LDMSWL 742

RESULT 4

ID 08ZC91 PRELIMINARY; PRT; 1139 AA.

AC 08ZC91; 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DE Putative potassium efflux system (Putative alpha helix protein).
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.
 NCBI_TaxID=632;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebald M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooke K., Cerdano-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Felwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Meule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,
 RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
 RL Nature 413:523-527(2001).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIMS / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liao P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Niles M.L., Mason J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL; AJ414155; CAC92364.1; -
 DR EMBL; AE013709; AAM84635.1; -
 DR InterPro; IPR006685; MSion_channel.
 DR InterPro; IPR006686; MS_channel_dom.
 DR Pfam; PR00924; MS_channel; 1.
 DR PROSITE; PS01246; UPR0003; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1139 AA; 128409 MW; 7B54108BFC39A6B1 CRC64;

Query Match 95.0%; Score 38; DB 16; Length 1139;

Best Local Similarity 83.3%; Pred. No. 6.5e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
Db 480 LDMSWL 485

RESULT 5

ID 08ESU2 PRELIMINARY; PRT; 173 AA.

AC 08ESU2; 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE Hypothetical protein.
 OS Streptococcus agalactiae (serotype III).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=216495;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MEM316 / Serotype III;
 RX MEDLINE=2242508; PubMed=12354221;
 RA Glaeser P., Rusniok C., Buchrieser C., Chevallier F., Frangoul L.,
 RA Madak T., Zouine M., Couve E., Lalloui L., Poyart C., Tlieu-Cuot P.,
 RA Kunst F.;
 RT "Genome sequence of *Streptococcus agalactiae*, a pathogen causing
 RT invasive neonatal disease.";
 RL Mol. Microbiol. 45:149-1513 (2002).
 DR EMBL; AL766847; CAD46531.1; -.
 DR Sagsalst; SPS0887; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 173 AA; 20135 MW; F5F34044F0224CD1 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 173;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
 DB 125 LDMAWL 130

RESULT 6

O8E065 PRELIMINARY; PRT; 173 AA.

AC O8E065; 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Acetyltransferase, GNAT family.
 GN SAG0870.
 OS *Streptococcus agalactiae* (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 CC Streptococcus.
 OX NCBI_TaxId=216466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=2222988; PubMed=12200547;
 RA Tettein H., Maignan V., Cieslewicz M.J., Eisen J.A., Peterson S.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margalit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beaman M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
 RA Carey H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 RA Jacobini E.T., Bretoni C., Galli G., Mariani M., Vega F., Malone D.,
 RA Rinaldo D., Rappunli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V *Streptococcus agalactiae*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
 DR EMBL; AB014231; AAM99756.1; -.
 DR TIGR; SAG0870; -.
 KW Transferase; Complete proteome.
 SQ SEQUENCE 173 AA; 20135 MW; 0081677125975921 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 173;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
 DB 125 LDMAWL 130

RESULT 7

O9XB57 PRELIMINARY; PRT; 310 AA.

AC O9XB57; 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Putative carboxymethylglutaminylase.
 GN DLH.
 OS *Zymomonas mobilis*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
 OC Sphingomonadaceae; Zymomonas.
 OX NCBI_TaxId=542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ZM4;
 RA Um H.W., Kang H.S.;
 RT "The sequence analysis of 42D7 fosmid clone of *Zymomonas mobilis*
 RT ZM4.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF157453; AAD42398.1; -.
 DR InterPro; IPR002925; DLH.
 DR InterPro; IPR003379; Ser_estr_5ite.
 DR Pfam; PF01738; DLH; 1.
 SQ SEQUENCE 310 AA; 34092 MW; 34AC821E1F91259D CRC64;

Query Match 92.5%; Score 37; DB 2; Length 310;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
 DB 153 VDMSWL 158

RESULT 8

O8YK7 PRELIMINARY; PRT; 322 AA.

AC O8YK7; 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE NADH-quinone oxidoreductase chain H (EC 1.6.5.3).
 GN BMR1151.
 OS *Brucella melitensis*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxId=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16W / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756588;
 RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mijer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jablonaki L., Larsen N., D'Souza M., Bernal A., Mazur M., Gotsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Lelsson J.-J.,
 RA Haackhorn R., Kyriades N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT *Brucella melitensis*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
 DR EMBL; AE009594; AAL52332.1; -.
 DR InterPro; IPR001694; Resp_NADH_dhl.
 DR Pfam; PF00146; NADHdh; 1.
 DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 322 AA; 35966 MW; D5B5B123AB2C13B7 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 322;
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
 DB 174 LDMAWL 179

RESULT 9

O9BK3 PRELIMINARY; PRT; 347 AA.

AC Q98KR3;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE NADH-ubiquinone dehydrogenase chain 8.
 GN ML1361.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OC NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAF303039;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Maruabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti."
 RL DNA Ref. 7:331-338(2000).
 DR EMBL; AP002997; BAB48751.1;
 DR InterPro; IPR001694; Resp_NADH_dh1.
 DR Pfam; PF00146; NADHdh; 1.
 DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
 DR KJ041001; Complete proteome.
 KW Urdiquinone; Complete proteome.
 SQ SEQUENCE 347 AA; 38370 MW; 1092F351BD97EC57 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 347;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6
 Db 199 LDMSWL 204

RESULT 10
 Q981B0 PRELIMINARY; PRT; 347 AA.
 AC Q981B0;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE NADH dehydrogenase I, H subunit.
 GN NUOH OR BR0809.
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OC NCBI_TaxID=29461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umeyam L., Brinkac L.M., Beaman M.J.,
 RA Daugherty S.C., Debey R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J., Van Aken S.E.,
 RA Riedmuller S., Tectelin H., Gill S.R., White O., Salzberg S.L.,
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 GN EMBL; AB014385; AA29738.1;
 DR TIGR; BR0809;
 KW Complete proteome.
 SQ SEQUENCE 347 AA; 38428 MW; DA7F7471PD34D127 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 347;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6
 Db 199 LDMSWL 204

RESULT 11
 Q98P55 PRELIMINARY; PRT; 361 AA.
 AC Q98P55;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Exopolysaccharide biosynthesis protein.
 GN XCC2011.
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OC NCBI_TaxID=340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528,
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral L.M., Bertolini M.C., Camargo L.B.A.,
 RA Camarotte G., Camarvan P., Cardoso J., Chambergo P., Clapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.U.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Mendes J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena U.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezsa R.I.D.,
 RA Trindade dos Santos M., Truffi D., Teal S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities."
 RL Nature 417:459-463(2002).
 DR EMBL; AB012305; AA041300.1;
 DR InterPro; IPR002656; Acyl_transf_3.
 DR Pfam; PF01757; Acyl_transf_3; 1.
 DR KJ041001; Complete proteome.
 KW Complete proteome.
 SQ SEQUENCE 361 AA; 39147 MW; 37AB21791BE0393F CRC64;

Query Match 92.5%; Score 37; DB 16; Length 361;
 Best Local Similarity 83.3%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6
 Db 117 LDMSWL 122

RESULT 12
 Q9X6C6 PRELIMINARY; PRT; 645 AA.
 AC Q9X6C6;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Beta-galactosidase.
 GN BGLT.
 OS Thermus brockianus.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OC NCBI_TaxID=56956;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IT1360;
 RX MEDLINE=99402735; PubMed=10473401;
 RA Fridjerson O., Walzlawick H., Genweiller A., Rohrlirsch T., Matos R.,

RT "Cloning of the gene encoding a novel thermostable alpha-galactosidase
 RT from *Thermus brockianus* IT1360."
 RL Appl. Environ. Microbiol. 65:3955-3963(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IT1360;
 RX MEDLINE=20203878; PubMed=10741834;
 RA Fridjansson O., Matzlawick H., Mattes R.;
 RT "The structure of the alpha-galactosidase gene loci in *Thermus*
 RT *brockianus* IT1360 and *Thermus thermophilus* TH125."
 RL Ectromophilus 4:23-33(2000).
 DR EMBL; AF135398; AAD33667.1; -
 DR InterPro; IPR001584; Glyco_hydro_14.
 DR InterPro; IPR003476; Glyco_hydro_42.
 DR Pfam; PF01373; Glyco_hydro_14.1.
 DR Pfam; PF02449; Glyco_hydro_42.1.
 SQ SEQUENCE 645 AA; 73420 MW; C79A9E1C0020EC40 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 645;
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
 DB 48 LDMAWL 53

RESULT 13

ID Q8FBL8 PRELIMINARY; PRT; 85 AA.
 AC Q8FBL8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN C4754.
 OS *Escherichia coli* O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxId=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=06.H1 / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Rosch P.,
 RA Rasko D., Buckles E.L., Lou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 RT of uropathogenic *Escherichia coli*."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL; AE016769; AAN83187.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 85 AA; 9675 MW; 47DADB502F570A8B CRC64;

Query Match 90.0%; Score 36; DB 16; Length 85;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6
 DB 19 IDMSWL 24

RESULT 14

ID Q9ACR5 PRELIMINARY; PRT; 205 AA.
 AC Q9ACR5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein SCPI.253.
 GN SCPI.253.

OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomyces; Streptomyces; Streptomyces.
 OX NCBI_TaxId=1902;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kiese H.,
 RA Harper D., Balem A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,
 RA Huang C.-H., Kiese T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitch B., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RT *coelicolor* A3(2)."
 RL Nature 417:141-147(2002).
 DR EMBL; AL590464; CAC36779.1; -
 DR KW Hypothetical protein; Plasmid; Complete proteome.
 SQ SEQUENCE 205 AA; 23051 MW; 6602396CF93F2D9 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 205;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
 DB 11 DMSWL 15

RESULT 15

ID Q8IXK8 PRELIMINARY; PRT; 227 AA.
 AC Q8IXK8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to hypothetical protein BC017335.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC040173; AAH40173.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 227 AA; 25487 MW; F1A71EA57062A05 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 227;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
 DB 114 DMSWL 118

Search completed: February 18, 2004, 14:35:34
 Job time : 19.3684 secs